



BRIDGING SCIENCE & BUSINESS

Cost-Benefit Analysis of Genomic Tools for the Alberta Beef Industry

Prepared for

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May 2013

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CONTENTS

EXECUTIVE SUMMARY	3
THE PROJECT	3
KEY FINDINGS	3
RECOMMENDATIONS	4
EXTENDED SUMMARY	5
BACKGROUND	9
TERMS OF REFERENCE	10
Objective	10
Project outcomes	10
APPROACH	11
Outline	11
Background	12
Methodology	13
Breeding objectives and selection index modelling	13
THE BREEDING OBJECTIVE	14
THE SELECTION CRITERIA	15
THE INDUSTRY AND THE RATE OF GENETIC GAIN	16
THE INDUSTRY MODEL	16
CURRENT RATE OF GENETIC GAIN	17
APPLICATION OF GENOMIC TECHNOLOGIES	18
COST-BENEFIT ANALYSIS	20
MODEL DEVELOPMENT	20
APPLICATIONS OF THE OVERALL MODEL	22
DEVELOPMENT OF AN INDUSTRY MODEL	29
OPPORTUNITIES TO FOCUS GENOMICS RESEARCH	31
Background	31
STRATEGIC OVERVIEW	31
PROFITABILITY THROUGH THE VALUE CHAIN	31
DEVELOPMENT OF NOVEL TRAITS	32
POTENTIAL BEST PRACTICES	33
FRAMEWORKS AND PRACTICES	33
RECOMMENDATIONS	35
ACKNOWLEDGEMENTS	36
ADDENDIV	^-

Executive Summary

The project

Livestock Gentec is engaged in helping ensure that Alberta (and Canada) are global leaders in profitable and environmentally-sustainable beef production. The recent Strategic Plan defined priorities and goals which focus on *production efficiency, quality of products, health and food safety, traceability,* and *knowledge translation.* In terms of the latter, the major focus is on the uptake of genomics technology. Therefore the objective of this project is to estimate the potential value of applying genomic technologies in the industry.

This project is driven off an analysis of the *rate of genetic gain* for participants in the cow-calf sector using current quantitative approaches that utilise BLUP. An estimate of the profitability of the value chain from the calf through to the carcase product provides the basis for analysis of the *economic benefit of genetic gain*. We then assess the *impact of the application of genomic technologies*, before considering opportunities to *focus genomics research* on traits expected to provide the greatest benefit. A framework for *the evaluation and application of potential best practices* in the use of genomic tools follows.

Key findings

The analysis operates at a relatively high level and considers the impact of an investment in genomic technologies on profitability at a cow and then at an industry level. We have defined the breeding goal as the *profitability of the cow-calf sector* within the Alberta (and Canadian) beef cattle industry. Our analysis also considers the whole value chain from the breeder to the cow-calf producer to the backgrounder to the feed-lotter/packer, and therefore we partition the additional value across the whole value chain. However much of our focus is on the cow-calf sector, where the value proposition is much clearer.

The Breeding Objective is a **profit function** and is defined as \$ per breeding cow mated per year. The model is designed to assess the impact of the application of various technologies in genetic improvement within beef stud herds.

The **estimated current rate of gain** in the Canadian beef industry is \$3.90 of profit per cow mated per year. This is due to an increase in growth rate, and the accompanying efficiency gains. The issue of who gains the benefit of genetic improvement is important and, in this respect, we estimate that about 40% of the overall gain (due to weaning weight) accrues directly to the cow/calf producer and 17% to the feedlot/packer sector. The beneficiaries of improvements in post-weaning gain (43%) are not clear. We have used the value of \$3.90 to assess the level of selection pressure that is being applied within the industry. We then show how, through a more intensive level of recording without any change in selection pressure, that gain could increase by around 23% (to \$4.81) for 'comprehensive' recording.

The *application of genomic selection* provides an opportunity to further increase rate of gain. Rather than define the actual genomic technology, we have assessed the impact as the response to selection assuming an accuracy of the Genomic Breeding Values (GBV) of 0.25 (25%) or 0.50. At an accuracy of 0.25, the impact of applying multi-trait GBVs is to increase the estimated gain to \$6.58, while at an accuracy of 0.50, it increases to \$9.43.

We estimated the *industry value of selection* using a model where the annualised rate of progress is used to estimate the benefits of 10 years of cumulative genetic progress over a 15 year period at 7% discount/year for a population of 4.7 million females mated annually; benefits are realised two years following instigation of selection and assume 100% penetration of recording (an over-estimate, but benefits are directly proportional to this assumption). The annualised equivalent benefit of the current genetic improvement regime is estimated at \$127 mn, while the application of comprehensive recording increases this to \$156 mn. The impact of applying multi-trait genomic breeding values at an accuracy of 0.25 (25%) is estimated at \$214 mn, whereas an accuracy of 0.50 (50%) would increase this to \$306mn.

Genomics offers a paradigm shift in that a breeding program can be structured such that data can be collected on a smaller number of animals within a well-structured nucleus population. Such populations must be designed so that they incorporate the key sources of genetics from within the wider (e.g. breed) population so that the data and information generated are relevant to the wider population. In addition there is the need to collect progeny test data through commercial ventures (accuracy of pedigree is no longer a problem as it can effectively be re-constructed using genomic approaches through gBLUP) for

both standard and novel traits. Examples of such novel traits include health traits for animals in feedlots, meat quality traits at slaughter, and maternal traits such as longevity and cow health.

The economic analysis provides a framework for evaluation of *potential best practices* in the use of genomic tools, including the opportunity to *generate additional data through the value chain*. While there is considerable potential to capture new value from genomic selection, this is limited without a change in structure of data collection and evaluation practices and further development of the technology. The realisation of the importance of genetic relationships to successful implementation of genomic technologies is fundamental to this process. This reality puts a premium on the on-going generation and collection of high-quality data. Given these factors, there is a strong case for the development of Information Nucleus herds (at a breed level), improved processes for the collection and analysis of phenotypic data, better utilisation of males to enhance connectedness between herds, utilising the inherent structure and genetic relationships within breeds within the population (e.g. the co-ordinated collection of downstream, effectively progeny-test, data that are integrated through DNA-based relationship analysis), and the genotyping of influential individuals. Such technologies also provide opportunities to increase genetic gain in synthetic breeds and in crossbreeding. The importance of optimisation of the structure highlights the important role of the breed associations.

Practices that will *facilitate uptake* and encourage industry-wide adoption of genomic technologies within the beef cattle industry are critical. Canada has a well-developed breed association model that provides an obvious route to market.

A critical issue that will impact on the realisation of potential is the development of an integrated supply chain. This is important to both provide a strong incentive for investment in genetic improvement and to the realisation of many of the benefits of genetic improvement. This can only occur in the event that the feed-lotter/packer can assess the potential of genetic lines of cattle to perform in the feedlot and in the pack-house. However this will require integration from the breeder to the cow-calf producer and arguably the development of genomic tools for marker-assisted management, where genomic analysis coupled with analysis of early life phenotype provides a predictive tool for use in selection of individuals.

Recommendations

We have considered the current situation and the opportunities for genomic selection in terms of the value that it can deliver within the Alberta (and Canadian) beef industries, and therefore make the following recommendations.

We recommend that Livestock Gentec works with the Breed Associations to:

- 1. develop Information Nucleus herds within each of the major breeds that will facilitate more accurate genomic predictions;
- define traits of interest that would provide additional value to stakeholders keeping in mind the need
 for a broad and comprehensive view of productivity, and the need to be aware of potential
 unfavourable outcomes for cow productivity due to selection for young animal traits such as growth
 rate, and in particular residual feed intake;
- ensure that there is strong connectedness across herds and also to downstream herds (which can
 operate as progeny test herds) to ensure that the outcomes are sufficiently valuable (that is, provide
 an adequate return on investment) to drive uptake;
- 4. place a strong focus on uptake of genetic improvement, and in particular, uses new and innovative genomic technologies and strategies to drive performance recording and selection on estimated breeding values, rather than promoting genomic selection as an alternative to performance recording.

We further recommend that Livestock Gentec:

- 5. focuses its investment in genotyping of key individuals to those breeds that are prepared to co-invest as a means to help ensure an appropriate return on the overall investment;
- 6. promotes the value of an integrated supply chain in terms of the benefits that would accrue to all participants in the supply chain (bull breeder, cow-calf producer, backgrounder, and feed-lotter/packer).

Extended summary

Genetic gain in the beef industry

The underlying premise re the opportunities for genetic improvement in beef is that genetic improvement is generated by bull breeders who sell bulls to downstream producers who then utilise those bulls to produce replacements, with males and surplus females being slaughtered for beef after being finished in feedlots.

Hence the factors that impact on the rate of genetic improvement at an industry level are the genetic contribution to the observed variation in key economic traits (**heritability**), the extent to which genetically superior animals can be identified (**evaluation**), and the effectiveness of **dissemination** of superior genetics. The new genomic technologies provide potential opportunities to better identify genetically superior animals, and also to improve the effectiveness of dissemination of superior genetics through greater uptake by producers.

Background to the analysis

The analysis operates at a relatively high level and considers the impact of an investment in genomic technologies on profitability at a cow and then at an industry level. We have defined the breeding goal as the *profitability of the cow-calf sector* within the Alberta (and Canadian) beef cattle industry. Our analysis also considers the whole value chain from the breeder to the cow-calf producer to the backgrounder to the feed-lotter/packer, and therefore we partition the additional value across the whole value chain. However much of our focus is on the cow-calf sector, where the value proposition is much clearer.

The Breeding Objective is a **profit function** and is defined as \$ per breeding cow mated per year. The Objective is constructed as a series of trait weightings reflecting the value of improvement in these traits on commercial beef farms. Selection index modelling is then used to predict genetic superiority of selected individuals under various future beef industry breeding scenarios. These superiorities are then translated into predictions of annual rates of genetic progress in profitability (using economic weights), which is defined as the increase in returns (**benefit**) less the additional production costs (**cost**). Hence when applied together, these provide a **cost-benefit** model. In effect, this model operates at the individual animal level, so that it can be simply scaled up to deal with herds or the industry as a whole. The cost of investment in the development and use of the technologies provides the basis for an assessment of the impact at the whole industry level.

The application of genomic technologies

Genomic technologies are being applied in a number of industries throughout the world, but it is in dairy cattle that by far the greatest penetration has been achieved. However the accuracies of prediction commonly realised in beef cattle are far lower than those in dairy, so that currently the opportunities in beef are less.

It is important to consider how genomic selection works. The general consensus from recent literature is that genomic selection utilises relationship data so that it actually represents a more sophisticated and 'accurate' pedigree than recorded pedigree. Hence the genetic relatedness of the training set to the individuals in which the GBVs are to be estimated is critical. Therefore this essentially precludes the use of across-breed genomic selection approaches. It is conceivable, however, that the accuracies will increase with improved quality of phenotypes and both improved understanding and estimation of the contribution of linkage disequilibrium (LD) to the accuracy. While the prospects for the application of genomic selection in beef cattle within a breed are good, there is a strong case to review the breeding structures to ensure that genomic selection yields real value.

Current rate of genetic gain and the value of incorporating genomic technologies

We have assumed that the current rate of genetic gain is around 0.7 kg per year in weaning weight (direct) without any change in birth weight. Thus our estimate of the total annualised selection response within the recorded sector of the Canadian industry is estimated at \$3.90 per cow mated per year.

The model is designed to assess the impact of the application of various technologies in genetic improvement within beef stud herds. For the analysis, we have defined three trait groups. The **Base Trait** Group includes the base weights that are assumed to be recorded on all candidates (birth, weaning and yearling traits only). The **Maternal** and **Feedlot/packer Trait** Groups include traits which may or may not be recorded and which are available for use in making selection decisions.

We developed three models using current BLUP-based genetic improvement evaluation and selection. We then compared each with the **Base**. The models are the **Base** + maternal, the **Base** +

feedlot/packer, and the **Base + maternal + feedlot/packer** (the comprehensive model). Application of the comprehensive model increases the estimated gain from \$3.90 to \$4.81. The inclusion of the genomic option is managed as an addition to each of these models, with each of five single Genomic Breeding Values (GBVs) available on each bull type added individually, which is then contrasted with all five GBVs collectively. The GBVs are used in two different scenarios, namely the **Base + GBVs**, and the **Comprehensive + GBVs**.

Rather than define the actual genomic technology, we have assessed the impact as the response to selection (expressed as annual genetic trend per cow mated per year) assuming an accuracy of the Genomic Breeding Values (GBV) of 0.25 or 0.50. At an accuracy of 0.25, the impact of applying multi-trait GBVs is to increase the estimated gain to \$6.58, while at an accuracy of 0.50, it increases to \$9.43.

The beneficiaries of genetic improvement

The issue of who gains the benefit of genetic improvement is important. The current rate of genetic gain in the industry is estimated at \$3.90 per cow mated per year, of which 49% is due to the impact of selection on weaning weight (direct) and 43% to improvements in post-weaning gain. The response in maternal traits that are of value to the cow-calf producer is actually negative (due to the correlated changes in mature weight associated with selection for growth in the calf), while 17% is due to the impact on other traits that are beneficial to the feedlot/packer sector (carcase value, residual feed intake). In terms of benefit, about 40% of the overall gain accrues to the cow/calf producer and 17% to the feedlotter/packer sector. The beneficiaries of benefits due to improvement in post-weaning gain are not clear.

