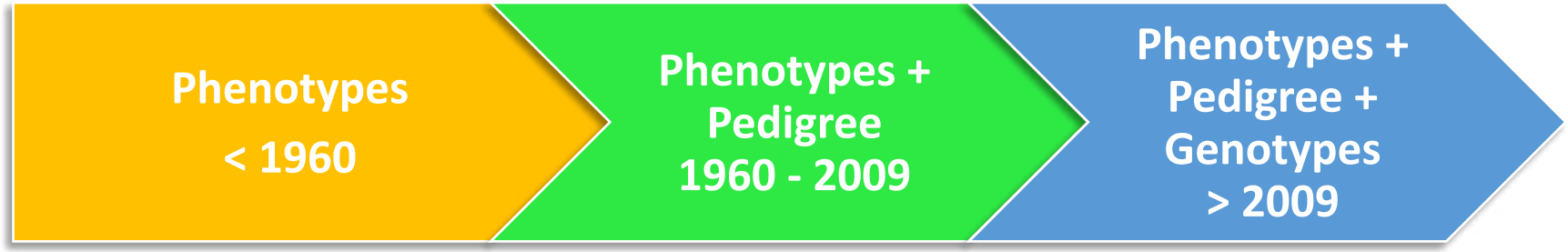
# Status of genomic selection in poultry

**Daniela Lourenco**

November 6, 2024


UNIVERSITY OF
GEORGIA
College of Agricultural & Environmental Sciences
*Animal Breeding and Genetics Group*

# Artificial selection over the years

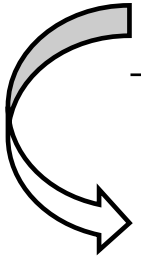



Increase the Genetic Gain

# Genomic Selection 15 years ago

**Dairy Cattle**

| | Age (yrs) | $Net Merit | Accuracy |
|---|---|---|---|
| Freddie | 4 | 918 | 83 |
| Al | 1 | 914 | 82 |
| Russell | 1 | 854 | 81 |
| Alan | 1 | 841 | 82 |
| O-Man | 10 | 778 | 99 |



40k daughters with records
Semen price: $40/unit
Income: > $5 million/year

"Lower accuracy for young genomic bulls almost prevented this technology from being adopted!"

Adapted from VanRaden (2009)

# Changes after genomics - dairy

- > 2x after genomics for Holsteins

J. Dairy Sci. 106:1110–1129
https://doi.org/10.3168/jds.2022-22205


**Changes in genetic trends in US dairy cattle since the implementation of genomic selection**

F. L. Guinan,[1]* G. R. Wiggans,[2] H. D. Norman,[2] J. W. Dürr,[2] J. B. Cole,[3] C. P. Van Tassell,[4] I. Misztal,[1] and D. Lourenco[1]

