Addressing the Phenomic Gap: Next generation genomic tools in beef

Basarab, Aalhus, Stothard, Wang, Crews, Dixon, Moore, Plastow

Deseret Ranches of Alberta

The Canadian beef cattle industry faces severe challenges in

- **global competitiveness,**
- **food safety and disease,**
- **environmental sustainability/change and**
- **bio-security.**

There is a critical need to optimize animal-based agriculture to;

- **improve efficiency of feed utilization,**
- **improve carcass and meat quality,**
- **improve product health and safety and**
- **reduce environmental impact.**

Past Success

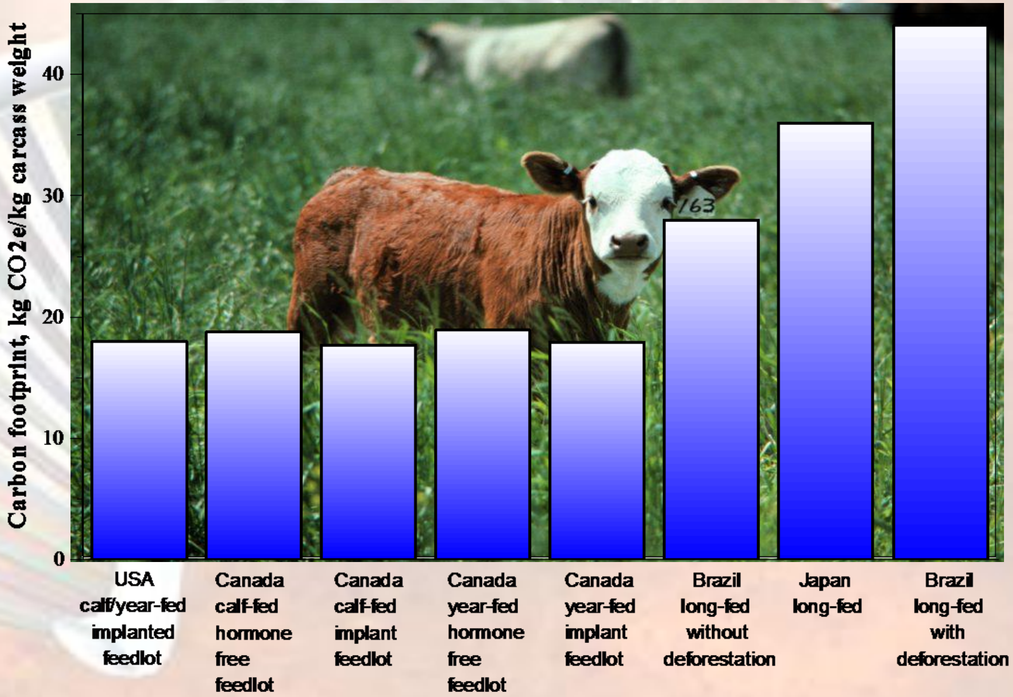
Production Efficiency 1977-2007

Same amount of beef now required

- ***70% of the animals***
- ***81% of the feed***
- ***88% of the water***
- ***67% of the land***
- ***resulting in a 16% decrease in the carbon footprint of beef***

(Capper 2011, Animal Frontiers)

Carbon footprint by region and beef production system (Basarab et al. 2012; Capper 2011)