In this context, the economic impact of incorporating or not incorporating feedlot/packer traits on the selection response is important. When selection pressure placed on these traits is removed, the response to selection for comprehensive recording drops from \$4.81 to \$2.88. However when bull breeders select for the feedlot/ packer traits but the value of this selection is not recognised due to failure in the supply chain, there is a further decline to \$1.34. This is a consequence of placing selection pressure on feedlot/packer traits with no direct value to the cow-calf producer who purchases a bull high in merit for these traits with no direct benefits, whereas the same selection pressure could have been applied to traits relevant to the cow-calf sector. However the cow-calf sector can benefit from improvements in feedlot/packer traits as extra profitability in the feedlot/packer sectors is quickly competed away through procurement competition for finishing and finished stock. This transfer of benefits back to the cow-calf sector occurs generically, and is effectively averaged over all cow-calf producers, irrespective of whether it is their calves that have contributed to greater production and quality benefits in the feedlot/packer sector. Thus paradoxically our analysis indicates that as the breeder (on behalf of the cow-calf producer) invests in recording for feedlot packer traits, the benefit to cow-calf clients of that breeder declines, while the benefit to the wider cow-calf sector still increases. The same situation applies with genomic selection (per GBVs for traits) where, with improved recording, the direct benefit accruing to the cow-calf producer purchasing genetically-improved bulls tends to be reduced. Thus in order to incentivise the bull breeder to continue to invest, it is important that benefits realised by the breeder's clients are recognised in payments by the feedlot-packer sector to the cow-calf producer. If this does not occur, then it will be much more profitable for breeders to focus all of their effort on what is directly relevant to their own businesses and to the cow-calf producer who sells calves at weaning.

These examples highlight the importance of an integrated supply chain to both the incentivisation, and also to the realisation of many of the benefits of genetic improvement. This can only occur in the event that the feedlot/packer can assess the potential of genetic lines of cattle to perform in the feedlot and in the pack-house. Such a strategy is likely to be particularly attractive to the feedlot/packer sector as the sector is often characterised by overcapacity, and genetic improvement initiatives can lead to strengthened and more committed supply agreements with the cow-calf sector. There are already examples of integrated models within the North American beef industry, but there is much potential for a greater future role of genetic improvement approaches within these in Canada.

Development of an industry model

We have estimated the total industry value of selection using a model where the annualised rate of progress is used to estimate the benefits of 10 years of cumulative genetic progress over a 15 year time frame. The analysis is based on a population of 4.7 million cows (and heifers) mated per annum, with benefits first realised two years following the instigation of selection (in 2013) and cumulated over 15 years (2015-2029). We assumed 100% penetration of recording (an over-estimate, but benefits are directly proportional to this assumption), and an annual discount rate of 7%.

The annualised equivalent benefit of the current genetic improvement regime is estimated at \$127 mn, while the application of comprehensive recording would increase this to \$156 mn. The impact of applying

multi-trait genomic breeding values at an accuracy of 0.25 (25%) is estimated at \$214 mn, whereas an accuracy of 0.50 (50%) would increase this to an annualised return of \$306mn.

Opportunities to focus genomics research

Bull breeders are in the business of breeding and rearing sound fertile bulls to sale age. Those using performance recording are seeking a premium over such an unimproved breeding bull. The new technologies of genomic selection represent both a threat and an opportunity to breeders and to their industry.

The threat comes through an ability of breeders to substitute their investment in recording with an investment in DNA testing (potentially at a lower cost). It is a threat because, paradoxically, the development of genomic selection is dependent on the on-going collection of phenotypic data to support the development of new traits and to provide data to continually assess the accuracy of such genomic technologies. Thus if breeders using DNA-based methods only are able to capture a significant share of the market for bulls marketed as "genetically-improved", there will be a disincentive for other breeders to continue recording at higher costs.

Genomic selection offers opportunities to generate value from incorporation of non-traditional traits in genetic selection. Good examples include meat quality and health traits. Pre-genomic methods such as BLUP are limited by the need to generate data through the recording of phenotypes and/or progeny testing on a relatively large scale. Consequently collection of such data can be prohibitively expensive and is often limited to industries that are either vertically-integrated (pigs and poultry) or where there are well-developed artificial breeding (AB) systems that enable the widespread utilisation of elite males through AB such as with dairy.

Genomics offers a paradigm shift in that a breeding program can be structured such that data can be collected on a smaller number of animals within a well-structured nucleus population(s). These populations must be designed so that they incorporate the key sources of genetics from within the wider (e.g. breed) population so that the data and information generated are relevant to the wider population. As there is a need to sample a smaller number of animals than in pre-genomic systems, the cost of individual assessments is much less of an issue. In addition there is the opportunity (and arguably the need to ensure good quality data) to collect progeny test data through commercial ventures as accuracy of pedigree is no longer a problem as it can effectively be re-constructed using genomic approaches through gBLUP. Good examples are health traits for animals in feedlots, meat quality traits at slaughter, and maternal traits such as longevity and cow health.

Potential best practices

The economic analysis provides a framework for the evaluation of **potential best practices** in the use of genomic tools to accelerate genetic gain. There is considerable potential to capture new value from genomic selection but this is limited without a change in structure of data collection and evaluation practices and further development of the technology. Hence there is a major opportunity to develop a new framework for the development and application of genomic tools in systems to accelerate genetic gain. Aspects include improved processes for collection and analysis of phenotypic data, utilisation of males to provide connectedness between herds, utilising the inherent structure and genetic relationships within breeds within the population, and the genotyping of influential individuals.

There is potential for the application of **genomic technologies** to generate additional data through the value chain. This could range from meat quality and the consumer eating experience through to detailed feedlot performance. This is effectively a DNA-enabled progeny testing approach. Such technologies also provide opportunities to increase genetic gain in synthetic breeds and in crossbreeding.

Practices that will **facilitate uptake** and encourage industry-wide adoption of genomic technologies within the beef industry are critical. Canada has a well-developed breed association model that provides an obvious route to market. The associations are enthusiastic adopters of genomic technology but the key factor is to ensure that the structures and systems are put in place and current structures enhanced to ensure that adequate amounts of good quality data are collected on industry-relevant animals. The realisation of the importance of genetic relationships to successful implementation of genomic technologies is fundamental to this process. However this reality also puts a premium on the on-going generation and collection of high-quality data. Hence there is a strong case for the development of Information Nucleus herds (at a breed level) and the co-ordinated collection of downstream (effectively progeny-test) data that are integrated through DNA-based relationship analysis.

The need to increase the rate of genetic gain in maternal traits represents both a challenge and an opportunity for breeding schemes. While there is a need for additional data, such data must include that

for complex (and difficult to measure) traits such as feed intake, especially in pregnant and lactating cows. Recording of breeding cow fertility, survival and performance will be critical to avoid costly unfavourable outcomes from selection on growth rate and residual feed intake in young growing animals.

A critical issue that will greatly impact on the realisation of potential is the effective development of an integrated supply chain. This is important to both provide a strong incentive for investment in genetic improvement and to the realisation of many of the benefits of genetic improvement. This can only occur in the event that the feed-lotter/packer can assess the potential of genetic lines of cattle to perform in the feedlot and in the pack-house. However this will require integration from the breeder to the cow-calf producer and arguably the development of genomic tools for marker-assisted management, where genomic analysis coupled with analysis of early life phenotype provides a predictive tool for use in selection of individuals.

Background

Livestock Gentec is engaged in helping ensure that Alberta (and Canada) are global leaders in profitable and environmentally-sustainable beef production.

In this respect, the application of genomic technologies is expected to play a major role in enhancing the overall profitability and efficiency of Alberta's livestock and meat sector through increasing the rate of genetic improvement. Although genomic technologies are at an early stage of development, there is strong evidence that they can contribute to an increased rate of genetic gain through earlier identification of superior individuals for breeding. This has been particularly evident in the dairy industry internationally.

Livestock Gentec has the key role in the development and application of these technologies in Alberta. Gentec operates as an integrated research, development, and technology pipeline delivering technology across all segments of the livestock industry. Established in 2010, Gentec's goal is to capitalize on world-leading genomic advances occurring at the University of Alberta and across Canada to ensure the translation of these advances across the Canadian livestock industry as guickly as possible.

The current quantitative approaches to genetic improvement (BLUP-based methods) require performance data (phenotypes) to be collected from individuals. The reality is that many traits of economic interest are expressed in only one sex (e.g. milk production) or later in life (fertility); this is a particular problem with the so-called maternal traits in beef cattle, which are actually the key components that drive profitability of a cow-calf enterprise. There are also other traits which are very difficult or impossible to measure in the live animal. These issues, along with the extensive nature of beef production and the weak market signals through the beef production supply chain mean that rates of genetic progress achieved with conventional BLUP-based genetic evaluation are well below the potential.

These factors highlight the potential value of genomic technologies, to increase effectiveness, and also help transform breeding and supply chain structures. These technologies require the analysis of a blood or tissue sample, in the earlier identification of superior individuals. However, the ability to deduce the genetic merit of an individual from DNA analysis is dependent on the development of a robust data set which can only be generated from the collection of phenotypic data (live weight by age, fertility, health status, etc). In the event that DNA collection is restricted to breeding bulls to reduce laboratory costs then parentage/pedigree data from herds of cattle is a further requirement. However, when genotypes are collected on the same individuals that have phenotypes, the new genomic technologies provide both accurate parentage and the necessary genotypic data for use in the subsequent analysis and prediction of genetic merit. Importantly the Alberta beef cattle industry is well-placed to exploit the new genetic technologies as it has built up a resource of phenotypic and genetic data over the last few decades.

The Livestock Gentec Strategic Plan (September 2012) defines the initial priorities and goals as:

- Improving production efficiency and lowering production costs while reducing the environmental footprint and GHG effect (Efficiency);
- Improving quality of livestock products through development of value-added product (Quality);
- Improving upon the health and safety of livestock and livestock products to ensure security of trade and public health safety (Health and Food Safety);
- Developing the infrastructure, tools, and people to enable the rapid uptake of genomics technology by the Canadian livestock industry (Knowledge Translation); and
- Verifying the traceability of livestock and livestock products (Traceability).

Terms of Reference

Objective

The overall objective is to estimate the potential value of applying genomic technologies in the Alberta beef industry.

Project outcomes

The economic analysis provides:

- 1. the beef industry with estimates of the *rate of genetic gain* through the application of genomic technologies compared with the current quantitative approaches that utilise BLUP;
- 2. a cost-benefit analysis for the application of genomic technologies based on #1 above;
- 3. information to researchers to enable them to *focus genomics research* on traits that are expected to provide the greatest cost-benefit within the overall value chain;
- 4. a framework for *the evaluation of potential best practices* in the use of genomic tools to accelerate genetic gain, including collection and analysis of phenotypic data, the utilisation of males for linkage across herds, the structure of the population, and the genotyping of influential individuals.

It is expected that the appropriate implementation of these technologies will allow Alberta (and Canada) to remain global leaders in genomics research which has direct relevance and application in the beef cattle industry through all sectors of the value chain.

Approach

Outline

The overall approach is outlined here.

The industry and the rate of genetic gain

1. The economic analysis is designed to provide the beef industry with estimates of the *rate of genetic gain* through the application of genomic technologies compared with the current quantitative approaches that utilise BLUP. It is important to note that the performance of genomic tools will continue to improve over time due to the on-going international investment in laboratory methods and statistical methodology – this will be reflected in the accuracy of predictions of genetic merit. The main components of the analysis and Report are:

identification of the main **economic drivers** in the Alberta (& Canadian) beef cattle industries and the development of a simple model of the Alberta (& Canadian) beef cattle industries to enable estimates of the current rate of genetic gain using current technologies (BLUP-based methods), and to enable an assessment of the potential for genomic technologies to enhance the rate of gain; an overview of the application of **genomic technologies** in the genetic improvement of livestock in selected areas.

Cost-benefit

2. The cost-benefit analysis considers the impact of the application of genomic technologies based on #2 above; this also provides a framework for the assessment of the value proposition for the development of customized tools to deliver genomic technologies to the industry. The approach involves:

cost-benefit analysis for the **application of genomic technologies** in the Canadian cattle industry with current technology, and with improvements that are expected to impact on the accuracy of prediction over the next 5 years; this will also provide a framework for the assessment of the value proposition for the development of customized tools to deliver genomics technologies to the industry.

Focus genomics research

3. The cost-benefit analysis highlights some opportunities to enhance profitability through the overall value chain; we therefore consider some options for researchers to enable them to focus genomics research on traits that are expected to provide the greatest cost-benefit. The report provides a definition of some methods for improving knowledge in respect of key economic traits in various sectors of the value chain;

consideration of the potential to generate value from the **incorporation of non-traditional traits** in genetic selection models through the application of genomic technologies, including the identification of knowledge gaps that can be met through genomics research.

Potential best practices

4. The analysis provides a framework for the evaluation and application of **potential best practices** in the application of use of genomic tools to accelerate genetic gain. This involves:

definition of a framework for **evaluation of alternatives** for the application of genomic tools, consideration of the potential for the application of **genomic technologies** through the value chain to provide additional value through **traceability** or **tracking** of products, and of practices that will **facilitate uptake** (i.e. encouraging industry-wide adoption) of genomic technologies within the beef cattle industry.

Background

The underlying premise with respect to the opportunities for genetic improvement in the Alberta (and Canadian) beef herd is that genetic improvement is generated by bull breeders who sell bulls to downstream producers who then utilise those bulls to produce replacements with males and surplus females being slaughtered for beef after being finished in feedlots. Therefore the factors that impact on the rate of genetic improvement at an industry level are:

- knowledge of the genetic contribution to observed variation in key economic traits (heritability);
- the extent to which genetically superior animals can be identified (evaluation); and
- the effectiveness of dissemination of superior genetics.

The new genomic technologies provide opportunities to better identify genetically superior animals, and also to improve the effectiveness of dissemination of superior genetics through greater uptake.

A generalised design for a genetic improvement program for production animals is presented in Figure 1.

Choose the breeding goal

Define the breeding objective

Choose selection criteria (traits to record)

Design the breeding scheme including the genetic evaluation system

Dissemination of superior animals

Figure 1. A generalised design for a genetic improvement program for production animals

The various steps within such a program are outlined below.

