Genomic tools for commercial beef herds

John Basarab

Fall Forum, Mayerthorpe
November 29, 2018

Improving feed efficiency, product quality, profitability, environmental impact and food security
MyHerdandMe.com
Genomic tools for cattle producers

“who’s your daddy” Parentage assignment

“Ancestry.com” Breed composition Mate matching

Others, Lethal recessives, relatedness

EnVigour HX™
gEPDs, Value indices

heterozygosity Hybrid Vigor Score

Copyright Alberta Agriculture and Forestry
“who’s your daddy”

Why It Pays to Parentage Test

- Lasting impact; progeny from sire can impact a herd for 10-25 years
- Developing replacement heifers approaches $2000
- Maintaining herd sire ~ $1800/year
- Parentage test $12-20/animal; 8 days turnaround
- Small price to pay for a long-term investment
- Record keeping is a pre-requisite
Number of progeny by sire (CCHMS, year 1)

118 sires;
0-44 progeny per sire
## Range in EPDs of sires from 3 different breeding programs for carcass value

<table>
<thead>
<tr>
<th>Breeding Program</th>
<th>sires used</th>
<th>EPD for carcass value</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>29</td>
<td>$-186 to $-19/head</td>
</tr>
<tr>
<td>2</td>
<td>48</td>
<td>$ -22 to $ 95/head</td>
</tr>
<tr>
<td>3</td>
<td>15</td>
<td>$ 4 to $169/head</td>
</tr>
</tbody>
</table>

**Conclusion:** There is sufficient range in the genetic value of sires for carcass merit, and that selection amongst yearling bulls using carcass traits improve carcass value (MacNeil, Basarab, Manafiazar and Plastow)
"Ancestry.com" for beef cattle

Genomic breed composition
Mate matching

"Precision breeding"
Crossbreeding

- To take advantage of hybrid vigor (heterosis) and breed differences
- Heterosis increases fertility, longevity and lifetime productivity by 20-30%.
- Fertility is the most important trait to cow-calf production (*10:2:1 rule of Thumb*)
- Calf Crop % has remained constant at 83-85% over the last 25-30 years
- Steady decline in hybrid vigor due to single breed use since early 2000s
- Asking producer to decide between branded beef premiums and fertility
Calf Crop percentage (%) has remained constant for >25 years

Calf Crop % = calves weaned per 100 females exposed to breeding
10-13 calves lost due to infertility
4-5 calves lost due to early calf death loss
Are crossbreds more variable than purebreds?

Coefficient of variation (CV) for purebreds vs. composite steers

<table>
<thead>
<tr>
<th>Traits</th>
<th>Purebreds CV, %</th>
<th>Composites CV, %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Birth weight</td>
<td>12</td>
<td>13</td>
</tr>
<tr>
<td>Wean weight</td>
<td>10</td>
<td>11</td>
</tr>
<tr>
<td>Carcass weight</td>
<td>8</td>
<td>9</td>
</tr>
<tr>
<td>Retail product</td>
<td>4</td>
<td>6</td>
</tr>
<tr>
<td>Marbling</td>
<td>27</td>
<td>29</td>
</tr>
<tr>
<td>Shear force</td>
<td>22</td>
<td>21</td>
</tr>
</tbody>
</table>

No difference in variability for reproduction, production and carcass traits
U.S. Meat Animal Research Center, Clay Center, NE;
Gregory et al. 1999
Inheritance of DNA 
& recombination

Sire – Angus 100%

Dam – Hereford 100%

F1 Progeny – AN50%; HE50%

Adapted from Mehdi Sargolzaei and Steve Miller, University of Guelph
Inheritance of DNA & recombination

Sire – Simmental 100%

Dam – AN50%; HE50%

Progeny – Expected SM50%; AN25%; HE25%
- Actual       SM50%; AN15%; HE35%

Adapted from Mehdi Sargolzaei and Steve Miller, University of Guelph
Genomic breed composition

MyHerdandMe ... genotyping for beef cattle
Genomic-based breed composition & retained heterozygosity

Heifer progeny
- Simmental: 17.6%
- Hereford: 2.4%
- Angus: 80.0%
Total: 100%
Retained Heterozygosity: 32.8%

Red Angus bull
- Simmental: 2.6%
- Hereford: 2.5%
- Angus: 94.9%
Total: 100%
Retained Heterozygosity: 19.8%