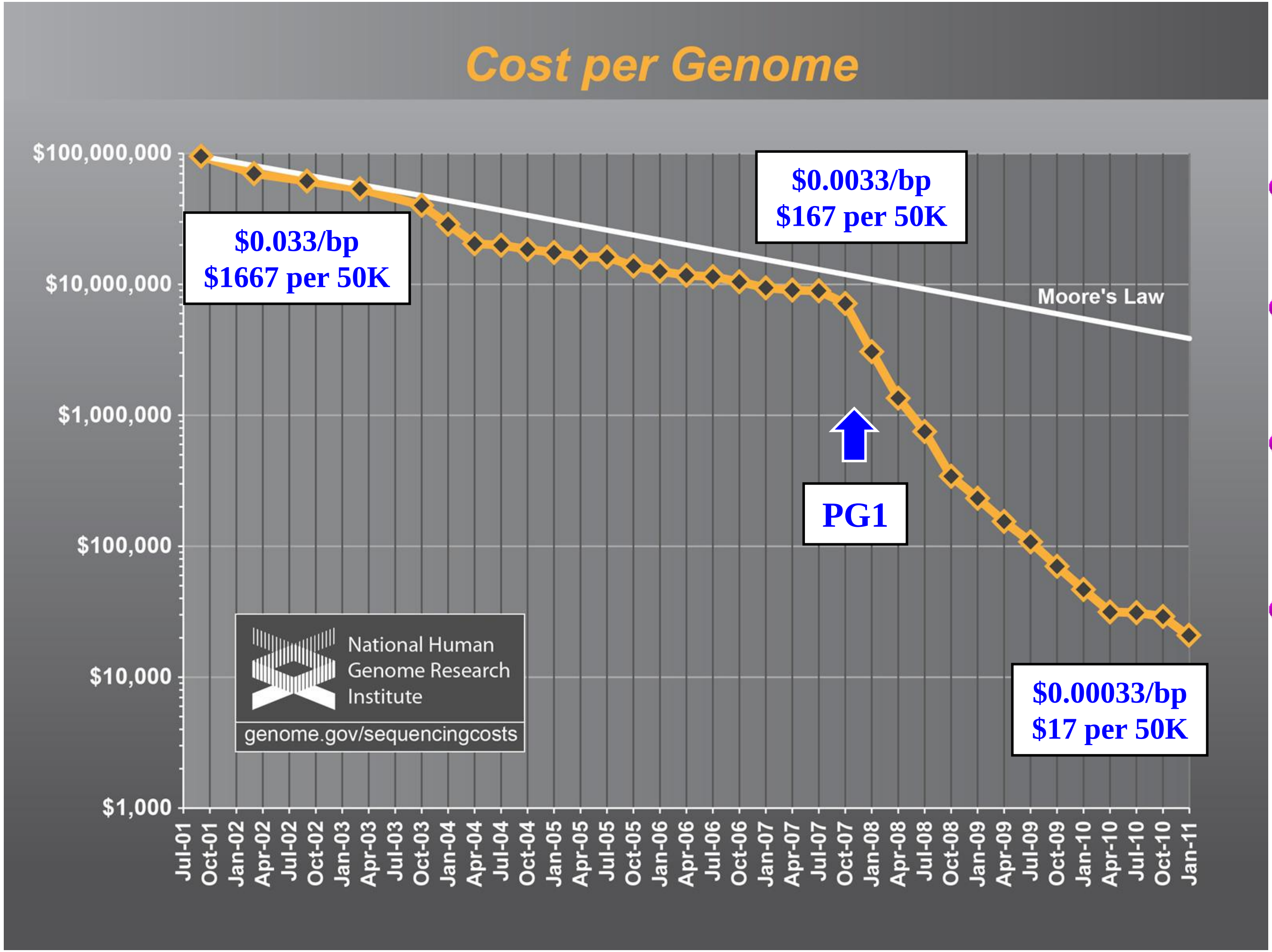


% Change in greenhouse gas emissions and global warning potential achieved through genetic improvement (1988-2007)

Species	CH_4	NH_3	N_2O	GWP_{100}
Chickens – layers	-30	-36	-29	-25
Chickens – broilers	-20	10	-23	-23
Pigs	-17	-18	-14	-15
Cattle – dairy	-25	-17	-30	-16
Cattle – beef	0	0	0	0
Sheep	-1	0	0	-1

CARBON FOOTPRINT (CO_2e/kg product); Pork 2.8-4.5 kg; Chicken 1.9-2.9; Dairy1.3 kg; **Beef 18-36 kg**

Sources: Project for DEFRA by Genesis Faraday Partnership and Cranfield University (AC0204) from Hume et al. (2011), J. Ag. Sci., doi:10.1017/S0021859610001188 .



Genomics

- **rapidly advancing sciences – provide solutions.**
- **10,000s of SNPs can be quickly identified**
- **However, not correlated to traits of economic importance.**
- **This lack of phenotypes, which is particularly true in beef cattle, is referred to as the "Phenomic Gap".**