- The analysis operates at a relatively high level and considers the impact of an investment in genomic technologies on profitability at a cow and then at an industry level. We have defined the breeding goal as the *profitability of the cow-calf sector* within the Alberta (and Canadian) beef cattle industry. Our analysis also considers the whole value chain from the breeder to the cow-calf producer to the back-grounder to the feed-lotter/packer, and therefore we partition the additional value across the whole value chain. However much of our focus is on the cow-calf sector, where the value proposition is much clearer. In this respect, it is appropriate to regard the economic impacts of breeding that occur downstream in the supply chain as being counted under an assumption that they are transmitted through to the cow-calf sector via market forces.
- Derivation of the breeding objective; this involves an assessment of the economic importance of
 improvement in a number of traits; these traits are linked to the profitability of the cow-calf system,
 and their improvement will contribute to attainment the breeding goal; the breeding objective also
 includes the development of gene-flow models and selection indexes.
- A description of what to measure (the phenotype of the animals or the recorded traits or **selection criteria**) in order to make improvements.
- Design of the **breeding scheme** including the **genetic evaluation system**; this involves decisions regarding the number of parents to be selected and age at mating, while the development of a genetic evaluation system involves designing statistical analysis systems to estimate the breeding value (additive genetic merit) of animals.
- Implementation which includes recording of selection criteria and evaluation of animals.
- Selection of superior animals and dissemination of that superiority throughout the industry.

Methodology

Overview

The Report provides assessments of the potential of genomic technologies to deliver economic benefit to producers and to the overall industry. Given the very rapid rate of development of DNA-based technologies (both in terms of output and price) and the diverse nature of the beef cattle breeding systems in Canada, the analysis operates at a relatively high level and considers the impact on profitability of an investment in genomic technologies at an industry level and at a herd level. A key issue to consider is the opportunity that these technologies provide to increase the rate of genetic gain through:

- an increased rate of gain within a herd which is actively engaged in performance recording and genetic improvement; and
- an increased uptake of genetic improvement due to the relative simplicity of obtaining EBVs without corresponding trait records using genomic methods¹

While current commercially-available offerings include DNA-based parentage, trait markers (especially for inherited defects)² and genome-wide prediction of merit for quantitative traits, the development of new technologies such as *genotyping by sequencing*, and very high-density SNP panels potentially offer new opportunities. The issues relating to across-breed versus within-breed approaches are also considered.

Breeding goal

We have defined the breeding goal as the profitability of the cow-calf sector within the Alberta (and Canadian) beef cattle industry.

The analysis considers partitioning the additional value across the whole value chain, but this is a non-trivial task. For example, determination of the actual value generated from an intervention can be very complex, and small changes in the relative value can have major effects. Therefore, while we consider the whole value chain, much of our focus is on the cow-calf sector, where the value proposition is much clearer.

Breeding objectives and selection index modelling

Overview

The Breeding Objective is a **profit function** and is defined as \$ per breeding cow per year. The breeding objective is constructed as a series of trait weightings reflecting the value of improvement in these traits on commercial beef farms. While there is general agreement at this level (as suppliers of seed-stock to the commercial sector) among the members of the Breed Associations, the Associations³ do not appear to have defined detailed breeding objectives, preferring to leave such decisions as to the relative importance of trait weightings that are used to their members, the seed-stock producers. In fact, the Associations do not appear to utilise selection indexes, with their breeder members tending to focus on specific traits of interest (such as calving ease, weaning weight, etc). However Beefbooster, which operates a very different genetic improvement model to those of the breed associations, does operate a selection index approach.

Defining costs and potential benefits

In the assessment of the value of investment in genetic improvement, we require **value trait weightings** to:

 quantify the benefits of genetic selection for purchasers of bulls from herds using good breeding practices;

¹ However in this respect, there is an important issue for Breed Associations to consider; phenotypes are fundamental to the accuracy of genomic methods and hence there is a need for on-going investment in phenotype development. This is likely to require incentives for those breeders who supply phenotypes; pricing mechanisms for tests would seem to provide a potential option.

² These include Color diluter, Idiopathic epilepsy, Hypotrichosis, Horned/polled (Hereford); Arthrogryposis Multiplex (AM) (Curly Calf Syndrome), Double Muscling (DM), Dwarfism (DW), Contractural Arachnodactyly (CA) (Fawn Calf Syndrome), Heterochromia Irides (HI) (White Eye), Hypotrichosis (HY), Mannosidosis (MA), Neuropathic Hydrocephalous (NH), Osteopetrosis (OS), Protoporphyria (PR), Syndactyly (SN), Tibial Hemimelia (TH) (Angus; www.cdnangus.ca);

³ With the exception of Beefbooster

- · define opportunities in recording of novel traits; and
- compare costs and benefits of alternative breeding strategies and specifically, the impact of genomic applications.

In this report, we develop a value model from the ranch (cow-calf operations) through back-grounding and the feedlot (the costs of additional phenotyping and genotyping are not included⁴). Selection index modelling is then used to predict genetic superiority of selected individuals under various future beef industry breeding scenarios. These superiorities are then translated into predictions of annual rates of genetic progress in profitability (using economic weights), which is defined as the increase in returns (benefit) less the additional production costs (cost). Hence when applied together, these provide a cost-benefit model. In effect, this model operates at the individual animal level, so that it can be simply scaled up to deal with herds or the industry as a whole. The cost of investment in the development and use of the technologies provides the basis for an assessment of the impact at the whole industry level.

Current rate of genetic gain

An important aspect of the overall evaluation was an assessment of the potential value that new technologies could add. Therefore it was necessary to establish the current rate of progress to provide the baseline. To do so, it was necessary to define the current structure of the beef industry in Alberta (and in Canada) and to estimate the rate of genetic progress. This, in itself, is somewhat complicated, so that we have applied the best estimates available from the breed association data (where available) and extrapolated those assessments across the industry.

Applications

The next stage is to use the outputs of the cost-benefit model to assess the impact of the application of various technologies in genetic improvement within beef breeding stud herds. Therefore we consider ways in which the various genetic improvement technologies might be applied and consider the impact on profitability of the cow-calf unit (the purchaser of stud bulls). We also provide indications of the sensitivity of the predicted outcome to changes in the relative costs of inputs and the value of outputs. We then consider the overall potential return on the investment in genomic technologies at an industry level.

The breeding objective

The cow-calf producer

Our focus is on the profitability of the cow-calf producer. This is defined as the net return (profitability) on a per cow basis at weaning.

While growth rate of the calf (direct growth) receives moderate emphasis, high priority is placed on maternal traits, and in particular on heifer and cow fertility and cow wastage (which impacts on the replacement rate). The relative emphasis on birth weight is designed so that there is no change in this trait. Maternal weaning weight (through cow milk yield) has moderate weighting reflecting the importance of cows that can wean heavy calves⁵. However, this weighting is counterbalanced, through a modest negative antagonism between milk yield and cow body condition and fertility. Mature cow weight also has moderate (negative) weighting reflecting the additional cost of feed for heavier cows. With selection on this index, any increase in mature cow weight should be modest reflecting the importance of a moderately-sized cow under extensive beef production systems.

We also include cow body condition score (an opportune time to record this may be at pregnancy diagnosis in late summer/early fall). In the breeding objective, this trait is positively weighted to ensure that there is positive selection pressure on cows that can gain body condition over spring-summer while still rearing good calves. The impact of the inclusion of feed efficiency (Residual Feed Intake, RFI) is assessed and the potential for disease resistance (such as resistance to bovine respiratory disease (BRD) and Johne's disease) is noted.

⁴ The costs are incurred by bull breeders; they have not been included at this point as in the context of the total enterprise (industry level), they are essentially a replacement of one cost for another cost.

⁵ No increase in feed intake has been included as the impact is small and it is assumed that feed supply is not limiting in spring.

The backgrounder and feedlot operator

The value of traits for the feedlot operator is complex as the model must make an assumption about whether or not this is recognised in the price paid by the feedlot for the young cattle. We have not actually defined a carcase quality trait but have simply assigned a value to a carcase trait, where selection criteria for the trait are ultrasonic measurements on a live animal. A proxy for some of the value to the feedlot is recognised in the difference in price paid for steers as compared with heifers, which recognises the higher growth potential (and feed conversion efficiency) of steers versus heifers⁶. Resistance to BRD is also of value to the feedlot operator but it would require definition of a phenotype.

Gene flow and the selection index

The maternal breeding objective is designed for the cow-calf operator, with an assumption of reasonably clear price signals down through the value chain from the price grid paid by the processor, and reflecting differences in genetic value to the feedlot. The selection index is presented with discounted genetic expression coefficients on an EBV basis, to represent the number of expressions (gene flow) of the bulls' genes per cow mated (\$ per cow mated). Thus, index values should be halved (to an Expected Progeny Difference or EPD basis) when predicting the index values for commercial progeny.

The selection criteria

Table 1 presents the selection criteria that are commonly recorded in the Canadian seed-stock industry along with some novel traits. The 'equivalent' profit trait is presented alongside. However it must be noted that the selection index actually includes recognition of the genetic correlations among recorded traits, along with the directly recorded trait.

Table 1. The recorded traits and their corresponding profit traits

Recorded trait	Corresponding profit trait						
Birth weight							
Weaning wei	ght (WW) direct						
WW mat	ernal (milk)						
Yearling weight	Post weaning ADG (kg/day)						
Heifer fertility	Heifer conception (N in calf)						
Cow fertility	Cow fertility (replacements per cow)						
Fat and muscle scan (as a predictor of carcase value)	Carcase value (per carcase)						
DELia avania a cainal (la DM asa da)	RFI feedlot animal (kg DM per day)						
RFI in growing animal (kg DM per day)	RFI annual cow (kg DM per day)						
Mature o	ow weight						
Cow body condition	on score (scale 1-5)						
No trait currently recorded for genetic selection purposes	Feedlot survival (Animals)						

⁶ In this respect, enquiries suggest that the relative purchase price of steers is about 15% higher per kg of live weight; however in our models we have applied a weighted average price across both sexes, where 67% of all cattle for slaughter are steers and 33% are heifers. The relative daily live weight gain in the backgrounding - feedlotting phase is also expected to be about 23% higher in steers, while in terms of feed conversion ratio (FCR, kg feed DM/ kg LWG) the expectation is that steer FCR is 89% that of heifers.

The Industry and the Rate of Genetic Gain The industry model

Economic drivers

The Alberta (and Canadian) beef cattle industries are an integral part of the global supply chain for beef. The rising income of developing countries is expected to place on-going pressure on demand for livestock products as consumption of livestock products is closely related to per capita income. Hence as incomes rise, people typically increase consumption of meat, milk and eggs until these products become fully integrated into their daily diet. Within the developed countries, meat consumption ranges from around 80 to 130 kg per person per year⁷, with beef being a significant component, especially in Canada's major export market in the US⁸. Hence even though the majority of Canadian beef is consumed within the country, demand from the far larger adjacent US market is such that the driver of demand for beef is effectively international demand. The Canadian industry is well aware of food safety and sustainability issues⁹ and these must be considered in any discussions around the future drivers of beef demand and hence of the industry. Whether this will be reflected in a significant demand for grass-fed beef is an important question although there is no clarity at present.

Industry statistics

Table 2 summarises statistics for the beef cattle industry that have been used to estimate the current rate of genetic gain (BLUP-based), and the inputs used in the development of the industry model.

Table 2. Summary of data for the Alberta and Canadian beef industries 10

		Alberta	Canada	Model parameters
Cow-calf	Breeding cows & bred heifers : July 2012	1.86 (1.58 + 0.28) mn	4.62 (3.96 + 0.66) mn	
herd	Breeding cows & bred heifers : Jan 2012	1.89 (1.66 + 0.23) mn	4.78 (4.23 + 0.55) mn	
Slaughter	Carcase weight of steers		873 lb (396 kg)	875 (397 kg)
cattle	Carcase weight of heifers		819 lb (371 kg)	820 (372 kg)
Percentage of	steers among steers & heifers slaughtered 11		57%	67%
Indicative bree	ed structure of the Canadian beef cow herd	(based on stud cattle re	egistrations)	
		Registrations	Percentage	Total
	Angus	126,000	54%	
	Hereford	29,000	13%	
	Simmental	27,400	12%	
	Charolais	22,000	9%	Say 230,000
	Limousin	9,300	4%	registered cows
	Other purebreds	10,000	4%	
	Total registered purebreds	224,000		
	Other including Beefbooster	Say 9,000	4%	

⁷ H Steinfeld, T Wassenaar & S Jutzi, Livestock production systems in developing countries: status, drivers, trends, *Rev. sci. tech.* Off. int. Epiz., 2006, 25 (2), 505-516

http://www.beefissuesquarterly.com/areconsumerseatinglessbeefacloserlookatsupplyanddemand.aspx), Are consumers eating less beef? A closer look at supply and demand. Beef Issues Quarterly, Winter 2012

⁸ John Lundeen & Ted Kalous,

⁹ http://www.canadianbeef.info/ca/en/rt/industry/CCPS/sustainability.aspx

¹⁰ Statistics from Canfax, July 2011 & 2012 data, with breed registration data from Canadian Beef Breeds Council (D Fee, pers. comm.)

¹¹The percentage of heifers in feedlots (as per recent statistics) is not sustainable in the long term but is due to a recent contraction in the beef cow herd. In the model, we assumed a percentage of heifers in feedlots that would allow a long-term stable cow herd size.

Industry performance data

Table 3 provides a summary of the key performance parameters for the Alberta beef industry.

Table 3. Performance data for the Alberta beef industry (statistics from AgriProfit, October 2012)

	Industry performance data							
	2006	2007	2008	2009	2010	Mean		
Calf crop (calves weaned per 100 cows mated)	85.5	83.9	83.9	85.1	80.9	83.9		
Weaned/Cow wintered (lbs)	526	505	525	512	526	519		
Wean wt/Cow wt %	42.2	41.8	43.2	42.3	44.0	42.7		
Feeding season days (winter)	151	141	136	142	141	142		
Tonnes fed per cow (winter)	4.2	3.8	3.6	3.7	3.4	3.7		
Weaning weight (Weight weaned/Calves weaned)	557	542	558	545	577	556		
Open cows (open cows & heifers/total exposed)	9.6	9.3	11.1	8.9	11.7	10.1		
Calf losses (% calves died/live births)	3.2	5	3.5	4.4	4.7	4.2		
Cow Weight (lbs, calculated)	1320	1297	1292	1288	1311	1302		

The assumptions for the herd structure and performance data inputs for the cost model from the ranch (cow-calf operations) through back-grounding and the feedlot are presented in Table 4.

