Updating APY core animals in the American Angus Association national evaluations

Garcia A, Miller S, Tsuruta S, Lourenco D, Misztal I, Lu D, Retallick K
Largest single breed beef cattle genetic evaluation

- Routine evaluations
  - 22 traits and 6 selection indexes
  - 11M animals
  - 1.1 M genotyped animals

- Weekly evaluations
  - BLUPF90 family of programs
Single Step evaluations

- Official release on July 7, 2017

- ssGBLUP with APY
  - 350K genotyped animals

- Choice of core animals:
  - 98-99% of variance in G
  - ~19K
  - Based on accuracy (high accuracy animals as core)
Motivation

• From 350K to 1M genotyped animals
  • 650K genotyped animals added
  • No changes in the core

• 3 questions to answer:
  1. Are we doing a good job with current set up?
  2. Can we improve convergence?
  3. What are the changes in GEBV and impact for breeders
Material and methods

• Official growth evaluation
  • 9.2 M BW ; 9.7 M WW ; 4.7 M PWG records
  • 11.8 M animals in the pedigree
  • 924 K genotyped animals

• Goals:
  • Test different samples of core animals
  • Compare with the official evaluation
1. Same number, from different generations (19K)
   - Y1: born up to 2010
   - Y2: born up to 2015 (same gen. as the HA core)
   - Y3: born up to 2017
   - Y4: born up to 2019 (all genotyped animals)

2. Random sample over all animals, different sizes
   - S1: 10 K animals
   - S2: 25 K animals
   - S3: 30 K animals
   - S4: 35 K animals
Results
Correlations with the official evaluation

• $\geq 0.99$ for all animals
• $\geq 0.98$ for genotyped animals and top 300 sires

• No difference in prediction accuracy or bias
### Absolute changes in GEBV

1. **Same number, from different generations (N core= 19K)**

<table>
<thead>
<tr>
<th>Scenario</th>
<th>BW (SDa= 5.4)</th>
<th>WW (SDa= 31)</th>
<th>PWG (SDa= 28)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Max</td>
<td>Mean</td>
</tr>
<tr>
<td>Y1 (2010)</td>
<td>0.02</td>
<td>1.31</td>
<td>0.02</td>
</tr>
<tr>
<td>Y2 (2015)</td>
<td>0.01</td>
<td>1.05</td>
<td>0.02</td>
</tr>
<tr>
<td>Y3 (2017)</td>
<td>0.01</td>
<td>0.93</td>
<td>0.02</td>
</tr>
<tr>
<td>Y4 (all)</td>
<td>0.01</td>
<td>1.27</td>
<td>0.02</td>
</tr>
</tbody>
</table>

* Changes expressed as SDa for each trait

---

* SDa = Standard Deviation in Absolute Changes.*
### Absolute changes in GEBV

#### Scenario

<table>
<thead>
<tr>
<th>Scenario</th>
<th>N core</th>
<th>BW (SDa= 5.4)</th>
<th>WW (SDa= 31)</th>
<th>PWG (SDa= 28)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Max</td>
<td>Mean</td>
<td>Max</td>
</tr>
<tr>
<td>S1</td>
<td>10 K</td>
<td>0.02</td>
<td>1.31</td>
<td>0.03</td>
</tr>
<tr>
<td>Y4</td>
<td>19 K</td>
<td>0.01</td>
<td>1.27</td>
<td>0.02</td>
</tr>
<tr>
<td>S2</td>
<td>25 K</td>
<td>0.01</td>
<td>0.82</td>
<td>0.02</td>
</tr>
<tr>
<td>S3</td>
<td>30 K</td>
<td>0.01</td>
<td>1.09</td>
<td>0.02</td>
</tr>
<tr>
<td>S4</td>
<td>35 K</td>
<td>0.01</td>
<td>1.07</td>
<td>0.02</td>
</tr>
</tbody>
</table>

- No clear pattern some scenarios better for one trait but worse for other
- Results always comparing with HA core (official evaluation)
Convergence

43% reduction in N rounds

19 K core animals

<table>
<thead>
<tr>
<th>Year</th>
<th>HA 2015</th>
<th>Y1 2010</th>
<th>Y2 2015</th>
<th>Y3 2017</th>
<th>Y4 All</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>3,449</td>
<td>4,643</td>
<td>3,904</td>
<td>3,120</td>
<td>1,981</td>
</tr>
</tbody>
</table>
Conclusions

• AAA updated the core set in official evaluations in 2021
  • Predictions from HA core were good, but slower convergence
  • 43% reduction in N rounds (avg. across all models)
  • Big reduction in run time

• Core choice does not matter for prediction
  • Correlations are high
  • Prediction accuracy is the same
  • When changing core, the magnitude of changes is the same

• Update was well received by AAA membership
QUESTIONS/CONTACT

Andre Garcia
Geneticist
agarcia@angus.org
Additional tests on core choices

1. Very old animals only
2. Only young animals
3. New sample of high accuracy animals
4. Only animals with genotyped progeny
5. Animals with no progeny
6. Rolling addition/replacement of animals (maintain previous, add some new)
7. Marginal contribution analyses to get influential sires in the population
8. Repeated random samples

• Results were the same, except convergence