Genotyping by sequencing

Genomic Potential

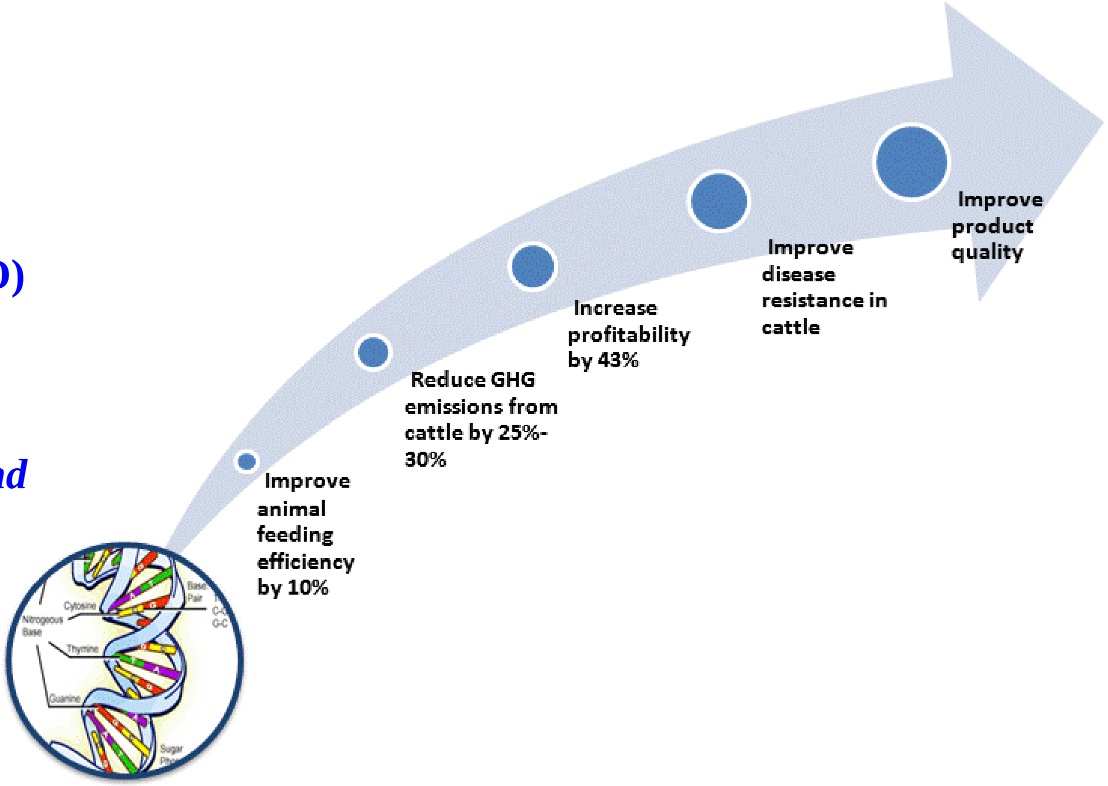
The Prospect of Improved Production Efficiency and Impacts

Safe, affordable, nutritious and environmentally

sustainable beef products

Increasing global population (FAO)

- ***8 billion by 2030***
- ***9 billion by 2050***
- ***55% increase in global demand for meat***



References:
Archer, J.A. et. al., (2004). Economic Evaluation of Beef Cattle Breeding Shcemes Incorporating Performance Testing of Young Bulls for Feed Intake. *Australian Journal Of Experimental Agriculture.*
Lazenby, M.T. et, al., (1996). Cost Benefit Analysis of Feed Efficiency Testing in Bull Evaluation Programs in Ontario. Ontario Beef Research Update (Published by University of Guelph).
Kahi, K.A. et. al., (2003) Economic Evaluation of Hereford Cattle Breeding Schemes Incorporating Direct and Indirect Measures of Feed Intake. *Australian Journal Of Agricultural Research.*
Paterson, John and McDonald Ty, The Value of Residual Feed Intake to Bull Buyers at the Midland Bull Test. Prime Cuts (Published by Montana State University).

ADDRESSING THE "PHENOMIC GAP" – PG1

Objectives:

- large scale phenotyping and genotyping
- - validate SNP panels for feed efficiency, carcass merit, & tenderness

40-50 sires
4 herds, 1000 cows/yr
670-800 progeny tested/yr under standard conditions

DNA
Blood
Tissues

GENOTYPES
50,000 SNP data base

Hard to Measure Traits
Residual Feed Intake (RFI)
Body composition
Carcass traits
Meat quality & palatability
Fatty acid profile