Table 4. Assumptions re herd structure and performance data for the Alberta and Canadian beef industries

	Age Structu	re of the Herd		Annual Rates	
Age at mating (years)	Mated	Pregnant	Age at calving		
Heifers	0.204	0.176	2	Heifer death rate	0.030
2	0.167	0.150	3	Heifer pregnancy rate	0.865
3	0.141	0.127	4	Cow pregnancy rate	0.894
4	0.119	0.107	5	Cow deaths & cull rate	0.050
5	0.100	0.090	6	Open heifer culling rate	0.135
6	0.085	0.076	7	Open cow culling rate	0.106
7	0.072	0.065	8	Calf deaths	0.054
8	0.061	0.055	9	Old cow cull rate	0.350
9	0.035	0.032	10	Steer calves weaned	0.420
10	0.020	0.018	11	Heifer calves weaned	0.420
TOTAL	1.00	0.896		Heifers retained	0.210
		Calves weaned	0.858	Heifers to feedlot	0.210
				Proportions	
				Steers as proportion of slaughter	0.667
Average age of the cow at birth of the calf (years)		4.93	Weaning weight as proportion of cow weight	0.43	

Current rate of genetic gain

We have derived the current rate of genetic gain in the industry from data sourced from the major breed associations and scientific and technical literature (see Table 8).

Penetration of recorded bulls within the industry

An important issue to consider when assessing the rate of genetic gain in the industry is the proportion of bulls that are used in commercial herds that are derived from recorded herds. There are two aspects:

the total demand for bulls and the capacity of registered herds to supply these; and

the proportion of bulls supplied ex registered herds that are actually from recorded herds.

<u>Supply/demand:</u> There are around 230,000 'registered' bull-breeding dams in Canada (Table 2). At a weaning rate of 87%, these will produce around 100,000 male calves. Of these, we estimate that one-half will be sold for commercial service. Hence these 50,000 bulls would be expected to service 1.25 mn cows at a ratio of 1 to 25. Thus an active life expectancy of 3.6 years would mean that all commercial cows (4.5 mn)¹² could be mated by bulls ex registered herds. This appears to be a reasonable assumption¹³.

Recorded herds: The second issue relates to the proportion of industry bulls that are sourced from recorded herds as opposed to non-recording but pedigree-registered herds. For the purposes of this report, we have used an estimate of 100%. Although we have sought an estimate, no data have been forthcoming but given that breeders who are recording have larger herds and sell a higher proportion of bulls, an appropriate estimate would have 80% of bulls being the products of herds that are base recording, 15% are from herds with maternal and/or comprehensive records and 5% are not recorded. Even though producers may not purchase bulls based on the data, they are still reaping the benefits of genetic improvement in the bull breeding herd.

Application of genomic technologies

Genomic technologies are being applied in a number of industries throughout the world, but it is in dairy cattle that by far the greatest penetration has been achieved.

Background

The applications of most relevance to this project are in beef cattle. There is a huge amount of effort going into genomic selection globally, but there is little evidence of any substantive utility yet, outside of dairy breeding schemes. There is some indication that genomic prediction methods are working reasonably well in Black Angus in the US. However, these predictions do not appear to transfer to Australian Angus, or to Red Angus. Several breed associations in the USA are progressing with genomic initiatives, although the approach of companies such as Pfizer has shifted away from developing a "global key" marketed as having wide and generic predictive ability towards working with industry partners to develop predictors that add value in the target population.

We have used accuracies of genomic prediction of 0.25 and 0.50 in our analyses presented here. We regard these values as realistic with current estimates of accuracies for Angus cattle in this range (see Swan AA *et al*¹⁴). However the reality is that GBV estimates are completely dependent on the quality of the training set, in terms of the genetic relatedness of the training set to the individuals for which the GBVs are to be estimated. It is still an unknown as to how large the training population size must be for accurate genomic prediction, and there is still some debate as to whether the prediction formulae of how genomic selection improves with an increased training population size are actually appropriate. However, in general, it is widely accepted that genomic selection works best with large training populations and selection candidates that are reasonably closely-related to animals in the training population.

For example in an analysis of the accuracies of GBVs in Hereford cattle using US or international training populations, it is clear the predictions for non-US animals were less accurate than those obtained for US Herefords; however among the non-US animals, genomic predictions were more accurate for Canadian animals reflecting the greater usage of US Herefords in Canada compared with the Argentinian and Uruguayan Hereford populations¹⁵.

How does genomic selection work?

The general consensus from the recent literature¹⁶ is that genomic selection utilises relationship data so that it actually represents a more sophisticated and 'accurate' pedigree than recorded pedigree for two

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¹² The total Canadian commercial cow herd is taken as 4.7 mn breeding cows & heifers less 230,000 'stud' cows

¹³ If the ratio was 1 to 30, then the average operational life expectancy of bulls in herds would be 3.0 years.

¹⁴Swan AA *et al* 2012. Integration of genomic information into beef cattle and sheep genetic evaluations in Australia, *Animal Production Science* 52: 126-132

¹⁵ Saatchi, Mahdi *et al* 2013. Genomic breeding values in Hereford cattle: Accuracies of direct genomic breeding values in Hereford cattle using national or international training populations. Journal of Animal Science (online. 23 Jan 2013)

¹⁶Clark, SA *et al* 2012. The importance of information on relatives for the prediction of genomic breeding values and the implications for the makeup of reference data sets in livestock breeding schemes. Genetics Selection Evolution, 44:4-9

reasons. Firstly, recorded pedigree is prone to human error, and secondly the genomic relationship accounts for Mendelian sampling which occurs at each conception. Increasingly, the contribution of linkage disequilibrium (LD) to the predictive ability of genomic selection is being considered to be minor with current approaches to genomic selection. Hence as noted above, the genetic relatedness of the training set to the individuals in which the GBVs are to be estimated is critical. Therefore this essentially precludes the use of across-breed genomic selection approaches. It is conceivable, however, that the accuracies will increase with improved quality of phenotypes and both improved understanding and estimation of the contribution of linkage disequilibrium (LD) to the accuracy.

It should be noted that the accuracies recorded for dairy cows are far higher than those recorded for beef cattle or sheep. There are three reasons. Firstly there is the pedigree structure within the various dairy breeds (and especially the Holstein-Friesian or HF), and secondly there is the population structure, and thirdly there is phenotype quality.

In terms of <u>pedigree structure</u>, the HF population features well-defined, deep pedigrees characterised by multi-generation sire lines and dam-sire lines that facilitate accurate detection of Mendelian inheritance of alleles and especially haplotype blocks across generations. Sensitivity to the depth of pedigree can be assessed through the impact of the progressive elimination of ancestral generations on the power of the analysis using gBLUP approaches where the genomic relationship matrix is substituted for the pedigree relationship.

Secondly the <u>population structure or population heterogeneity</u> has a major influence. The effective population size of the international HF population is very small; thus the haplotypes are relatively large (extensive LD) and the small population size also facilitates definition of the LD structure of the population (with relatively few SNPs). However it is these haplotype blocks which themselves are important in defining the actual Mendelian sampling.

Thirdly, there is the issue of the <u>quality of phenotypes</u>. The definition of phenotypes for dairy bulls is exceptional as it is based on the (sire)-daughter data; that is the phenotype is effectively a weighted value based on daughter records rather than on the individual itself.

However while the accuracies are far higher (exceeding 0.6 for production traits, noting that the square of accuracy represents reliability) there are issues with bias which means that genomic breeding values are subject to problems which must be dealt with when presenting results to industry stakeholders with high stakes in the outputs of genetic evaluation.

In summary, while the prospects for the application of genomic selection in beef cattle are good, there is a strong case to review the breeding structures to ensure that genomic selection yields real value (see *Opportunities to Focus Genomic Research*).

Wientjes, Yvonne CJ et al 2013. The Effect of Linkage Disequilibrium and Family Relationships on the reliability of Genomic Prediction, Genetics, 193: 621–631

Saatchi, Mahdi *et al* 2012. Accuracy of direct genomic breeding values for nationally evaluated traits in US Limousin and Simmental beef cattle. Genetics Selection Evolution, 44:38-47

Cost-Benefit Analysis

Model development

The industry cost model

A summary of the outputs of the cost model that are used as inputs into the selection model is presented in Table 5. While there are several systems that are used to produce beef in the Canadian system, we have taken an average system from data supplied by a feedlot operator based in Alberta.

Table 5. Outputs of the cost model from the cow-calf operation through to the feedlot (note that the averages are calculated assuming that two-thirds of the animals slaughtered are steers, and one-third are heifers)

neirers)										
Weani	ing weights	and growth rate	es of sla	aughter ca	attle (Ave	erage i	epresents 66.7%	of cattle	as ste	ers)
				Aver	age		Steers			Heifers
Weaning weight as proportion of cow weight			weight	0.43			0.445 (1.0)		().40 (0.9)
		Back-grou	unding	0.6	67	0.7	'0 (1.00) – 120 da	ıys (0.61 (0.	875) – 120 days
Average Daily G	Sain (ADG, g per day)	F	eedlot	1.4	12	1.5	54 (1.00) – 192 da	ıys	1.18 (0	.76) – 240 days
ng por ady)		(Overall	1.1	14		1.22 – 312 days		0.99	9 – 360 days
Food Convers	sion Botio	Back-grou	unding	9.8	36		9.63			10.35
(FCR, kg of feed	d per kg of	F	eedlot	6.8	35		6.53			7.51
	ADG)	(Overall	7.5	51		7.21			8.10
	Winte	r and summer f	eeding	costs for	pregnan	t or la	ctating cows (by	region)		
				Winter (sı	upplemer	ntary f	eed only)			Summer
	Proportion of the herd	Days of winter	Fed p	d per cow			Feed cost per short ton	Cost of per c		Cows at \$1.53 per day (1.8X heifers)
			Short tons		Long to	nnes				
North	0.25	167		4.8 4.36		6	\$60	\$29	90	\$303
Central	0.35	165	4.5 4.08 \$54 \$241		11	\$306				
South	0.40	118	:	2.2 2.		2.00 \$77		\$16	69	\$378
						We	ighted average	\$24	13	\$323
Wint	ter maintena	nce parameters	for co	ws: estima	ated cost	of a 1	kg increase in o	ow matu	ıre weiç	ght
				Chan	ge		Impact	on feed o	costs fo	or winter
	Liv	e weight (kg)		1.00)		Winter: North			\$0.37
MEI	Intake (MJ/da	y per kg LW)		0.083	37		Winter: Central			\$0.31
DI	M Intake (kg	d per kg LW)		0.009	93	Winter: South			\$0.21	
Back	<mark>k-grounding</mark>	costs for heife	rs (pre-	<mark>feedlot) a</mark>	nd summ	er fee	ding costs for re	placeme	nt heife	ers
	Back-grounding for hei			fers		-	Summer feeding			overall year for
	Days	Heifers a	at \$1.01	per day	Da	ıys	Heifers at \$0.8	5 per day	,	heifers
Summer: Nort	th 167		\$169		19	98	\$168			\$337
Summer: Centra	al 165		\$167		20	00	\$170			\$337
Summer: Sout	th 118		\$119		24	47	\$210			\$329
Weighted average	е		\$156				\$179			\$335

Genetic parameters and economic weights

Table 6 presents the set of genetic parameters and the **Economic Weights** for each of the **Profit Traits** that have been applied within the selection model to estimate the net present value (NPV) of genetic gain across a number of hypothetical scenarios (other genetic parameters are included in the Appendix). Thus we have the basic data for a **cost-benefit** model.

Table 6. Heritability, Phenotypic variance and Economic weights for Profit traits

Trait	Heritability	Phenotypic variance	Phenotypic standard deviation	Economic weight ¹⁷ (\$ per unit)
Birth weight (kg)	0.35	1.00	1.00	-\$11.3
Weaning weight direct (WWT, kg)	0.26	484	22.0	\$2.72
Post weaning ADG (kg/day)	0.40	0.058	0.24	\$238
Cow mature weight (kg)	0.40	4120	64.2	-\$0.22
Weaning weight maternal (WWTmat, kg)	0.10	484	22.0	\$0.89
Heifer conception (N in calf)	0.20	0.21	0.46	\$11.0
Cow fertility (replacements/ cow)	0.02	0.17	0.41	-\$340
Cow body condition score (1-5)	0.25	0.16	0.40	\$17.7
RFI annual cow (kg DM per day)	0.25	0.36	0.60	-\$55.5
Carcase value (\$ per carcase)	0.30	1.000	1.00	\$62.6
RFI in growing animal (kg DM per day)	0.35	0.55	0.74	-\$112
Feedlot survival (Animals)	0.05	0.034	0.18	\$946

Information sources

Table 7 provides data on the information sources that were assumed to be available for bulls as selection candidates. We then separated the traits into three groups that allow for various levels of recording of data within the herds. The **Base Trait** Group represents the base weights that are assumed to be recorded on all candidates, The **Maternal** and **Feedlot/packer Trait** Groups include traits which may or may not be recorded and available for use in making selection decisions.

Table 7. Information sources available for selection candidates (numbers of recorded relatives per bull), according to the age and status of bull candidates; the young bulls, herd bulls and AI bulls are aged 3, 5

and 8 years respectively

·	Selection proportion		Base traits (weight & date)				Matern	al traits		Feedlot/packer traits	
Bulls perconfith	(as a percentage of the bulls bred in the stud herd)	Information source	Birth	Wean- ing	Year -ling	Cow mature weight	Wean- ing weight	Fertility (Heifer concept -ion & cow)	Body Cond- ition Score (BCS)	Car- case scan	Residual feed intake (RFI)
		Self	1	1	1					1	1
Young	T 050/	Sibs	20	20	15					15	
bulls		Dam and female half-sibs				5	5	7	5		
		Self	1								1
		Sibs	20								
Herd	Ton 250/	Dam				1	1	1	1	1	
Bulls	Top 25%	Female parental half- sibs				5	5	7	5	5	
		Progeny	20	40	30					30	3
AI	ΔΙ	Daughters				60	50	60	60		
bulls	Top 15%	Progeny	300	300	300					300	20

-

¹⁷ Incorporates frequency & timing of expression of different traits through the life of the progeny of a bull

Applications of the overall model

Background to the individual models

The overall model is designed to assess the impact of the application of various technologies in genetic improvement within beef breeding stud herds. Within this model, we have assessed four trait recording models which reflect the different levels of recording as per Table 7.