Crossbred cow
- Simmental: 35.3%
- Angus: 60.0%
- Hereford: 4.7%
Total: 100%
Retained Heterozygosity: 51.4%
MyHermandMe ... genotyping for beef cattle
Genomic-based breed composition & retained heterozygosity

Heifer progeny
- Simmental: 17.6%
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Red Angus bull
- Simmental: 2.6%
- Hereford: 2.5%
- Angus: 94.9%

Total: 100

Crossbred cow
- Simmental: 35.3%
- Hereford: 4.7%
- Angus: 60.0%

Total: 100

Retained Heterozygosity:
- Heifer progeny: 32.8%
- Red Angus bull: 19.8%
- Crossbred cow: 51.4%
Who has more retained heterosis?
D6574

Angus = 52.9%
Simmental = 39.6%
Charolais = 5.9%
Others = 1.6%

RFI-fat = -0.02

Hybrid Vigor Score = 55.9%
D6543

Angus  = 80.4%
Simmental  = 13.6%
Charolais  = 4.2%
Others  = 1.8%

RFI-fat  = -0.41

Hybrid Vigor Score = 33.3%
Is low %RH and reduced hybrid vigor an opportunity?

Distribution of progeny and their dams for genomic-based retained heterozygosity (Hybrid vigor score)

- 2311 progeny and their dams from 13 commercial herds in Alberta
- 46% of progeny & 39% of cows could benefit from more VIGOR

Yes, 46% of calves and 39% of cows would benefit from more VIGOR
Distribution of progeny and their dams for genomic-based retained heterozygosity (Hybrid vigor score)

HERD 2, 161 progeny and their dams
84% of progeny & 55% of cows could benefit from more VIGOR
Hybrid Vigor Score and RFI\textsubscript{fat} in crossbred beef cattle.

<table>
<thead>
<tr>
<th>Groups</th>
<th>Type</th>
<th>n</th>
<th>Vigor Score</th>
<th>Linear effect, kg DM/day per 1% increase in Vigor Score</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>mean</td>
<td>SD</td>
</tr>
<tr>
<td>DW</td>
<td>steer</td>
<td>109</td>
<td>49.5</td>
<td>9.4</td>
</tr>
<tr>
<td>JM</td>
<td>steer</td>
<td>99</td>
<td>54.2</td>
<td>17.0</td>
</tr>
<tr>
<td>LRC</td>
<td>heifer</td>
<td>95</td>
<td>41.5</td>
<td>18.8</td>
</tr>
<tr>
<td>All</td>
<td></td>
<td>303</td>
<td>48.4</td>
<td>16.2</td>
</tr>
</tbody>
</table>

Each 10% increase in Hybrid Vigor Score improves feed efficiency by 0.08 kg DM/d. Thus increasing Vigor Score from 30% to 60% would save $18/head in feed costs over 250 days of feeding.
Genomic Hybrid Vigor, longevity, and profitability

412 replacement heifers followed over 5 calvings (1050 matings)
### Linear effects of genomic heterozygosity

<table>
<thead>
<tr>
<th>Trait</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>200-d weaning weight</td>
<td>+3 lb/10% change</td>
</tr>
<tr>
<td>Age at first calving</td>
<td>-2 days/10% change</td>
</tr>
<tr>
<td>Pregnancy rate</td>
<td>+2 percentile points/10% change</td>
</tr>
<tr>
<td>Weaning rate</td>
<td>+3 percentile points/10% change</td>
</tr>
<tr>
<td>Lifetime productivity</td>
<td>+79 lb over 5 parities/10% change</td>
</tr>
<tr>
<td>Days in the herd</td>
<td>+51 days/10% change</td>
</tr>
</tbody>
</table>

Genomic retained heterozygosity (gRH) and its effect on cumulative net income over 5 calvings in commercial beef heifers

Difference:
High gRH vs. Low gRH
= $80,938 per 100 cows over 5 calvings;
$161/female/year
## Correlations: RFI on other traits

<table>
<thead>
<tr>
<th>Traits</th>
<th>Direction in low RFI</th>
<th>phenotypic &amp; genetic correlation</th>
</tr>
</thead>
<tbody>
<tr>
<td>DMI</td>
<td>lower intake</td>
<td>0.60 to 0.79</td>
</tr>
<tr>
<td>FCR</td>
<td>improved</td>
<td>0.53 to 0.88</td>
</tr>
<tr>
<td>Feeding behaviours</td>
<td>lower</td>
<td>0.18 to 0.57</td>
</tr>
<tr>
<td>Cow productivity</td>
<td>no affect</td>
<td>0.03</td>
</tr>
<tr>
<td>34 meat quality traits</td>
<td>no affect</td>
<td>-0.09 to 0.12</td>
</tr>
<tr>
<td>DM &amp; CP digestibility</td>
<td>2-5% improv.</td>
<td>-0.33 to -0.34</td>
</tr>
</tbody>
</table>