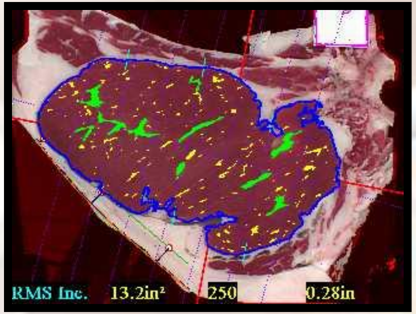
Genetic MARKER & MBV VALIDATION

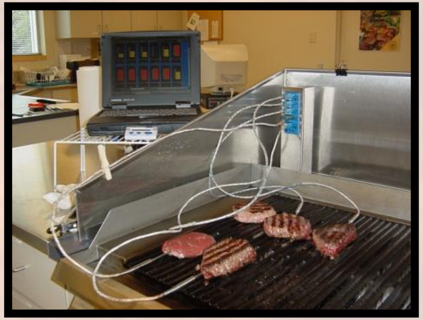
Individual Animal Feed Intake Facilities

Global GrowSafe capacity: ~68,000 animals; facilities in Canada (8%), US (76%), UK, Brazil, Aus (16%); Sunstrum 2012.

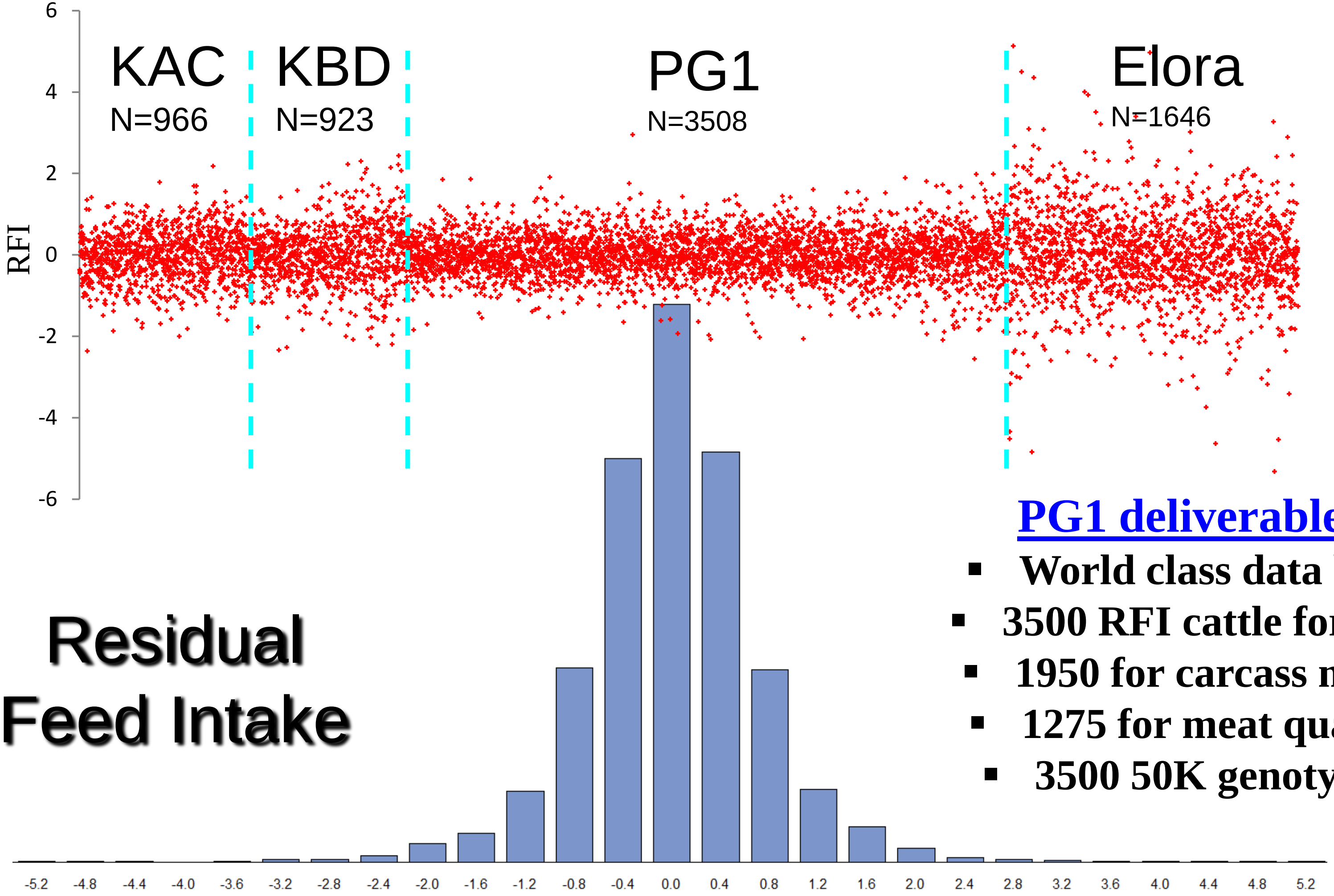
Carcass data: weight, backfat, ribeye area, marbling, yield & quality grade.