The Base (recording) Model uses the traits from the Base Trait Group as per Table 7 (birth - BW, weaning weight – WW, and yearling weight only). It does not include WW maternal, but this is partly accounted for through the genetic correlation (r_g) between BW & WW maternal and between WW direct & WW maternal. The additional models presented in the tables below build off the base model, and include:

Base + maternal

Base + feedlot/packer

Base + maternal + feedlot/packer (the comprehensive model)

The inclusion of the genomic option is managed as an addition to each of these models. The assumptions are that each of five single Genomic Breeding Values (GBVs) are available on each bull type individually, and are then contrasted with all 5 GBVs available on each bull type collectively. The GBVs are used in two different scenarios:

Base + GBVs

Base + maternal + feedlot/packer + GBVs (the comprehensive model with GBVs)

Overview: Estimation of the selection response

The **cost-benefit** model has been used to assess the impact of the current rate of genetic progress which is assumed to be a result of the use of BLUP procedures operating through the genetic evaluation programs operated by the various breed associations (Base).

In order to define the base, we have assumed that the current rate of genetic gain is around 0.7 kg per year in weaning weight (direct) without any change in birth weight (as per Table 8). The expected changes in other traits are as per the Base column in Table 10. Thus our estimate of the total annualised selection response within the recorded sector of the Canadian industry is estimated at \$3.90 per year. In order to estimate the rate of genetic gain for the whole Canadian herd, this value needs to be adjusted to account for the proportion of the herd which is impacted by herds involved in genetic improvement (this is addressed in the section under *Development of an industry model*). However we can expect that there will be some spill-over of genetic progress from recorded herds into the non-recorded part of the industry.

Using the base recording protocol, the estimated selection intensity applied to effect current levels of genetic gain implies that breeders are, on average, selecting young bulls, herd bulls and AI sires from the top 35%, 25% and 15% of bull candidates respectively (with average ages of 3, 5 and 8 years at the time their progeny are born). The equivalent average age of the cows is 4.93 years (as per Table 4). Our estimate of the Total annualised selection response of \$3.90 per cow mated per year is highlighted.

Table 8. Estimates of the current annual rate of genetic gain in the recorded sector of the Canadian beef cattle industry

Response	Economic weight (profitability)	Trait units	Selection response (per cow mated per year)	Proportion of total response	Accrual of benefits
Birth weight (kg)	-\$11.3	0.00164 kg/y	-\$0.07	-0.02	0
Weaning weight direct (kg)	\$2.72	0.70 kg/y	\$1.89	0.49	Cow-calf producer
Maternal traits (Table 11)			-\$0.30	-0.08	(39%)
Post weaning average daily gain (kg/day)	\$238	0.0071	\$1.69	0.43	Who (43%)
Feedlot/packer traits (Table 11)			\$0.68	0.17	Feedlot/ packer (17%)
Total a	\$3.90				

The model has then been used to assess the potential value from the application of genomic technologies in the Canadian cattle industry. Rather than define the actual technology, we have assessed the impact

assuming an accuracy of the Genomic Breeding Values (GBV) of 0.25 or 0.50¹⁸. The analysis also provides a framework for the assessment of the value proposition for the development of customized tools to deliver genomics technologies to the industry. A summary of the scenarios that we consider is shown in Table 9.

Table 9. Scenarios

	Units	Reference
Current recording protocols with value recognised	Trait units	Table 10
throughout the supply chain	\$value units	Table 11
Current recording protocols where the value chain is disrupted such that breeders place no value on the traits expressed in the feedlot and packer segments of the chain	Trait units	Table 12
Current recording protocols (base or comprehensive) but	Trait units & \$	Table 14 (Base)
incorporating genomic breeding values with value recognised throughout the supply chain	Accuracy of GBV of 0.25 (25%)	(Comprehensive)
recognised unoughout the supply chain	Accuracy of GBV of 0.50 (50%)	Table 16
Industry impact		Table 17

In Tables 10 and 11, we have presented the annualised responses to selection (expressed in trait units in Table 10 or \$ value units in Table 11) in a breeding program as per the current protocols, albeit with increased recording.

Table 10. Annualised breeding program response to selection (in trait units) per current protocols

Recording Protocol	Profit trait	Base (current)	Base + Maternal	Base + Feedlot/Packer	Comprehensive
	Birth weight (phenotypic standard deviations) ¹⁹	0.0064	0.0140	0.0052	0.0112
Base	Weaning weight direct (kg)	0.70	0.71	0.56	0.57
	Post weaning average daily gain (kg/day) ²⁰	0.0071	0.0076	0.0058	0.0062
	Cow mature weight (kg)	0.90	1.09	0.73	0.89
	Weaning weight maternal (kg)	0.060	0.068	0.049	0.055
	Heifer conception (number in calf)	0.00030	0.00073	0.00033	0.00062
Matamal	Cow fertility (number less heifers per cow in the herd) ²¹	-0.00067	-0.00060	-0.00052	-0.00048
Maternal	Cow body condition score (1-5 scale)	0.00040	0.0010	0.00092	0.0013
	Residual feed intake annual cow (kg DM per day) – note: correlated response as RFI is recorded in young animals	-0.0024	-0.0024	-0.0062	-0.0062
	Carcase value (\$ per carcase)	0.17	0.17	0.70	0.69
Feedlot & Packer ²²	Residual feed intake growing animal (kg DM per day)	-0.0046	-0.0046	-0.0121	-0.0120
	Feedlot survival (animals)	0.0000	0.0000	0.0000	0.0000

¹⁸ These values are realistic with current estimates of accuracies for Angus cattle are in this range (see Appendix 1).

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¹⁹ The index weighting applied to birth weight was derived so that there would be a minimal genetic trend in birth weight; no units were used in the analysis.

²⁰ Corresponds to Yearling Weight as a recorded trait

²¹ A positive trait change for fertility is favourable, because of less expenditure on replacements; it is a major contributor to longevity in the herd.

²² The recorded trait for carcase value is an ultrasound record (fat and muscle); feedlot survival is not actually recorded, and given that we have assumed that it is not genetically correlated with any other trait, then no genetic gain is achievable. However there is potential to utilise genomic predictions if the phenotypic data could be collected in the backgrounding - feedlotting stage.

Table 11. Annualised breeding program response to selection (in \$ value units per cow mated per year) as per current protocols

Recording Protocol	Profit trait	Economic weight	Base (current)	Base + Maternal	Base + Feedlot/Packer	Comprehen sive
	Birth weight	-\$11.3	-\$0.07	-\$0.16	-\$0.06	-\$0.13
_	Weaning weight direct (kg)	\$2.72	\$1.89	\$1.92	\$1.52	\$1.56
Base	Post weaning average daily gain (kg/day)	\$238	\$1.69	\$1.81	\$1.37	\$1.48
		Sub-total	\$3.51	\$3.57	\$2.83	\$2.91
	Cow mature weight (kg)	-\$0.22	-\$0.20	-\$0.24	-\$0.16	-\$0.19
	Weaning weight maternal (kg)	\$0.89	\$0.05	\$0.06	\$0.04	\$0.05
	Heifer conception (number in calf)	\$11.0	\$0.00	\$0.01	\$0.00	\$0.01
Maternal	Cow fertility (number of replacements per cow)	\$340	-\$0.23	-\$0.20	-\$0.18	-\$0.16
	Cow body condition score (1-5 scale)	\$17.7	\$0.01	\$0.02	\$0.02	\$0.02
	Residual feed intake annual cow (kg DM/day)	-\$29.7	\$0.07	\$0.07	\$0.18	\$0.18
		Sub-total	-\$0.30	-\$0.28	-\$0.10	-\$0.09
	Carcase value (\$ per carcase)	\$6.26	\$0.16	\$0.16	\$0.65	\$0.64
Feedlot & Packer	Residual feed intake growing animal (kg DM/ day)	-\$112	\$0.52	\$0.52	\$1.35	\$1.34
	Feedlot survival (per animal)	\$946	\$0.00	\$0.00	\$0.00	\$0.00
		Sub-total	\$0.68	\$0.68	\$2.00	\$1.98
	Total annualised respons	e to selection	\$3.90	\$3.97	\$4.75	\$4.81

Table 11 indicates a negative response to selection in terms of the value of maternal traits. This is due to the correlated changes in cow genetic trends associated with the positive trends in economically-valuable traits in the young animals. For example, the responses in *weaning weight (direct)* and *post-weaning gain* in the progeny of cows are associated with an increase in mature size of the cows. It is important to note that selection for negative *residual feed intake* makes a significant contribution in the maternal traits (especially considering that the overall impact is negative). However the impact on *cow RFI* is overwhelmed by the genetic responses in growth traits within the Base protocol.

The response in terms of RFI (-0.0024 to -0.0062 kg DM/day) is much lower than that reported by by Arthur *et al* (2001)²³ for single trait selection lines for RFI (the annual response in their work was -0.125 kg DM/day over a five year selection period). The nature of the assumptions that underlie our estimates of genetic gain are important here, especially in respect of genetic correlations with other traits. In this respect the only assumption that we have made is that of a genetic correlation between RFI in the growing animal and RFI in the cow.

Table 12 shows the impact of selection when the supply chain is disrupted and breeders place no value on traits expressed in the feedlot and packer segments. In this analysis, economic weights associated with feedlot/packer value traits were reduced to zero, with no selection pressure applied. The affected traits and their original economic weights were as per Table 11.

²³ Arthur PF et al 2001. Response to selection for net feed intake in beef cattle. Proc. Assoc. Advmt. Anim. Breed. Genet. 14: 135-8

Table 12. Annualised breeding program responses to selection (trait units), when the value chain is disrupted and breeders place no value on the traits expressed in the feedlot and packer segments of the supply chain.

Recording Protocol	Profit trait	Economic weight	Base	Base + Maternal	Base + Feedlot/Packer	Comprehensive
	Birth weight (kg)	-\$11.3	-0.12	-0.13	-0.12	-0.13
Base	Weaning weight direct (kg)	\$2.72	0.20	0.15	0.20	0.15
Dase	Post weaning average daily gain (ADG, kg/day)	\$0.00	-0.0036	-0.0044	-0.0036	-0.0044
	Cow mature weight (kg)	-\$0.22	-1.21	-1.45	-1.20	-1.45
	Weaning weight maternal (kg)	\$0.89	0.075	0.054	0.074	0.054
	Heifer conception (number in calf)	\$11.0	0.0038	0.0047	0.0038	0.0047
Maternal	Cow fertility (number of replacements per cow)	\$340	0.0013	0.0017	0.0013	0.0017
	Cow body condition score (1-5 scale)	\$17.7	0.00040	0.0011	0.00042	0.0011
	Residual feed intake annual cow (kg DM per day)	-\$29.7	-0.00052	-0.00052	-0.0014	-0.0013
	Carcase value (\$ per carcase)	\$0.00	0.0056	0.0056	0.0217	0.0206
Feedlot & Packer	Residual feed intake growing animal (kg DM per day)	\$0.00	-0.0010	-0.0010	-0.0028	-0.0026
	Feedlot survival	\$0.00	0.0000	0.0000	0.0000	0.0000

The economic impact of either incorporating or not incorporating feedlot/packer traits on the selection response is shown in Table 13. When the selection pressure placed on these traits is removed, the annualised response to selection for comprehensive recording drops from \$4.81 to \$2.88.

An additional calculation was undertaken to assess the impact of breeders actually selecting for the feedlot/ packer traits but the value that this selection generates is not recognised as a consequence of failure in the supply chain. This results in a further loss in value to \$1.34. This is a consequence of placing selection pressure on feedlot/packer traits with no direct value to the cow-calf sector that results in a reduction in progress made in other cow-calf traits that do have direct value to the cow-calf producer.

Table 13. Economic impact of either incorporating or not incorporating feedlot/packer traits

	Recording protocols							
Value model	Base	Base + Maternal	Base + Feedlot/Packer	Comprehensive				
Feedlot/Packer traits selected and valued (Tables 10 & 11)	\$3.90	\$3.97	\$4.75	\$4.81				
Feedlot/Packer traits not selected	\$2.74	\$2.87	\$2.75	\$2.88				
Feedlot/Packer traits selected but not valued (trait responses, but EV = 0; Table 12)	\$1.53	\$1.48	\$1.34	\$1.34				

Incorporating genomic technologies

In Tables 14 and 15, we present an analysis of the impact of incorporating genomic technologies where breeders apply GBV in association with the **base** (Table 14) or **comprehensive** protocols (Table 15).

Rather than define the actual technology, we have assessed the impact assuming an accuracy of the Genomic Breeding Values (GBV) of 0.25 (note that in the summary in Table 17, we also present estimates for an accuracy of 0.50).

Table 14. Annualised response to selection with breeders applying **base recording** plus single- or multitrait GBV (full genomic selection) to select bulls (the prediction accuracy for all GBV traits is 0.25).