8.0 to 2.2

5.0 to 2.2

# Changes after genomics - dairy

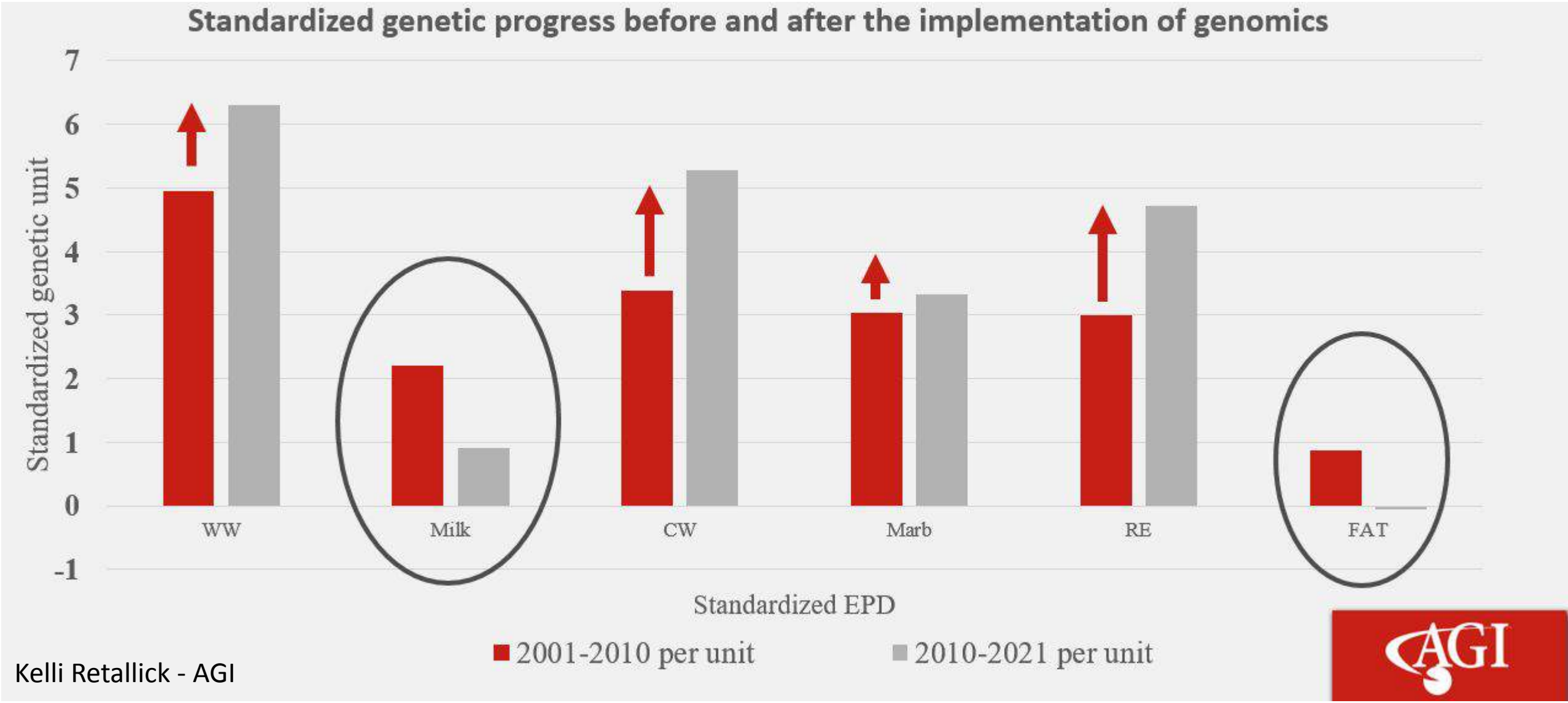
J. Dairy Sci. 106:1110–1129
https://doi.org/10.3168/jds.2022-22205


## Changes in genetic trends in US dairy cattle since the implementation of genomic selection

F. L. Guinan,[1]* G. R. Wiggans,[2] H. D. Norman,[2] J. W. Dürr,[2] J. B. Cole,[3] C. P. Van Tassell,[4] I. Misztal,[1] and D. Lourenco[1]