Meat quality, retail acceptability: shear force, 3 & 29 days ageing; pH, temperature, colour, drip loss, proximate analysis; sensory taste, flavour and texture





Residual Feed Intake



PG1 deliverables

- World class data base
- 3500 RFI cattle for RFI
- 1950 for carcass merit
- 1275 for meat quality
- 3500 50K genotypes

- Sequencing: Sires from PG1 (13), KAC (8), KBD (9) and Elora (30) have been selected for sequencing.

CFCC_4415P; 50 progeny

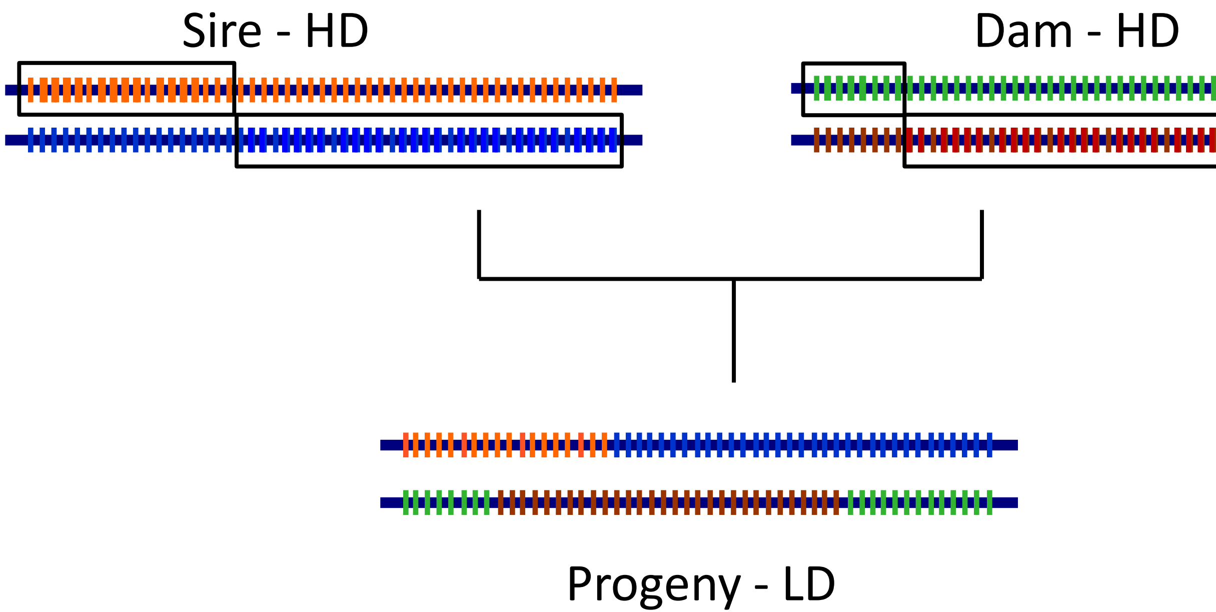
XO_7729T; 40 progeny

LLB_113T; 35 progeny

Three sires from the Phenomic Gap (PG1) project that will undergo full DNA sequencing

These will join 300 other fully sequenced animals from CCGP and 1000 animals under the "1000s Bulls Project"

