Advances in Selection

Beef Improvement Federation – Calgary AB, July 5, 2023

Steve Miller – AGBU, a joint venture of NSW Department of Primary Industries and University of New England, Armidale, Australia.
Advances in Selection

• Selection is a verb “the action or fact of carefully choosing someone or something as being the best or most suitable” Wikipedia
Who does selection?
Who does selection?

Owns no Cattle
Makes no decisions

Owns all the Cattle
Makes all the decisions
Who is responsible for the home run?

The Batter or the Bat?
Home Run History

762
Barry Bonds
2007

755
Hank Aaron
1976

714
Babe Ruth
1935
Changes in Technology
Knowing that the genetic material which will ensure the domestic and international competitiveness of Canada’s livestock industries ... we are pleased to provide the facts on 2,862 proven bulls and 3,165 young bulls of 13 different breeds.
Composites were the promise of the 1990's

Major conclusions from this experiment documented in this technical bulletin are:

- Composite breeds provide a simple procedure to use high levels of heterosis.

- Composite breeds provide a highly effective procedure to use breed differences or breed complementarity to **achieve** and **maintain** optimum breed composition for production and carcass traits.

- Composite breeds have the same uniformity for production and carcass traits as contributing purebreeds both within and between generations.

- Composite breeds offer herds of any size an opportunity to use high levels of heterosis and breed complementarity simultaneously.
Composites were the promise of the 1990's

Composite Breeds To Use Heterosis and Breed Differences To Improve Efficiency of Beef Production

In cooperation with the Institute of Agriculture and Natural Resources, University of Nebraska-Lincoln
Cross-breeding research was hot in Canada as well.

Roy Berg, a pioneer in the cattle industry, surrounded by animals that represented his passion. Photo: Courtesy Ruth Ball  photo: Courtesy Ruth Ball
The Breeds they are a changing

• Do we provide good tools to help with this selection?

![Graph showing the number of cattle registered by breed over years](image_url)

- Angus
- Total Hereford
- Shorthorn
- Simmental
- Wagyu
- Speckle Park

Australian Registered Cattle Breeders Association 2023
There is no clearer signal than at POS

Producers may not know what their true costs are, but they all know what they sell their calves for.

This influences selection
Everything old is new again
Everything old is new again

Beef Breed

Dairy Breed

Time to consider the other ½ of the genome?
Everything old is new again

Where is the rest of the profit equation?

Such as Carcass ie. Marbling

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<th>Trait</th>
<th>Ayrshire</th>
<th>Holstein</th>
<th>Jersey</th>
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<tr>
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</table>
Everything old is new again

Beef Breed

Dual Purpose Breed
Twice as good and twice as many

The production of twins in beef cattle utilizing embryo transfer technology

W.H. Johnson 1, W.G. Etherington 1, F.P. de Rose 2, J.W. Wilton 2, N.C. Savage 1

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2 Department of Animal Science University of Guelph Guelph, Ontario, Canada N1G 2W1

Dual Purpose Breed
Halve your Mothers methane debt
A Career like Gump
Does paying for measurements work?

Example of paying ON beef farmers to record weaning weights in the late 80s and early 90s

Data Source

AgSights
Paying for measurements post-weaning doesn’t work either.

- Subsidies for Performance testing bulls did not have a lasting impact

- Ontario Bull Evaluation was world leading
  - Ultrasound
  - Feed Intake
  - Economic Indexes

Data Source: AgSights
Now a company that is more than just genetic improvement
The USA offers a significant market for Canadian breeders.

Breeders wanted numbers comparable with the US market.
$Profit: A Game Changer in the Seedstock Industry

In today's cattle business, it's easy for producers to get overwhelmed with a large volume of data, some of it meaninglessly created under artificial seedstock conditions.

Lee Leachman had a mission to change that...to simplify the selection process, and create a set of indexes that take into consideration the factors that make an impact on the rancher's bottom dollar, economic factors, and now even genomic predictions.
Polymorphisms in the bovine leptin promoter associated with serum leptin concentration, growth, feed intake, feeding behavior, and measures of carcass merit

J D Nkrumah \textsuperscript{1}, C Li, J Yu, C Hansen, D H Keisler, S S Moore

Affiliations + expand
PMID: 15583038 DOI: 10.2527/2005.83120x

Abstract

Leptin is the hormone product of the obese gene synthesized and secreted predominantly by white adipocytes. It functions as a lipostatic signal regulating BW, food intake, energy expenditure, and adiposity. The leptin arg25cys affects performance, carcass traits and serum leptin concentrations in beef cattle

F C. Buchanan\textsuperscript{1}, A G. Van Kessel\textsuperscript{1}, Y R. Boisclair\textsuperscript{2}, H C. Block\textsuperscript{1}, and J J. McKinnon\textsuperscript{1}

\textsuperscript{1}Department of Animal and Poultry Science, 51 Campus Drive, University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5A8 (e-mail: fiona.buchanan@usask.ca); and \textsuperscript{2}Department of Animal Science, Cornell University, 258 Morrison Hall, Ithaca, NY, 14853-4801 USA. Received 10 August 2006, accepted 24 January 2007.