- Adoption: 2013 vs 2009
- Genotypes: 16k vs. 5.5M

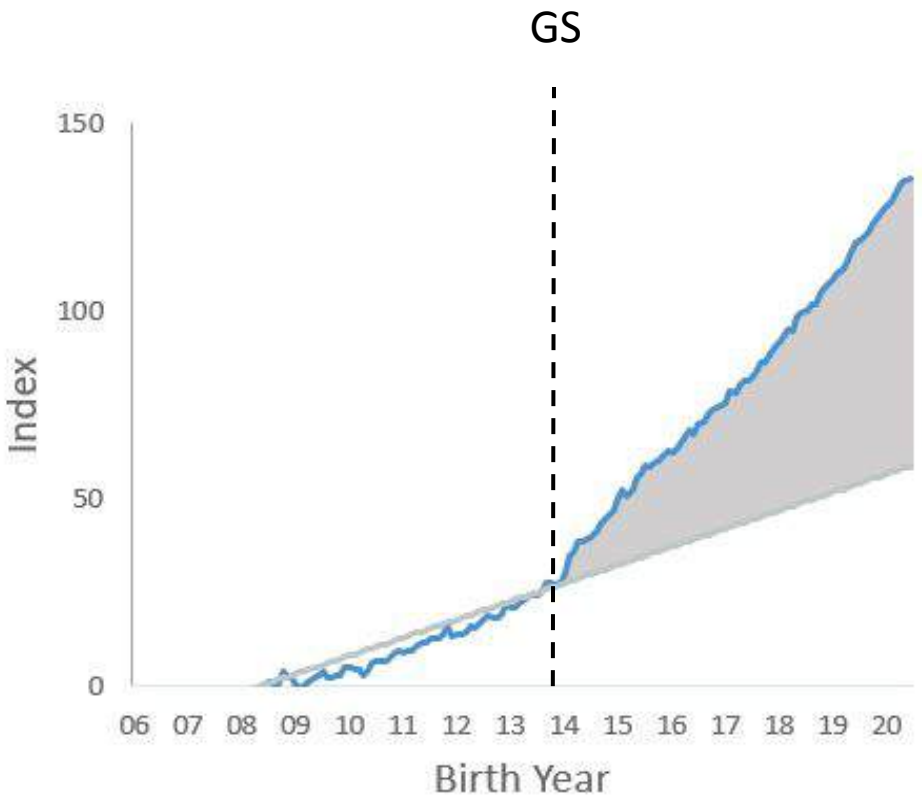
# Changes after genomics - beef



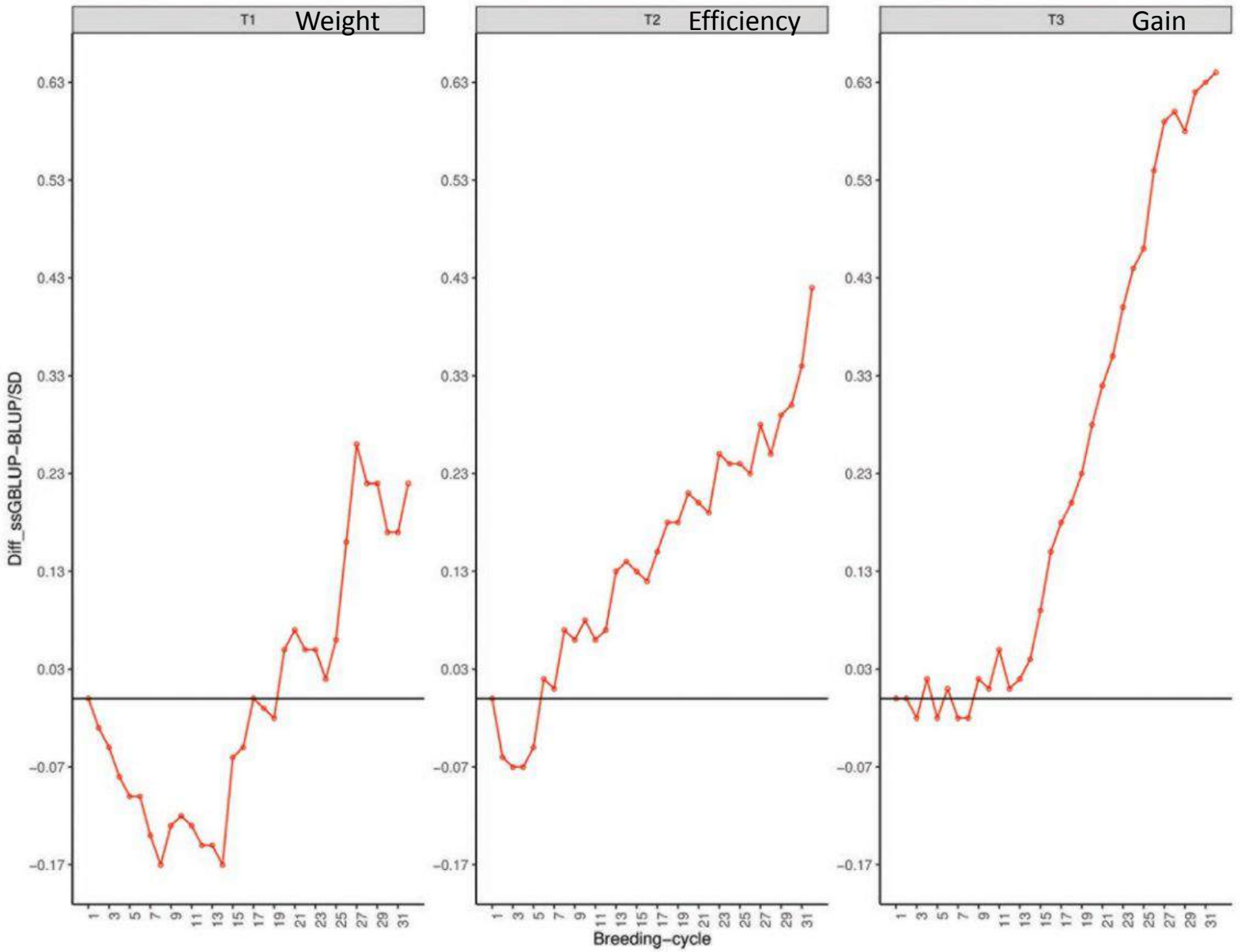

Kelli Retallick - AGI

# Changes after genomics - Pigs

PIC



# Genomics vs non-genomic - Poultry




JOURNAL ARTICLE

**Detecting effective starting point of genomic selection by divergent trends from best linear unbiased prediction and single-step genomic best linear unbiased prediction in pigs, beef cattle, and broilers**

Rostam Abdollahi-Arpanahi, Daniela Lourenco, Ignacy Misztal

*Journal of Animal Science*, Volume 99, Issue 9, September 2021, skab243, https://doi.org/10.1093/jas/skab243

- Difference (in SD) between ssGBLUP and BLUP

# BLUP vs ssGBLUP

- BLUP

Henderson (1949 - 1976)

$$\begin{bmatrix} \mathbf{X'X} & \mathbf{X'W} \\ \mathbf{W'X} & \mathbf{W'W}+\mathbf{A}^{-1}\frac{\sigma_e^2}{\sigma_u^2} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\mathbf{u}} \end{bmatrix} = \begin{bmatrix} \mathbf{X'y} \\ \mathbf{W'y} \end{bmatrix}$$

Pedigree

Phenotypes

- Single-step GBLUP (ssGBLUP)

Aguilar et al. (2010)
Christensen and Lund (2010)