Inheritance of DNA

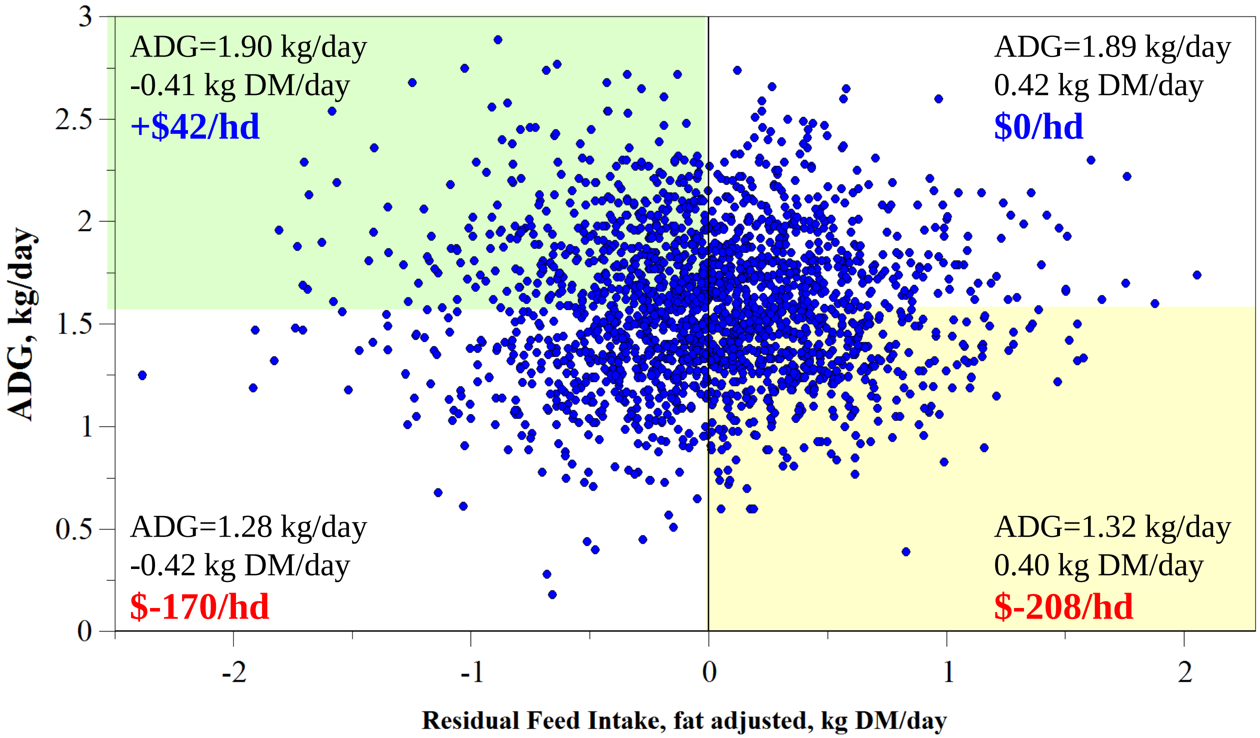


Bovine Genome

30 pairs of chromosomes
~3,000,000,000 bp
~10,000,000 SNPs
~ 30,000 genes

Source: Mehdi Sargolzaei and Steve Miller, University of Guelph

Economic Potential of RFI & Growth in feeder cattle (N =2029)