,	,	,	Annualis	ed trait resp	onse to sele	ection (trait u	units & \$)	
Recording Protocol	Profit trait	Base	+ GBV Growth	+ GBV RFI	+ GBV Fertility	+ GBV Carcass	+ GBV health	Multi- trait GBV
	Birth weight	0.0064	-0.0032	0.0052	0.0064	0.0060	0.0056	-0.0008
Base	Weaning weight direct (kg)	0.70	0.62	0.52	0.65	0.61	0.57	0.42
Busc	Post weaning average daily gain (kg/day)	0.0071	0.0093	0.0053	0.0067	0.0062	0.0059	0.0061
	Cow mature weight (kg)	0.90	0.40	0.68	0.85	0.79	0.75	0.32
	Weaning weight maternal (kg)	0.060	0.020	0.045	0.057	0.053	0.050	0.018
	Heifer conception (N in calf)	0.0003	-0.00088	0.00034	0.0022	0.00032	0.00031	0.00070
Maternal	Cow fertility (number of replacements per cow)	-0.00070	-0.00086	-0.00046	0.00060	-0.00056	-0.00053	0.00018
	Cow body condition score,1-5	0.00040	0.00040	0.00039	0.0012	0.00037	0.00038	0.00082
	Residual feed intake annual cow (kg DM per day)	-0.0024	-0.0024	-0.0093	-0.0024	-0.0023	-0.0023	-0.0076
	Carcase value (\$ per carcase)	0.17	0.17	0.17	0.17	1.12	0.16	0.75
Feedlot & Packer	Residual feed intake growing animal (kg DM per day)	-0.0046	-0.0046	-0.0209	-0.0046	-0.0046	-0.0044	-0.0168
	Feedlot survival (animals)	0.0000	0.0000	0.0000	0.0000	0.0000	0.0014	0.0010
Total ann	nualised response to selection	\$3.90	\$4.30	\$5.11	\$4.13	\$4.38	\$4.63	\$6.37
	Added response compared	\$0.40	\$1.21	\$0.23	\$0.48	\$0.73	\$2.47	

Table 15. Annualised response to selection with breeders applying **comprehensive recording** plus single- or multi-trait GBV (full genomic selection) to select bulls (the prediction accuracy for all GBV traits is 0.25).

			Annualis	ed trait resp	onse to sele	ection (trait u	units & \$)	
Recording Protocol	Profit trait	Compre- hensive	+ GBV Growth	+ GBV RFI	+ GBV Fertility	+ GBV Carcass	+ GBV health	Multi- trait GBV
	Birth weight	0.0112	0.0036	0.0096	0.0100	0.0092	0.0088	0.0036
Base	Weaning weight direct (kg)	0.57	0.47	0.49	0.48	0.48	0.45	0.42
Buse	Post weaning average daily gain (kg/day)	0.0062	0.0072	0.0053	0.0052	0.0051	0.0049	0.0063
	Cow mature weight (kg)	0.89	0.46	0.75	0.75	0.73	0.70	0.42
	Weaning weight maternal (kg)	0.055	0.024	0.047	0.048	0.046	0.044	0.023
	Heifer conception (N in calf)	0.0006	-0.0002	0.0006	0.0018	0.0006	0.0006	0.0008
Maternal	Cow fertility (number of replacements per cow)	-0.00048	-0.00055	-0.00038	0.00039	-0.00036	-0.00034	0.00016
	Cow body condition score,1-5	0.0013	0.0012	0.0012	0.0016	0.0010	0.0011	0.0012
	Residual feed intake annual cow (kg DM per day)	-0.0062	-0.0101	-0.0105	-0.0104	-0.0102	-0.0097	-0.0088
	Carcase value	0.69	0.58	0.60	0.59	1.04	0.56	0.90
Feedlot & Packer	Residual feed intake growing animal (kg DM per day)	-0.012	-0.020	-0.022	-0.020	-0.020	-0.019	-0.018
	Feedlot survival	0.0000	0.0000	0.0000	0.0000	0.0000	0.0010	0.0009
Total anı	nualised response to selection	\$4.81	\$5.75	\$5.53	\$5.62	\$5.69	\$5.98	\$6.58
	Added response		\$0.94	\$0.72	\$0.81	\$0.88	\$1.17	\$1.77

There is considerable interest in the opportunities afforded by selection for RFI to improve efficiency by reducing feed requirements. Therefore Table 16 summarises the impact on RFI through various selection protocols. The analysis indicates that even by applying genomic selection at a high accuracy of 0.50 (which requires considerable investment in phenotyping of key animals), there is still a loss of around

40% in terms of overall economic response (R7 versus R4). However should the genetic correlations with other traits prove to be positive, the outcome will be improved, but the time-lag (due to both logistics in terms of the number of animals phenotyped and technical complexity) required to generate data with an accuracy of 0.5 is non-trivial. In fact it seems likely that selecting solely for RFI would lead to an adverse outcome for the Canadian beef industry as unfavourable correlations and responses with other traits would develop rapidly, even if they do not exist already. These results highlight the importance of taking a broad approach to improvement of productivity.

Table 16. Responses in Residual Feed Intake (RFI) to selection (expressed as annual genetic trend per cow mated per year) without and with the application of genomic breeding values at accuracies of 0.25

(25%) and 0.50 (50%)

(23/	o) and 0.50 (50%)	1		1		1	
	Basis of selection	trait units	e in RFI in (kg DM per ly)	as perce	expressed entage of mum	tage of Economic	
	24315 01 0310011011	Growing	Cows	Growing	Cows	Value	Percentage of Base (R1)
R1	Base (birth, weaning and yearling traits)	-0.0047	-0.0024	10%	13%	\$3.90	100%
R2	Comprehensive (all traits)	-0.0120	-0.0062	26%	35%	\$4.81	123%
R3	Comprehensive + multi-trait GBV at accuracy of 0.25	-0.0180	-0.0088	38%	49%	\$6.58	169%
R4	Comprehensive + multi-trait GBV at accuracy of 0.50 (ex Table 17 below)	-0.0291 (\$3.25)	-0.0108 (\$0.32)	62%	61%	\$9.43	242%
	Selection for improved RFI only						
R5	RFI only	-0.0299	-0.0153	63%	86%	\$3.79	97%
R6	RFI + GBV for RFI only at accuracy of 0.25	-0.0305	-0.0153	65%	86%	\$3.86	99%
R7	RFI + GBV for RFI only at accuracy of 0.50	-0.0471	-0.0178	100%	100%	\$5.78	148%

Summary: Estimation of selection response

Table 17 provides a summary of a number of scenarios that compare the current rate of progress (selection response) with those involving the application of genomic technologies (as per Table 9). The genetic responses apply to the whole industry but are the result of producers purchasing bulls from herds where the recording protocols are being applied. Producers are not required to invest directly in genomic technologies.

Table 17. Responses to selection (expressed as annual genetic trend per cow mated per year) without

and with the application of genomic breeding values

Scenario (as per T	Economic \$ value	Percentage of Base	
	Base recording	\$3.90	100%
Current estimated selection response	Base + Maternal trait recording	\$3.97	102%
using BLUP-based procedures only	Base + Feedlot/packer recording	\$4.75	122%
	Comprehensive recording	\$4.81	123%
Impact of applying multi-trait genomic	Base recording	\$6.37	163%
breeding values (Accuracy of GBV of 0.25)	Comprehensive recording	\$6.58	169%
Impact of applying multi-trait genomic	Base recording	\$8.78	225%
breeding values (Accuracy of GBV of 0.50)	Comprehensive recording	\$9.43	242%

Perspective: Who gets the benefits?

The current rate of genetic gain and the estimated future gain under various scenarios may appear low when compared against what is theoretically possible. However the structure of the herd has a major impact on the realised rate of gain.

The issue of who gains the benefit of genetic improvement is important. Table 18 extends the data in Tables 8 & 11 and provides an indication of where the benefit will be realised under various regimes. The estimated current rate of gain is \$3.90 of profit per cow mated per year. Of this, about half is realised through traits expressed directly within the cow-calf system (as per Table 8). The remainder requires that they also benefit from the gains in growth potential of the offspring in particular, and secondly from trait

benefits that are realised directly by the feedlot-packer sector. To realise these benefits would require an integrated supply chain where the benefits of investment in genetic improvement are apportioned appropriately. Table 19 then compares the potential benefits of enhanced recording protocols presented in Tables 12 & 13. It is important to note that inclusion of a focus on feedlot/packer traits actually reduces the benefit to the cow-calf producers.

Table 18. The potential benefit to the cow-calf producer based on the current annual rate of genetic

gain (profit per cow mated) in the recorded sector of the Canadian beef cattle industry

Potential benefit to the cow-calf producer	Traits included	Components of selection response	Total response	Percentage of response
Directly-relevant traits only	Weaning weight (WW) direct & birth weight (BW) & maternal (M, cow) traits	\$1.89 (WW) - \$0.07 (BW) - \$0.30 (M) = \$1.52	\$1.52	40%
Including full recognition for growth potential	Post weaning average daily gain (ADG, kg/day)	+\$1.69 (ADG) = \$1.69	\$3.21	83%
Including full recognition for feedlot & packer traits	Carcase value (CV) & RFI	\$0.16 (CV) + \$0.52 (RFI) = \$0.68	\$3.90	100%

In Table 19, we present our assessment of the benefits of enhanced recording protocols without using GBV whereas in Tables 20 & 21, the values incorporate the impact of genomic selection to the cow-calf producer.

Table 19. The potential benefit to the **cow-calf producer** based on enhanced recording protocols (traits

are as per Table 18) without using GBV in the recorded sector of the Canadian beef cattle industry

Potential benefit to the cow-calf producer	Base (current)		Base + Maternal trait recording		Base + Feedlot/Packer trait recording		Comprehensive	
Directly-relevant traits only	\$1.52	40%	\$1.38	35%	\$1.36	29%	\$1.34	28%
Including full recognition for growth potential	\$3.21	83%	\$3.19	80%	\$2.73	57%	\$2.82	59%
Including full recognition for feedlot & packer traits	\$3.90	100%	\$3.97	100%	\$4.75	100%	\$4.81	100%

Table 20. The potential benefit to the **cow-calf producer** based on the **base** recording protocol (traits as per Table 18) together with GBV (accuracy of 0.25) in the recorded sector of the Canadian beef cattle industry

Potential benefit to the cow-calf producer	Base	Base + GBV for Growth	Base + GBV for RFI	Base + GBV Fertility	Base + GBV Carcass	Base + GBV health	Base + multi-trait GBV
Directly-relevant traits only	\$1.52	\$1.43	\$1.38	\$1.88	\$1.35	\$1.27	\$1.41
Including full recognition for growth potential	\$3.21	\$3.64	\$2.64	\$3.47	\$2.83	\$2.67	\$2.86
Including full recognition for feedlot & packer traits	\$3.90	\$4.31	\$5.12	\$4.14	\$4.38	\$4.63	\$6.37

Table 21. The potential benefit to the **cow-calf producer** based on the **comprehensive** recording protocol (traits as per Table 18) together with GBV (accuracy of 0.25) in the recorded sector of the Canadian beef cattle industry

Potential benefit to the cow-calf producer	Compre- hensive	Comp + GBV Growth	Comp + GBV RFI	Comp + GBV Fertility	Comp + GBV Carcass	Comp + GBV health	Base + multi-trait GBV
Directly-relevant traits only	\$1.34	\$1.29	\$1.31	\$1.56	\$1.29	\$1.21	\$1.38
Including full recognition for growth potential	\$2.82	\$3.00	\$2.57	\$2.80	\$2.50	\$2.37	\$2.87
Including full recognition for feedlot & packer traits	\$4.81	\$5.77	\$5.58	\$5.57	\$5.70	\$5.96	\$6.57

However the cow-calf sector can benefit from improvements in feedlot/packer traits as extra profitability in the feedlot/packer sector is quickly competed away through procurement competition for finishing and finished stock. This transfer of benefits back to the cow-calf sector occurs generically, and is effectively averaged over all cow-calf producers, irrespective of whether it is their calves that have contributed to greater production and quality benefits in the feedlot/packer sector. Thus paradoxically our analysis

(Table 19) indicates that as the breeder (on behalf of the cow-calf producer) invests in recording for feedlot packer traits, the benefit to cow-calf clients of that breeder declines, while the benefit to the wider cow-calf sector still increases. The same situation applies with genomic selection (per GBVs for traits) where, with improved recording, the direct benefit accruing to the cow-calf producer purchasing genetically-improved bulls tends to be reduced.

Thus in order to incentivise the bull breeder to continue to invest, it is important that benefits realised by the breeder's clients are recognised in payments by the feedlot-packer sector to the cow-calf producer. This can only occur in the event that the feedlot-packer sector can assess the potential of genetic lines of cattle to perform in the feedlot and in the pack-house. This would require a fully-integrated supply chain.

In this respect there are some studies that provide further support for the proposition that commercial producers (users of the genetics generated by the bull breeders) may actually be the direct beneficiaries of genetic progress, even for traits that do not directly affect the performance of their improved progeny on-farm, as they realise benefits through increased consumption. For example, Australian studies have suggested that Australian consumers are significant beneficiaries of genetic improvement (e.g. Farquharson et al. 2003²⁴, Zhao *et al* 2000²⁵, Mounter *et al* 2008²⁶) through greater consumption and/or through reduced prices. However, in our view, this benefit seems unlikely where product prices are set by the international market, which is the case for the Canadian beef industry. Such studies also endorse the proposition that feed-lotters and meat processors receive a very small share of any gain due to genetic improvement. The reason is that they face intense competitive pressures in both procurement and onselling such that any gains in feedlot performance or carcase quality either get passed back through the supply chain to producers, or passed on through the supply chain to consumers.

However, feed-lotters and meat processors can benefit through ensuring the long-term supply of superior animals and they may be able to maintain an advantage over competitors though capturing exclusive access to desirable lines of animals. This then provides a case for the feedlot-packer sector to invest in genetic improvement. Such a strategy is likely to be particularly attractive to this sector as they are often characterised by overcapacity. There are examples of such integrated models within the North American beef industry but there is potential for a greater role of such approaches to genetic improvement within Canada.

Development of an industry model

Conversion from an individual model to an industry model

We have estimated the total industry value of selection using a value model where the annualised rate of progress (in \$) is used to estimate the benefits of 10 years of cumulative genetic progress over a 15 year time frame (assuming constant rates of genetic gain).

Table 22 shows the value of phenotypic recording and selection for the four recording protocols. The analysis is based on a population of 4.7 million cows (and heifers) mated per annum, with benefits that are first realised two years following the instigation of selection (in 2013) and cumulated over 15 years (2015-2029).