Buchanan, F. C., Van Kessel, A. G., Boisclair, Y. R., Block, H. C. and McKinnon, J. J. 2007. The leptin arg25cys affects performance, carcass traits and serum leptin concentrations in beef cattle. Can. J. Anim. Sci. 87: 153–156. A single nucleotide polymorphism (SNP) in the bovine leptin gene has been associated with carcass traits and elevated gene expression. To examine the relationship between leptin genotype with serum leptin concentration and carcass traits, blood samples were collected 24 h prior to slaughter in 89 head of cattle. Cattle were predominantly of Angus (n = 26). Hereford (n = 31) and Charolais (n = 32) breed types with approximately half homozygous for the T allele or the C allele. Cattle were fed limited to achieve 1 kg d\textsuperscript{-1}

Association of a single nucleotide polymorphism in the calpastatin gene with carcass and meat quality traits of beef cattle

F S Schenkel\textsuperscript{3}, S P Miller, Z Jiang, I B Mandell, X Ye, H Li, J W Wilton

Affiliations + expand
PMID: 16424255 DOI: 10.2527/2006.842291x

Abstract

Calpastatin (CAST) is a naturally occurring protein that inhibits the normal tenderization of meat as it ages postmortem. A SNP was identified in the CAST gene (a G to C substitution) and genotyped on crossbred commercially fed heifers (n = 163), steers (n = 226), and bulls (n = 61) from beef feedlots, and steers (n = 178) from a University of Guelph feeding trial. The association of the CAST SNP with carcass and meat quality traits was studied. Carcass traits included fat, lean, and bone yield; grade fat; LM area; and HCW. Meat quality traits included marbling grade; i.e., fat content of LM; tenderness evaluation of LM (Warner-Bratzler shear force) at 2, 7, 14, and 21 d of postmortem aging; and tenderness evaluation of semitendinosus muscle at 7 d of postmortem aging. The mixed model used
Disruptive Innovation

The chip that changed the game

• 2005 – Can we make genomic selection work in livestock?
• 2009 – Can beef experience the genomic selection success seen in Dairy?
• 2023 - The above is history

image provided by Illumina
Predicted a Doubling in Rate of Genetic Change


Strategy for applying genome-wide selection in dairy cattle

L R Schaeffer

Abstract

Animals can be genotyped for thousands of single nucleotide polymorphisms (SNPs) at one time, where the SNPs are located at roughly 1-cM intervals throughout the genome. For each contiguous pair of SNPs there are four possible haplotypes that could be inherited from the sire. The effects of each interval on a trait can be estimated for all intervals simultaneously in a model where interval effects are random factors. Given the estimated effects of each haplotype for every interval in the genome, and given an animal's genotype, a 'genomic' estimated breeding value is obtained by summing the estimated effects for that genotype. The accuracy of that estimator of breeding values is around 80%. Because the genomic estimated breeding values can be calculated at birth, and because it has a high accuracy, a strategy that utilizes these advantages was compared with a traditional progeny testing strategy under a typical Canadian-like dairy cattle situation. Costs of proving bulls were reduced by 92% and genetic change was increased by a factor of 2. Genome-wide selection may become a popular tool for genetic improvement in livestock.
A large and diverse collection of bovine genome sequences from the Canadian Cattle Genome Project

Paul Stothard¹, Xiaoping Liao¹,², Adriano S. Arantes¹, Mary De Pauw¹, Colin Coros³, Graham S. Plastow¹, Mehdi Sargolzaei⁵, John J. Crowley¹, John A. Basarab¹,⁶, Flavio Schenkel⁵, Stephen Moore¹,⁴* and Stephen P. Miller¹,⁵,⁷*

Abstract

Background: The Canadian Cattle Genome Project is a large-scale international project that aims to develop genomics-based tools to enhance the efficiency and sustainability of beef and dairy production. Obtaining DNA sequence information is an important part of achieving this goal as it facilitates efforts to associate specific DNA differences with phenotypic variation. These associations can be used to guide breeding decisions and provide valuable insight into the molecular basis of traits.
Over 500,000 genotypes in BREEDPLAN analyses

- Approximately 63 separate genetic evaluations
- 40 beef cattle breeds
- 14 million animals across 14 countries
Average selection accuracy - all breeds & EBVs

single-step increasing EBV accuracies all breeds

D. Johnston et al. AAABG 2023
**Size of genomic reference – all breed & EBVs**

- Bigger reference more accuracy from single-step

D. Johnston et al. AAABG 2023
More is More

Genomic selection accuracy continues to increase with more data

K. Moore et al. AAABG 2023
Universal Truth in Beef cattle selection

Data = Accuracy = Progress

Wheel of Selection

More Data → More Accuracy → More Traits → More Progress

More Progress → More Traits → More Data → More Accuracy
Universal Truth in Beef cattle selection

“Without data, we can do nothing.”
A BLUPers view on the Monarchy

Phenotype

Genotype
Average age of parents declining is a symptom of earlier selection with genomics.

Declining age most dramatic in sires.

Miller 2022 Reprod. Fertil. Dev. 35(2) 98-105
We can make them bigger

- No matter what the technology
- Angus EPD increase by about 3lb/year
- 2050 YW AVE EPD = 200
Cows are increasing in merit with greater differential identified.

Tools are identifying Elite females to target for advanced breeding technologies such as ET.

Miller 2022 Reprod. Fertil. Dev. 35(2) 98-105
Marbling Trend is kicking up

2018 to 2022 trend is double the previous 5 years
Increasing Trends post Genomics

- ~50% increase in Merino
- ~20% increase in Angus

Source: Datagene, Angus Australia and Sheep Genetics (2023)

Miller AAABG 2023
Increasing Trends post Genomics

- ~50% increase in Merino
- ~20% increase in Angus
- 4 fold increase in Friesiens

Source: Datagene, Angus Australia and Sheep Genetics (2023)

Miller AAABG 2023
Final Thoughts

• The ‘big change’ has happened and it is genomic selection
• The black box reigns is powerful
• Limiting factor is data – it is a scramble for data to get ahead
• The recipe is clear – more data, more accuracy, more progress – just about any trait