Summary of 20 studies from Australia, Canada, Ireland and USA
CH4, CO2 and feed intake in high and low RFI cattle
Data – Respiration vs. Eructation

Rumen and Lung CO$_2$ and CH$_4$ from Four Animals over a 25 Minute Period
Summer Sampling
Two basic hypotheses: low RFI & low CH\textsubscript{4}

**Feed intake driven** low RFI, lower DMI and lower CH\textsubscript{4} production (g/day) but no effect on digestibility or CH\textsubscript{4} yield (g/kg DMI)

**Relationship between CH\textsubscript{4} emission and DMI**

Aus \( r^2 = 0.454; \) Can \( r^2 = 0.677 \)

Grainger et al. (2007), J. Dairy Sci.

IPCC 2006: CH\textsubscript{4} production =

\[
\left( (\text{DMI}, \text{kg DM/day} \times 18.45 \text{ MJ/kg DM}) \times \left( \frac{6.5\%}{100} \right) \right) / 0.05565 \text{ MJ/g CH}_4
\]
Two basic hypotheses: low RFI & low CH$_4$

Inherent differences in feeding behaviours, lower feed intake, longer rumen retention time → differences in rumen microbial communities, increased digestibility, more H$^+$ and increased ᵘ CH$_4$ yield (g/kg DMI)

What did we observe?

LOW RFI heifers
consumed 7.1% less feed
8.09±0.26 vs. 8.71±0.21 kg DM/day

emitted 6.5% less daily CH$_4$
196±1.4 vs. 210±1.4 g/day

BUT
emitted 2.7% more CH$_4$/kg DMI
compared to HIGH RFI heifers
Economic and Environmental Benefits

Selection for feed efficiency (annual rate of genetic progress=0.8%)

Feedlot Operation
16,000 market ready feeders
512 Tons of Barley Saved!!!!!

Large Cow-calf Operation
794 cows
50 round bales Saved!!!!!

2.9 million feeders – 92,800 tons/yr

4.7 million cows – 296,000 bales/yr
Increase accuracy of gEPDs & Value Indices

34 million variants screened for functional impact on feed efficiency and carcass quality traits;

gEPDs for 18 traits with > 35% accuracy in crossbred cattle;
Canadian Angus Animal Details
RED WILBAR REPLICA 904Z

Registration #: 1696969
Colour: Red
Sex: Male
Tattoo: WDM 904Z
Birth Date: 03/04/2012
Calving Year: 2012
Status: Active
Registration Status: Registered
Certificate Electronically Stored: No
Sire: RED WILBAR REPLICA 836T
Dam: RED WILBAR HELGA 612S
Breeder: Wilbar Cattle Co
Current Owner: Lacombe Research Centre
Progeny: None
Pedigree: View
EPD Graph: View
Performance Data: View

Based on November 2018 EPDs Angus

<table>
<thead>
<tr>
<th>EPD</th>
<th>Birth Weight</th>
<th>Weaning Weight</th>
<th>Yearling Weight</th>
<th>Milk</th>
<th>Total Maternal</th>
<th>Scrotal Circ.</th>
<th>Calving Ease</th>
<th>Mat Calving Ease</th>
<th>Yield Grade</th>
<th>REA</th>
<th>Carcass Weight</th>
<th>Marbling</th>
<th>Fat</th>
<th>Stay</th>
<th>HPG</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.69</td>
<td>+1.6</td>
<td>+43</td>
<td>+57</td>
<td>+23</td>
<td>+45</td>
<td>-</td>
<td>+1.0</td>
<td>+7.0</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>0.69</td>
<td>36</td>
<td>31</td>
<td>19</td>
<td>18</td>
<td>-</td>
<td>-</td>
<td>17</td>
<td>12</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>0.69</td>
<td>30</td>
<td>55</td>
<td>85</td>
<td>30</td>
<td>40</td>
<td>-</td>
<td>70</td>
<td>55</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