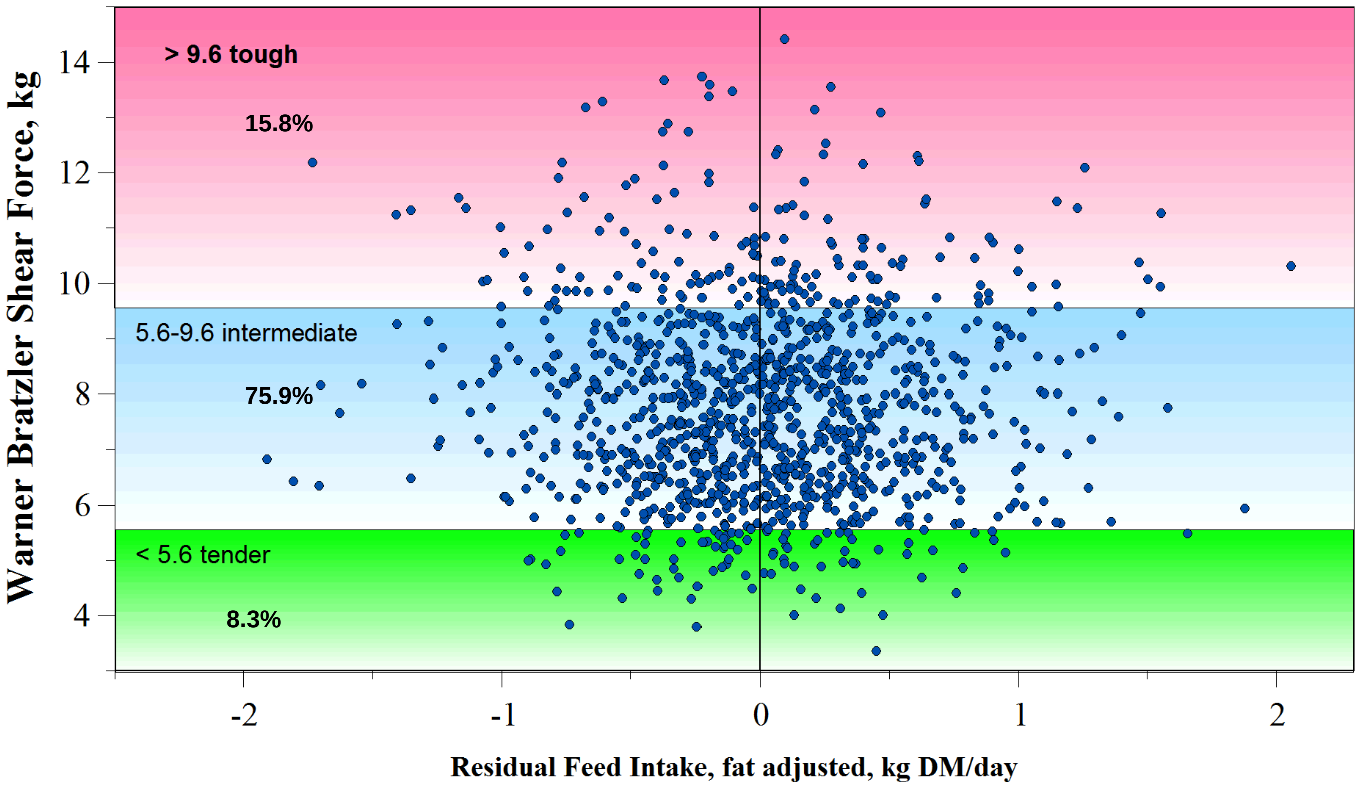


No relationship between growth (ADG) and RFI

NOTE: Same feeder cost and price, transportation, vet & medicine, interest, yardage, death loss and marketing costs

Arthur et al. 2001;
Basarab et al. 2003, 2013;
Crews et al. 2003; Jensen et al. 1992

Relationship between RFI_{fat} and tenderness in striploin steaks aged for 3 days (Basarab & Aalhus, 2013)