For the purposes of the analysis, we have assumed 100% penetration of recording (which is an overestimate). An annual discount rate of 7% was applied (where year 0 = 2013). Results are also presented as an annualised equivalent for each year of selection.

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²⁴ Farquharson, RJ, GR Griffith, SA Barwick, RG Banks and WE Holmes 2003, *Estimating the Returns from Past Investment into Beef Cattle Genetic Technologies in Australia*, Economic Research Report No. 15, NSW Agriculture, Armidale.

²⁵ Zhao, X, WE Griffiths, GR Griffith and JD Mullen 2000, *Probability distributions for economic surplus changes: the case of technical change in the Australian wool industry*, Australian Journal of Agricultural Economics 44(1), 83-106.

²⁶ Mounter, S, G Griffith et al 2008. Potential Returns to the Australian Sheep and Wool Industries from Effective R&D and Promotion Investments and their Sensitivities to Assumed Elasticity Values. Australasian Agribusiness Review **16**.

Table 22. Assessment of impact: discounted industry value of cumulative genetic progress over a total of 15 years (progress is due to 10 years of selection of superior breeding bulls, where year 0 is 2013).

	_	etic trend (per cow ed per year)	Cumulative discounted value (s	•				
Scenario	\$ value	Increase over Base Recording Protocol	Annualised equivalent	Total Benefits				
Base recording	\$3.90		\$127 M	\$952 M				
Base + Maternal trait recording	\$3.97	2%	\$129 M	\$969 M				
Base + Feedlot/packer recording	\$4.75	22%	\$154 M	\$1,160 M				
Comprehensive recording	\$4.81	23%	\$156 M	\$1,174 M				
Impact of applying multi-trait genor	mic breeding v	values (Accuracy of GE	3V of 0.25)					
Base recording	\$6.37	63%	\$205 M	\$1,541 M				
Comprehensive recording	\$6.58	69%	\$214 M	\$1,606 M				
Impact of applying multi-trait genomic breeding values (Accuracy of GBV of 0.50)								
Base recording	\$8.78	125%	\$285 M	\$2,143 M				
Comprehensive recording	\$9.43	142%	\$306 M	\$2,302 M				

Potential impact of changes in the industry in application of genetic information

In Table 23, we consider the potential impact of changes in the way that the Canadian beef industry utilises genetic information. For these purposes, we have assumed that all breeders currently use the base recording protocol²⁷. The scenarios evaluated include the following (the detailed assumptions are in the footnotes²⁸).

- 1. Increase selection intensity of breeding bulls to effect a 50% change in the rate of genetic gain
- Change the selection protocol to increase the proportion of breeders using comprehensive recording²⁹
- 3. Change the selection protocol to implementation of some genomic selection

Table 23. Impact of industry change on base recording models

	Scenario	Total benefits	Benefits over base
	Base recording	\$952 M	
1	Increase selection intensity (50% increase in rates of genetic gain)	\$1,428 M	\$476 M
2	20% of breeders shift from base to comprehensive recording	\$996 M	\$44 M
3	20% of base + 10% of comprehensive breeders use GBV (Accuracy of 0.25)	\$1,120 M	\$168 M

Assessment of net benefit: Accounting for the costs of additional investment

In theory, the cost of the additional investment in genomic technologies should be included in the assessment of net benefit. However the reality is that the new approach is almost certainly going to result in new structures such that the cost is not actually estimable. This is discussed further in the sections below.

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²⁷ Using the base recording protocols, the estimated selection intensity applied to effect current levels of genetic gain, shows that breeders are on average selecting bull candidates from the top 35%, 25% and 15% of young bulls, herd bulls and AI sires respectively.

²⁸ 1) breeders select bulls from the top 14%, 7.5% and 2.6% of bull candidates; 2) 20% of breeders who are currently using the base protocol switch to the comprehensive recording protocol; 3) 20% of breeders are recording according to the comprehensive recording protocols thus providing the training sets for the application of genomic technologies and that half of these breeders (10% of the total) plus one-quarter (20% of the total) of those using the base recording protocols take advantage of the genomic technologies, with the full breakdown of recording protocols as: 60% base recording, 20% base + multi-trait genomic selection, 10% comprehensive recording, and 10% comprehensive + multi-trait genomic selection.

²⁹As per the note on page 13, no data have been forthcoming but given that breeders who are recording have larger herds and sell a higher proportion of bulls, an appropriate estimate would have 80% of bulls being the products of herds that are base recording, 15% are from herds with maternal/ comprehensive records and 5% are not recorded. Even though producers may not purchase bulls based on the data, they are still reaping the benefits of genetic improvement in the bull herd. There are also opportunities to further enhance comprehensive recording, through practical schemes that could be introduced by some breeders (see Potential Best Practices).

Opportunities to Focus Genomics Research

Background

Bull breeders are in the business of breeding and rearing sound fertile bulls to sale age. Those using performance recording are seeking a premium over the base product of a sound unimproved breeding bull.

The new technologies of genomic selection represent both a threat and an opportunity to breeders and to their industry. The threat comes through an ability of breeders to substitute their investment in recording with an investment in DNA testing (potentially at a lower cost).

It is a threat because, paradoxically, the development of genomic selection is dependent on the on-going collection of phenotypic data to support the development of new traits and to provide data to continually assess the accuracy of such genomic technologies. Thus if breeders using DNA-based methods only are able to capture a significant share of the market for bulls marketed as "genetically-improved", there will be a disincentive for other breeders to continue recording at higher costs.

The opportunity arises through the potential for breeders to differentiate themselves as "performance recorders" and extract extra value. The balance between threat and opportunity depends on how structure changes to accommodate new opportunities and the way in which structural/pricing mechanisms operate.

Strategic overview

The *cost-benefit* analysis has highlighted some opportunities to enhance profitability through the overall value chain. Here we consider some options for researchers to enable them to *focus genomics research* on traits that are expected to provide the greatest cost-benefit. In this respect, the Gentec Strategic Plan (September 2012) defines the initial priorities and goals as:

- Improving production efficiency and lowering production costs, while reducing the environmental footprint and GHG effect (Efficiency);
- 2) Improving quality of livestock products through development of value-added product (Quality);
- 3) Improving upon the health and safety of livestock and livestock products to ensure security of trade and public health safety (Health and Food Safety);
- 4) Developing the infrastructure, tools, and people to enable the rapid uptake of genomics technology by the Canadian livestock industry (Knowledge Translation); and
- 5) Verifying the traceability of livestock and livestock products (Traceability).

Genomics research can make meaningful contributions to all five of these priorities. However, as noted previously, a fully-integrated value chain is necessary to incentivise any investment in traits other than those that will directly benefit the cow-calf producer. In this respect, only priorities 1 and 4 are likely to have a positive impact for the cow-calf producer. In addition components of 3 and 5 may impact on the price through demand for higher quality products, although the potential contribution of genetics/genomics may be limited.

Profitability through the value chain

There are opportunities to enhance the level of knowledge around key economic traits through the value chain. These relate mainly to the merits of a fully-integrated value chain (such as Friona³⁰) as per the Table 19 commentary: thus in order to incentivise the bull breeder to continue to invest, it is important that benefits realised by the breeder's clients are recognised in payments by the feedlot-packer sector to the cow-calf producer. This can only occur in the event that the feedlot-packer can assess the potential of genetic lines of cattle to perform in the feedlot and in the pack-house. This would require a fully-integrated supply chain.

³⁰Goldberg RA et al 2007. Friona Industries: Delivering better beef. Harvard Business School, 9-906-405

Development of novel traits

Genomic selection offers opportunities to generate value from incorporation of non-traditional traits in genetic selection. Good examples include meat quality and health traits. Pre-genomic methods such as BLUP are limited by the need to generate data through the recording of phenotypes and/or progeny testing on a relatively large scale. Consequently collection of such data can be prohibitively expensive and is often limited to industries that are either vertically-integrated (pigs and poultry) or where there are well-developed artificial breeding (AB) systems that enable the widespread utilisation of elite males through AB such as with dairy.

Genomics offers a paradigm shift in that a breeding program can be structured such that data can be collected on a smaller number of animals within a well-structured nucleus population(s). These populations must be designed so that they incorporate the key sources of genetics from within the wider (e.g. breed) population so that the data and information generated are relevant to the wider population. As there is a need to sample a much smaller number of animals than in pre-genomic systems, the cost of individual assessments is much less of an issue. A good example is the use of CT (computed tomography) approaches in sheep breeding schemes.

In addition there is the opportunity to collect progeny test data through commercial ventures as accuracy of pedigree is no longer an issue as pedigree can effectively be re-constructed using genomic approaches through gBLUP³¹. Good examples are health traits for animals in feedlots, meat quality traits at slaughter, and maternal traits such as longevity and cow health.

A critical advantage of genomic selection will be the major reduction in generation interval that is achievable given the availability of good quality phenotypic data both in the nucleus and in downstream related herds through the capture of data where the value is realised through pedigree re-construction. The Australian Merino Information Nucleus³² provides an example of the operation of the nucleus, although the utilisation of the outputs downstream through the industry is a work in progress.

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³¹ See previous section *How does genomic selection work?*

³² See Clark, SA et al 2012. Genetics Selection Evolution, 44:4-9

Potential Best Practices

The analysis provides a framework for *the evaluation of potential best practices* in the application of use of genomic tools to accelerate genetic gain. There is considerable potential to capture new value from genomic selection but this is limited without a change in structure of data collection and evaluation practices and further development of the technology. Without a change in the way that data are collected, the result could well be an increase in cost without a parallel increase in value.

Frameworks and practices

New opportunities in evaluation

There is a major opportunity to develop a new framework for the development and application of genomic tools in systems to accelerate genetic gain. These include:

- improved processes for the collection and analysis of phenotypic data,
- utilisation of males to provide genetic connectedness between herds,
- utilising the inherent structure and genetic relationships within breeds within the cattle population,
- the genotyping of influential individuals.

Given these factors, there is a strong case for the development of Information Nucleus herds³³ and the co-ordinated collection of downstream (effectively progeny-test) data that are integrated through DNA-based relationship analysis. The need to increase the rate of genetic gain in maternal traits represents both a particular challenge and an opportunity for breeding schemes with a focus on investment in genetic progress and who are prepared to undertake detailed recording.

Role for genomic technologies through the value chain

There is potential for the application of **genomic technologies** to generate additional data through the value chain. This could range from data collection such as that around meat quality and the consumer eating experience through to detailed feedlot performance. As noted above, this is effectively a DNA-enabled progeny testing approach.

There is also the opportunity to utilise genomic technologies in **traceability** of meat products. However the costs of such approaches which require that a DNA sample is taken in the processing plant and stored in the event that a product must be sourced back to its origin, means that such systems have been adopted only in specific higher value supply chains; such systems include SureTRAK (Australia), and IdentiGEN³⁴ (Ireland). This blockage to widespread adoption will only be overcome when real-time DNA analysis is available at a cost that will enable its application in the meat processing plant so that data are stored rather than samples.

Arguably the greatest value will come from integrating data ex the supply chain back into breeding and production systems, especially as DNA systems provide the opportunity to identify problems that are relatively uncommon but important. These include 'symptoms' of problems such as diseases of animals in feedlots or a high incidence of poor quality meat products from a particular meat plant where, in such cases, a genetic link might now be suspected but undetectable. DNA-based systems will enable such analysis.

Facilitating uptake

Practices that will **facilitate uptake** and encourage industry-wide adoption of genomic technologies within the beef cattle industry are critical. Canada already has a well-developed breed association model that provides an obvious route to market. The associations are enthusiastic adopters of genomic technology but the key factor now is to ensure that the structures and systems are put in place and current structures enhanced to ensure that adequate amounts of good quality data are collected. The realisation of the importance of genetic relationships to successful implementation of genomic technologies is fundamental

³³ The value of the training set is a function of the relatedness of that set of animals to the population under evaluation. Hence it is essential that they are closely-related (see Saatchi, Mahdi *et al* 2013. Genomic breeding values in Hereford cattle: Accuracies of direct genomic breeding values in Hereford cattle using national or international training populations. Journal of Animal Science (online. 23 Jan 2013))

³⁴ http://animalgenetics.pfizer.com/sites/PAG/nz/Documents/SureTRAK_Brochure_NZ.pdf; www.identigen.com/

to this process. However this reality also puts a premium on the on-going generation and collection of high-quality data. Such data must include that for complex and difficult to measure traits such as feed intake, especially in pregnant and lactating cows. Recording of breeding cow fertility, survival and performance will be critical to avoid costly unfavourable outcomes from selection on growth rate and residual feed intake in young growing animals.

A critical issue that will greatly impact on the realisation of potential is the effective development of an integrated supply chain. This is important to both provide a strong incentive for investment in genetic improvement and to the realisation of many of the benefits of genetic improvement. This can only occur in the event that the feed-lotter/packer can assess the potential of genetic lines of cattle to perform in the feedlot and in the pack-house. However this will require integration from the breeder to the cow-calf producer and arguably the development of genomic tools for marker-assisted management, where genomic analysis coupled with analysis of early life phenotype provides a predictive tool for use in selection of individuals.

Genomic technologies also provide new opportunities to increase genetic gain in synthetic breeds such as Beefbooster and for crossbreeding. In this respect, there are reasons to believe that, while genetic analysis based on DNA- relationships offers the potential to evaluate bulls as sires for meat production, it may also offer the opportunity to dissect the contributions of parental breeds and the contribution of heterozygosity.

The overall value proposition

It is at this point that we turn to the question of **what would I have to believe** to justify this investment in genomic technologies? The primary question relates to

what level of increase in profitability of the cow-calf sector within a breed is sufficient to justify the investment?

The specific analysis is beyond the scope of this report but the facets to consider include:

- the magnitude of the investment required to establish and operate *Information Nucleus* herds (note that this must be considered for each breed although there is potentially scope to integrate with US breed operations);
- what level of uptake through the industry is required?
- what level of development of a fully-integrated value chain is necessary?
- what time-scale for the development and introduction of genomic selection is required?
- what level of accuracy of estimation is necessary to make a difference to the current rate of improvement?