Average EPDs for all Calves born in 2018

<table>
<thead>
<tr>
<th>EPD</th>
<th>Birth Weight</th>
<th>Weaning Weight</th>
<th>Yearling Weight</th>
<th>Milk</th>
<th>Total Maternal</th>
<th>Scrotal Circ.</th>
<th>Calving Ease</th>
<th>Mat Calving Ease</th>
<th>Yield Grade</th>
<th>REA</th>
<th>Carcass Weight</th>
<th>Marbling</th>
<th>Fat</th>
<th>Stay</th>
<th>HPG</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.69</td>
<td>+1.9</td>
<td>+41</td>
<td>+71</td>
<td>+20</td>
<td>+40</td>
<td>+0.69</td>
<td>+2.9</td>
<td>+6.5</td>
<td>n/a</td>
<td>+0.37</td>
<td>+0.32</td>
<td>+0.010</td>
<td>n/a</td>
<td>n/a</td>
<td>n/a</td>
</tr>
</tbody>
</table>

23 November 2018
Birth weight and 205-day weaning weight for sire WDM_904Z (Red Angus)

- 20 progeny born in 2016
- Avg birth wt=83 lb (10), SD=10
- 205-day wean wt=656 lb, SD=83
- Age of dam = 2-10 years of age
- $R^2 = 0.52$

1. Different genetic merits
2. Different maternal effects
3. Poor accuracy of sire EDP
4. Hybrid vigor
5. Gene combining of sire and dam
6. Different management or Dam age
D6520 (female)
22Mar16, 80 lb
26Sep16, 538 lb
188 days at weaning
205 day = 579 lb

WDM 904Z (AR)
Z3012
(4 yr old; 75%AN: 17%HE: 7%CH)
Birth weight = 82 lb
Weight at weaning = 1355 lb

DUA 74X (AR)
X3379 (ARCH)

D6537 (female)
30Mar16, 92 lb
26Sep16, 710 lb
180 days at weaning
205 day = 796 lb

WDM 904Z (AR)
P3028
(4 yr old; 82%AN: 3.1%HE: 3.4%CH: 7.1% SM)
Birth weight = 92 lb
Weight at weaning = 1535 lb

HXF 100X (AR)
L3130

Same year, mating group (AI), sire, cow age, but very different wean wt. WHY?
Accuracy of progeny gEPDs and relationship between gEPD and actual progeny performance

<table>
<thead>
<tr>
<th>Traits</th>
<th>gEPD accuracy</th>
<th>Correlation (r) gEPD vs. actual trait</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Range</td>
</tr>
<tr>
<td>Marbling</td>
<td>32.6</td>
<td>28-45</td>
</tr>
<tr>
<td>Grade fat, mm</td>
<td>35.0</td>
<td>30-48</td>
</tr>
<tr>
<td>Rib eye area, cm²</td>
<td>38.1</td>
<td>33-51</td>
</tr>
<tr>
<td>Lean Meat Yield, %</td>
<td>37.1</td>
<td>32-50</td>
</tr>
<tr>
<td>Yield Grade</td>
<td>36.1</td>
<td>31-50</td>
</tr>
<tr>
<td>DMI, kg DM/day</td>
<td>43.3</td>
<td>36-58</td>
</tr>
</tbody>
</table>
Sire gEPD for marbling is related to progeny carcass marbling score (79 sires; 3 or more calves)

1 units of gEPD = 1.5 units change in carcass marbling

\[ y = 444 + 1.5x, \quad R^2 = 24.5\% \]

Accuracy = 49.5\%
Conclusions

- Genomic tools – EnVigour HX™
  (>200 return; cost $45/DNA test)

- Use to make better mating and culling decisions
- Use for more accurate genetic selection
- Use to refine branding programs
Project Team Members

From top left: John Basarab, Donagh Berry, John Crowley, Paul Stothard

From middle left: Dawn Trautman, Michelle Miller, Graham Plastow, Changxi Li,

From bottom left: Mohammed Abo-Ismail, Kirill Krivushin, Tara Carthy, Tiago Da Silva Valente
Livestock are a producer of man-made Greenhouse Gases (GHG) through the belching of methane from cattle, sheep and goats. Methane is 25 times more powerful as a GHG than CO₂.