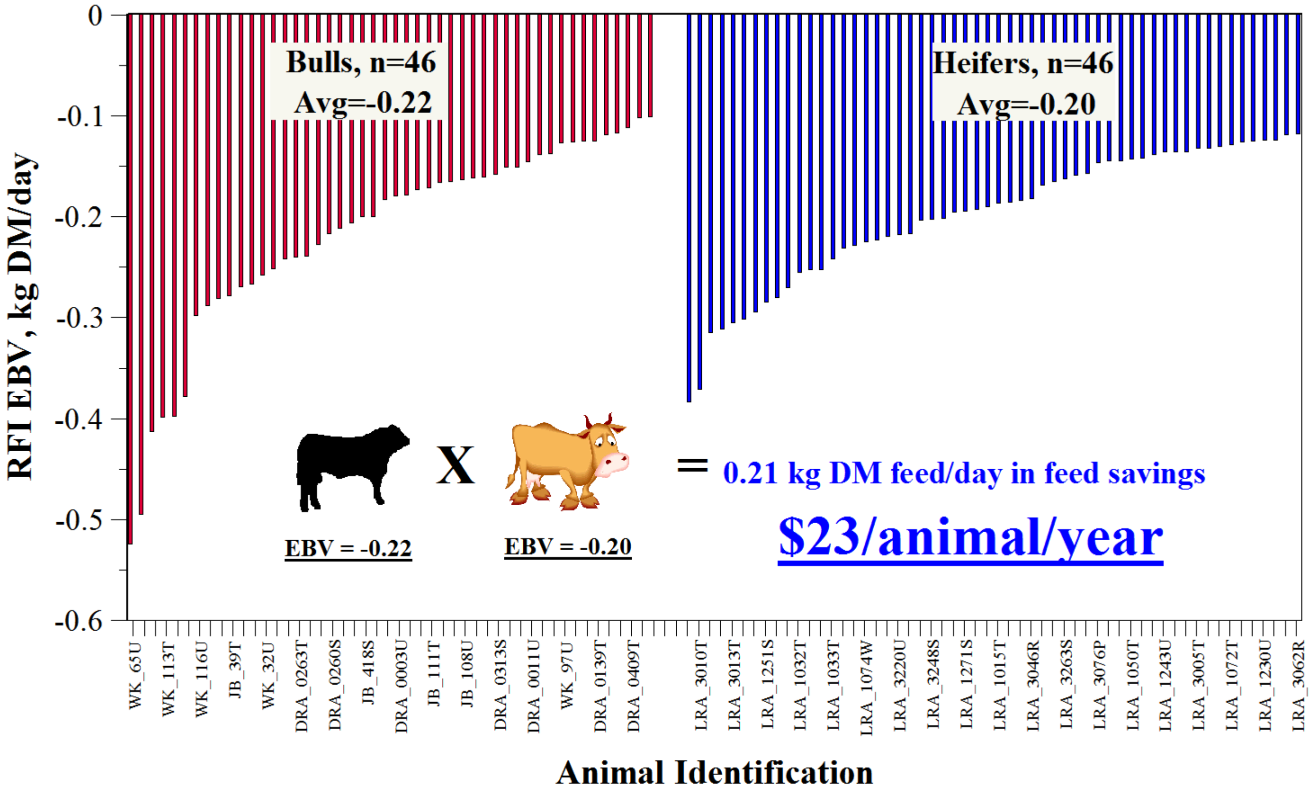


1186 heifers & steers striploins identified by DNA match to post-weaning blood sample

No or low relationship to 34 meat quality, sensory panel and retail quality traits
r_p = -0.09 to 0.12

Top bulls and heifers for RFI across participating herds

(Estimated Breeding Values [EBVs] 5770 cattle; accuracy 34-95%, mean accuracy =72%).



PG1

50K SNPs parentage on >3000 Offspring = 1-61/sire

NOTE: $0.30/kg DM feed x 365 days x 0.21 kg DM/day = $23/hd/yr

Validation of MBVs for RFI, marbling and tenderness in beef cattle (>364)

Everestus Akanno, John Basarab and Graham Plastow

MBV_{RFI} vs. actual RFI = 14% of additive genetic variability; rg = 0.37

$MBV_{marbling}$ vs. actual marbling = 21% of additive genetic variability; rg = 0.46

$MBV_{tenderness}$ vs. actual tenderness = 16% of additive genetic variability; rg = 0.40

"Early in life" genomic enhance breeding values (GEBVs) have been developed with prediction accuracy of 0.3-0.6 (Li et al. 2012).

Genetic correlations (r_g) between MBV and actual trait and progeny equivalents for marker panels

Adopted from (www.angus.org/AGI/Genomicchoice011102011)

Traits	Heritability	r_g Igenity (384 SNP)	Progeny equivalents
Birth weight	0.42	0.32	4
Marbling	0.26	0.42	10
Back fat thickness	0.26	0.25	4

In our project: RFI, r_g = 0.37; marbling, r_g = 0.40, tenderness, r_g = 0.44

Progeny eq. needed to achieve similar genetic evaluation = 4-5

Savings RFI: $1600 for GrowSafe, feed/yardage + 6-8 months of time

RFI & SNP genotyping in beef cattle populations

50k genotypes in multi-trait indices

Deseret Ranches of Alberta

40 bulls/yr at Olds
130 bulls/yr at Elite herd, Utah

90 bulls/yr, Kinsella Research Ranch

50 bulls/yr, Kinsella Research Ranch

150 bulls/yr Lakeland College

440 bulls/yr, Elora Beef Research Station
6k animals requiring parentage verification

>900 bulls in 3 yrs, Olds College, Cattleland

What can Genomics do now?

- Create predictors for hard to measure traits (weak to moderate, but have improved to 14-20% of genetic variation).
- Increase accuracies of EPDs “early in life”.
- Identify Parentage
- Marker Assisted Management

Conclusion

"In the era of genomics and genotypes, **phenotypes are still KING**."

Mike Coffey, Scottish Agricutural College

"…..**beginning of a revolution in livestock genomics** … short time …. envisioned ... $5 parentage panel plus ……… trait markers … deliver $50 in value … "

- Steve Miller, December 2012, University of Guelph

"Groups that can organize themselves **technologically and structurally** to … marry entire supply chain phenotypes and genotypes, plus take advantage … declining genotyping costs …. will have a substantial competitive advantage"

- Alison Van Eenennaam, University of California