Recommendations

We have considered the current situation and the opportunities for genomic selection in terms of the value that it can deliver within the Alberta (and Canadian) beef industries, and therefore make the following recommendations.

We recommend that Livestock Gentec works with the Breed Associations to:

- 1. develop Information Nucleus herds within each of the major breeds that will facilitate more accurate genomic predictions;
- 2. define traits of interest that would provide additional value to stakeholders keeping in mind the need for a broad and comprehensive view of productivity, and the need to be aware of potential unfavourable outcomes for cow productivity due to selection for young animal traits such as growth rate, and in particular residual feed intake;
- 3. ensure that there is strong connectedness across herds and also to downstream herds (which can operate as progeny test herds) to ensure that the outcomes are sufficiently valuable (that is, provide an adequate return on investment) to drive uptake:
- 4. place a strong focus on uptake of genetic improvement, and in particular, uses new and innovative genomic technologies and strategies to drive performance recording and selection on estimated breeding values, rather than promoting genomic selection as an alternative to performance recording.

We further recommend that Livestock Gentec:

- 5. focuses its investment in genotyping of key individuals to those breeds that are prepared to co-invest as a means to help ensure an appropriate return on the overall investment;
- 6. promotes the value of an integrated supply chain in terms of the benefits that would accrue to all participants in the supply chain (bull breeder, cow-calf producer, backgrounder, and feed-lotter/packer).

Acknowledgements

The authors gratefully acknowledge the input of the following people who hosted Peter Amer, Mike Coffey and Peter Fennessy in Alberta, and willingly provided their time and inputs into the discussions.

Livestock Gentec/ University of Alberta and Delta Genomics Centre: Dr. Graham Plastow, Tom Lynch-Staunton, Dr. Colin Coros, Delta Genomics, Dr. John Crowley, Livestock Gentec, Beefbooster Inc., Dr. Steve Miller, Livestock Gentec, CGIL, University of Guelph, Dr. John Basarab, Livestock Gentec, ARD

Alberta Agriculture and Rural Development (ARD): Dale Kaliel, Chris Panter, Darren Chase

Beef Cattle Research Council (BCRC): Dr. Reynold Bergen

Alberta Beef Producers (ABP): Karin Schmid

Canadian Beef Breeds Council (CBBC): Doug Fee, Doris Rempel, Mauricio Arcila

Beefbooster Inc.: Jennifer Stewart-Smith, and the breeders

Namaka Farms: Stuart Thiessen

Canadian Angus Association: Kajal Devani, Michael Latimer, and the producers

Canadian Charolais Association: Wade Beck Canadian Hereford Association: Jeff Hyatt

Canadian Limousin Association: Anne Brunet-Burgess

Canadian Simmental Association: Bruce Holmquist, Sandy Russell

Canadian Gelbvieh Association: Wendy Belcher

Canfax: Brian Perillat

Appendix

Appendix Table 1. Genetic parameters (Heritability, Phenotypic variance and Repeatability) of **Recorded traits**

Trait	Heritability	Phenotypic Variance	Repeatability
Birth weight	0.30	1.00	0
Weaning weight (WW) direct	0.18	1.00	0
Weaning weight maternal (milk)	0.10	1.00	0
Yearling weight	0.30	1.00	0
Heifer fertility (conception, N in calf)	0.10	1.00	0
Cow fertility (replacements /cow)	0.02	1.00	0
Fat and muscle scan (as a predictor of carcase value)	0.20	1.00	0
Residual feed intake (RFI) in the growing animal	0.35	1.00	0
Cow mature weight	0.40	1.00	0
Cow body condition score (1-5 scale)	0.25	1.00	0
Genomic Breeding Values			
Growth rate (kg/day)	0.25	1.00	0
Residual feed intake (RFI) in the growing animal	0.25	1.00	0
Cow fertility	0.25	1.00	0
Carcase value	0.25	1.00	0
Feedlot health	0.25	1.00	0

Appendix Table 2. Numbers of Angus bulls transferred per year in 2011 and 2012 (source, Kajal Devani)

	Recorded bulls tra	nsferred				
	20)11	2012			
Recorded traits	Number	Proportion	Number	Proportion		
Performance	422	3.0%	410	2.8%		
Birth Weight only	2,342	16.4%	2,224	15.4%		
Weaning Weight	3,124	21.9%	3,609	25.1%		
Yearling Weight	6,528	45.7%	6,185	43.0%		
Ultrasound Scan	1,857	13.0%	1,968	13.7%		
Total	14,273		14,396			
	Herd detail	s				
Total cows recorded	126,000					
Estimated male calves weaned	55,000					
Number & percentage of bull calves transferred	14,300	23%				

Appendix Table 3. Genetic correlations for recorded traits and for recorded traits with the Genomic Breeding Values (GBV)

түртийн тимг от от от		Weight pa	rameters (kg)	Other traits							Genomic Breeding Values (GBV)				
Recorded trait	Birth weight	Wean wt (WW) direct	WW maternal (milk)	Yearling weight	Heifer fertility	Mature cow weight	Body condition score	Cow fertility	Fat and muscle scan	RFI	Growth rate	RFI	Cow fertility	Carcase value	Feedlot health	
Birth weight	1.00	0.60	0.10	0.60	-0.10	0.70	0.00	-0.20	0.00	0.00	0.70	0.00	0.00	0.00	0.00	
Weaning weight direct	0.60	1.00	0.10	0.70	-0.15	0.60	0.00	-0.10	0.00	0.00	0.90	0.00	0.00	0.00	0.00	
Yearling weight	0.60	0.70	0.00	1.00	-0.30	0.70	0.00	-0.30	0.00	0.00	0.90	0.00	0.00	0.00	0.00	
Weaning weight maternal (milk)	0.10	0.10	1.00	0.00	0.00	0.10	-0.50	-0.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
Cow mature weight	0.70	0.60	0.10	0.70	-0.30	1.00	0.30	-0.30	0.00	0.00	0.70	0.00	-0.10	0.00	0.00	
Heifer fertility	-0.10	-0.15	0.00	-0.30	1.00	-0.30	0.00	0.60	0.00	0.00	-0.30	0.00	0.50	0.00	0.00	
Cow fertility	-0.20	-0.10	-0.20	-0.30	0.60	-0.30	0.30	1.00	0.00	0.00	-0.20	0.00	0.95	0.00	0.00	
Cow body condition score	0.00	0.00	-0.50	0.00	0.00	0.30	1.00	0.30	0.00	0.00	0.00	0.00	0.20	0.00	0.00	
Fat and muscle scan	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.60	0.00	
Residual feed intake (RFI) in the growing animal	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.95	0.00	0.00	0.00	

Appendix Table 4. Phenotypic correlations for recorded traits and for recorded traits with the Genomic Breeding Values (GBV)

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		Weight	parameters		Other traits							Genomic Breeding Values (GBV)					
Recorded trait	Birth weight	Wean wt (WW) direct	WW maternal (milk)	Yearling weight	Heifer fertility	Mature cow weight	Body condition score	Cow fertility	Fat and muscle scan	RFI	Growth rate	RFI	Cow fertility	Carcase value	Feedlot health		
Birth weight	1.00	0.60	0.10	0.60	-0.10	0.70	0.00	-0.20	0.00	0.00	0.70	0.00	0.00	0.00	0.00		
Weaning weight direct	0.60	1.00	0.10	0.70	-0.15	0.60	0.00	-0.10	0.00	0.00	0.90	0.00	0.00	0.00	0.00		
Yearling weight	0.60	0.70	0.00	1.00	-0.30	0.70	0.00	-0.30	0.00	0.00	0.90	0.00	0.00	0.00	0.00		
Weaning weight maternal (milk)	0.10	0.10	1.00	0.00	0.00	0.10	-0.50	-0.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00		
Cow mature weight	0.70	0.60	0.10	0.70	-0.30	1.00	0.30	-0.30	0.00	0.00	0.70	0.00	-0.10	0.00	0.00		
Heifer fertility	-0.10	-0.15	0.00	-0.30	1.00	-0.30	0.00	0.60	0.00	0.00	-0.30	0.00	0.50	0.00	0.00		
Cow fertility	-0.20	-0.10	-0.20	-0.30	0.60	-0.30	0.30	1.00	0.00	0.00	-0.20	0.00	0.95	0.00	0.00		
Cow body condition score	0.00	0.00	-0.50	0.00	0.00	0.30	1.00	0.30	0.00	0.00	0.00	0.00	0.20	0.00	0.00		
Fat and muscle scan	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.60	0.00		
Residual feed intake (RFI) in the growing animal	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.95	0.00	0.00	0.00		

Appendix Table 5. Genetic correlations for profit traits

	•					Profit	traits					
		Base				Mate	ernal			F	eedlot/Packe	er
Profit traits	Birth weight	Weaning weight direct (kg)	Post weaning ADG (kg/day)	Cow mature weight (kg)	Weaning weight maternal (kg)	Heifer fertility (concept- ion, N in calf)	Cow fertility (replace- ments /cow)	Cow body condition score (1- 5)	RFI annual cow (kg DM per day)	Carcase value (\$ per carcase)	RFI in growing animal (kg DM per day)	Feedlot survival
<u>Base</u>												
Birth weight	1.0	0.6	0.5	0.7	-	- 0.1	- 0.2	-		-	-	-
Weaning weight direct (kg)	0.6	1.0	0.6	0.5	0.1	-	- 0.2	-		-	-	-
Yearling weight (kg/day)	0.5	0.6	1.0	0.6	-	- 0.3	- 0.3	-		-	-	0.2
<u>Maternal</u>												
Cow mature weight (kg)	0.7	0.5	0.6	1.0	-		- 0.3	0.3		-	-	-
Weaning weight maternal (kg)	-	0.1	-	ı	1.0	-	-	- 0.5		-	-	-
Heifer fertility (conception, N in calf)	- 0.1	-	- 0.3	1	-	1.0	0.6	-		-	-	-
Cow fertility (replacements/ cow)	- 0.2	- 0.2	- 0.3	- 0.3	-	0.6	1.0	0.3		-	-	-
Cow body condition score (1-5)	-	-	-	0.3	- 0.5	-	0.3	1.0		-	-	1
RFI annual cow (kg DM per day)									1.0			
<u>Feedlot/Packer</u>												
Carcase value (S per carcase)	-	-	-	-	-	-	-	-		1.0	-	-
RFI in growing animal (kg DM per day)	-	-	-	-	-	-	-	-		-	1.0	-
Feedlot survival	-	-	0.2	-	-	-	-	-		-	-	1.0

Appendix Table 6. Genetic correlations between recorded traits and profit traits, and GBVs and profit traits

Appendix rabio or conode					•		fit traits					
		Base				Ma	aternal			Fe	edlot/Packe	er
	Birth weight	Wean weight direct	Post weaning ADG	Cow mature weight	Weaning weight maternal	Heifer fertility (conception, N in calf)	Cow fertility (replacements/ cow)	Cow body condition score (1-5)	RFI annual cow (kg DM per	Carcase value \$	RFI in growing animal (kg DM	Feedlot survival
Recorded traits		(kg)	(kg/day)	(kg)	(kg)	,	,	` ,	day)	carcase)	per day)	<u> </u>
Birth weight	0.95	0.60	0.40	0.70	0.00	-0.10	0.00	0.00	0.00	0.00	0.00	0.00
Weaning weight direct (kg)	0.60	0.95	0.50	0.60	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Yearling weight (kg)	0.60	0.70	0.80	0.60	0.00	-0.20	-0.30	0.00	0.00	0.00	0.00	0.00
Cow mature weight (kg)	0.70	0.60	0.70	0.95	0.10	-0.30	-0.30	0.30	0.00	0.00	0.00	0.00
Weaning weight maternal (milk)	0.00	0.10	0.00	0.10	0.95	0.00	-0.20	-0.50	0.00	0.00	0.00	0.00
Heifer fertility (conception, N in calf))	-0.10	-0.15	-0.15	-0.30	0.00	0.95	0.60	0.00	0.00	0.00	0.00	0.00
Cow fertility (replacements/cow)	-0.20	-0.10	-0.10	-0.30	-0.20	0.60	0.95	0.30	0.00	0.00	0.00	0.00
Fat and muscle scan	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.60	0.00	0.00
Cow body condition score (1 -5)	0.00	0.00	0.00	0.30	-0.50	0.00	0.30	0.95	0.00	0.00	0.00	0.00
<u>Derived traits</u>												
RFI annual cow (kg DM per day)	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.60	0.00
Genomic Breeding Values												
Growth rate (kg/day)	0.70	0.90	0.90	0.60	0.00	-0.20	-0.20	0.00	0.00	0.00	0.00	0.00
Residual feed intake (RFI) in the growing animal	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.60	0.00	0.95	0.00
Cow fertility	0.00	0.00	0.00	0.00	0.00	0.60	0.95	0.20	0.00	0.00	0.00	0.00
Carcase value	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.95	0.00	0.00
Feedlot health	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.95

Appendix Table 7. Ration composition

		Feed c	osts: Back-gro	unding				Assumptions: Back-grounding					
Diet composition	Component	ME (MJ per kg DM)	Ration	Price per tonne component	Cost per tonne fed	Cost per day			Proportion	ME (MJ per	Ration		
	proportion		(ME/kg DM)			Steers	Heifers	Component	of diet	kg DM)	(ME/Kg DM)		
Rumensin & minerals	0.015			\$500	\$7.50								
Grain	0.099	12.5	1.23	\$240	\$47.28	\$1.08	\$1.01	Grain	0.20	12.5	2.46		
Roughage	0.887	9.9	8.78	\$80	\$110.32			Roughage	0.80	10.0	7.88		
			10.0		\$165						10.34		
		Fe	ed costs: Feed	llot					Assumptio	ns: Feedlot			
Rumensin & minerals	0.015			\$500	\$7.50								
Grain	0.837	12.5	10.47	\$240	\$200.94	\$2.24		Grain	0.85	12.5	10.63		
Roughage	0.148	9.0	1.33	\$80	\$11.82		\$1.97	Roughage	0.15	9.0	1.35		
			11.8		\$220						11.98		