Environmental Sustainability

- Global livestock production is 14.5% of global man-made GHG
- Global beef production is 5.95% of global man-made GHG

- Canada’s beef production is 0.072% of global man-made GHG
- Canada’s beef production is 3.6% of Canada’s man-made GHG

- conversion of perennial grassland into annual cropland, or worse yet, urban-industrial areas, typically leads to a 20-60% reduction in soil C
Genomic breed composition


Y = 0.0134 + 0.00891x
n = 404, r-square = 0.961
C CGP reference databases

- 379 sequences; 7 breeds and 3 xbreds;
- 4800 HD and 5600 50K genotypes
- 34 million variants identified.
- >10,000 DMI, ADG, RFI all with 50K genotypes
- >8500 carcass traits; 2995 WBSF

1000 Bull Genomes Project

- International coordination

- 2000 DMI, ADG, RFI; 1500 WBSF; 40000+ carcass traits all with 50K genotypes; 138 new sequences

- 3000 DMI, ADG, RFI, carcass traits, WBSF all with 50K genotypes
Relationship between genomic retained heterozygosity (gRH) and longevity in crossbred beef heifers

Survival is defined as whether or not a replacement heifer or cow survived to parity 1, 2, 3, 4 and 5 (had a calving record).
## Estimated increase in performance from different mating systems

<table>
<thead>
<tr>
<th>Mating Type</th>
<th>Estimated increase in calf wean weight per cow exposed to breeding (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pure breeds</td>
<td>0</td>
</tr>
<tr>
<td>2-breed rotation</td>
<td>15.5</td>
</tr>
<tr>
<td>3-breed rotation</td>
<td>20.0</td>
</tr>
<tr>
<td>Composites</td>
<td></td>
</tr>
<tr>
<td>F3-5/8A, 3/8B;</td>
<td>0.9</td>
</tr>
<tr>
<td>F3 - 3/8A, 3/8B</td>
<td>5.3</td>
</tr>
<tr>
<td>F3 - 1/4A, 1/4B, 1/4C, 1/8D, 1/8E</td>
<td>18.2</td>
</tr>
<tr>
<td>F3 - 1/4A, 1/4B, 1/8C, 1/8D, 1/8E, 1/8F</td>
<td>18.9</td>
</tr>
<tr>
<td>F3 - 3/16A, 3/16B, 1/8C, 1/8D, 1/8E, 1/8F</td>
<td>19.8</td>
</tr>
<tr>
<td>F3 - 1/8A, 1/8B, 1/8C, 1/8D, 1/8E, 1/8F, 1/8G</td>
<td>20.4</td>
</tr>
</tbody>
</table>

Each 10% increase in %RH (Vigor) results in 2.3% increase in calf weight weaned per cow exposed to breeding.

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Gregory et al. 1990
Trait variation in high vs. low vigor replacement heifers

- **High Vigor**: >0.4863 gRHET
- **Low Vigor**: <=0.4863 gRHET

Co-efficient of variation, %

- Birth wt
- Wean wt
- 200-d wean wt
- Pre-wean ADG
- On-test wt
- Off-test wt
- Off-test fat
- On-test ADG
- On-test DMI
- On-test FCR
- Age 1st calving
- Pre-check wt
- Pre-calving wt
Selection for low RFI-fat will:

- Have no effect on growth, carcass yield & quality grade
- Reduce feed intake at equal weight and ADG
- Improve feed to gain ratio by 10-15%
- Reduce NE$_m$ and methane production
Life Cycle assessment of GHG emissions from high vs. low Vigor herds

<table>
<thead>
<tr>
<th>Carbon Footprint</th>
<th>HIGH Vigor</th>
<th>LOW Vigor</th>
</tr>
</thead>
<tbody>
<tr>
<td>kg CO₂e/kg carcass beef</td>
<td>22.48</td>
<td>24.14</td>
</tr>
<tr>
<td>kg CO₂e/385 kg (850 lb) carcass</td>
<td>8655</td>
<td>9294</td>
</tr>
</tbody>
</table>

Difference: 639 kg CO₂e/animal slaughtered worth $19 at $30/t carbon

Assuming:
- 30% replacement rate
- 40% of cows could benefit from increase in hybrid vigor
- 4.9 million beef cows
- 375,732t CO₂e/yr = $11 million/yr

Includes enteric CH₄, manure N₂O, manure CH₄, cropping N₂O and energy CO₂ and is based on procedures described by Basarab et al. 2012, animals 2, 195-220
Trends in estimated breeding values for residual feed intake (RFI) for High and Low feed efficiency selection lines from 1993 to 1999

Trangie Agricultural Research Centre, NSW, Australia. Adapted from Arthur et al. 2001

Annual direct selection response = -0.125 kg DM/day compared to average.
Feed costs of $0.20/kg DM represents savings of $9/hd after Year 1, $18/head after Year 2 and $55/hd in year 6 over 365 days of feeding.