

# Updating APY core animals in the American Angus Association national evaluations

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# 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



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**Genomic selection in the US: where it has been and where it is going?**

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**Kelli Retallick**  
AGI President

**Session 38.** Challenges – Delivering genetic progress in systems around the world




# 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)



Genetic evaluation using single-step genomic best linear unbiased predictor in American Angus<sup>1</sup> 

D. A. L. Lourenco , S. Tsuruta, B. O. Fragomeni, Y. Masuda, I. Aguilar, A. Legarra, J. K. Bertrand, T. S. Amen, L. Wang, D. W. Moser ... [Show more](#)

*Journal of Animal Science*, Volume 93, Issue 6, June 2015, Pages 2653–2662,  
<https://doi.org/10.2527/jas.2014-8836>



# 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

**Core-dependent changes in genomic predictions using the Algorithm for Proven and Young in single-step genomic best linear unbiased prediction**

Ignacy Misztal ✉, Shogo Tsuruta, Ivan Pocrnic, Daniela Lourenco

*Journal of Animal Science*, Volume 98, Issue 12, December 2020, skaa374,

<https://doi.org/10.1093/jas/skaa374>

**Changes in genomic predictions when new information is added** 

Jorge Hidalgo ✉, Daniela Lourenco, Shogo Tsuruta, Yutaka Masuda, Stephen Miller, Matias Bermann, Andre L S Garcia, Ignacy Misztal

*Journal of Animal Science*, Volume 99, Issue 2, February 2021, skab004,

<https://doi.org/10.1093/jas/skab004>

# 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

# Material and methods

## 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)

Scenario	BW (SDa= 5.4)		WW (SDa= 31)		PWG (SDa= 28)	
	Mean	Max	Mean	Max	Mean	Max
Y1 (2010)	0.02	1.31	0.02	1.21	0.02	1.08
Y2 (2015)	0.01	1.05	0.02	1.23	0.01	1.21
Y3 (2017)	0.01	0.93	0.02	1.29	0.01	1.03
Y4 (all)	0.01	1.27	0.02	0.89	0.01	0.86

\* Changes expressed as SDa for each trait

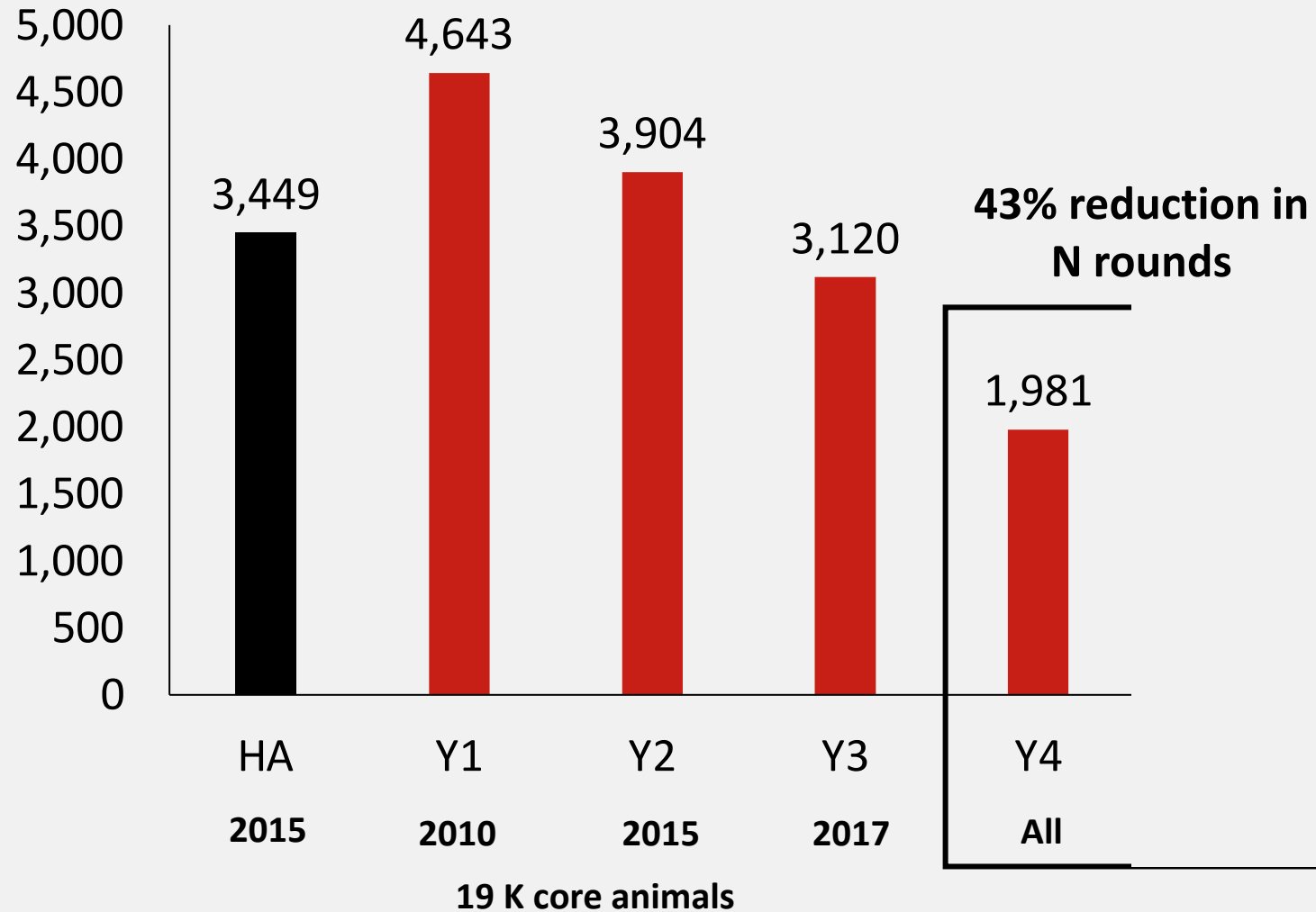
# Absolute changes in GEBV

## 2. Random sample over all animals, different sizes

Scenario	N core	BW (SDa= 5.4)		WW (SDa= 31)		PWG (SDa= 28)	
		Mean	Max	Mean	Max	Mean	Max
S1	10 K	0.02	1.31	0.03	1.18	0.02	1.07
Y4	19 K	0.01	1.27	0.02	0.89	0.01	0.86
S2	25 K	0.01	0.82	0.02	1.24	0.01	1.07
S3	30 K	0.01	1.09	0.02	0.90	0.01	0.97
S4	35 K	0.01	1.07	0.02	1.09	0.01	0.77

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

# Convergence



# 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

# Acknowledgements



**Kelli Retallick**  
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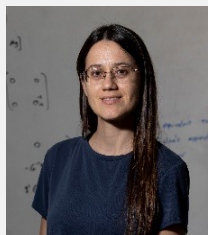
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# QUESTIONS/CONTACT

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# 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