$$\begin{bmatrix} \mathbf{X'X} & \mathbf{X'W} \\ \mathbf{W'X} & \mathbf{W'W}+\mathbf{H}^{-1}\frac{\sigma_e^2}{\sigma_u^2} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\mathbf{u}} \end{bmatrix} = \begin{bmatrix} \mathbf{X'y} \\ \mathbf{W'y} \end{bmatrix}$$

Phenotypes

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} \end{bmatrix}$$

Pedigree  Genomic  Pedigree for genotyped

# Single-step GBLUP

- Animals


J. Dairy Sci. 93:743–752
doi:10.3168/jds.2009-2730
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***Hot topic:*** **A unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation of Holstein final score**[1]

I. Aguilar,*†[2] I. Misztal,* D. L. Johnson,‡ A. Legarra,§ S. Tsuruta,* and T. J. Lawlor#


J Anim Sci. 2015 Jun;93(6):2653-62. doi: 10.2527/jas.2014-8836.

**Genetic evaluation using single-step genomic best linear unbiased predictor in American Angus**

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, I Misztal

PMID: 26115253 DOI: 10.2527/jas.2014-8836


J. Dairy Sci. 105
https://doi.org/10.3168/jds.2021-21505
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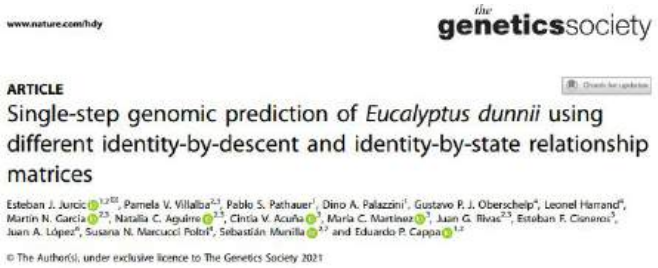
**Multibreed genomic evaluation for production traits of dairy cattle in the United States using single-step genomic best linear unbiased predictor**

A. Cesarani,[1]* D. Lourenco,[1] S. Tsuruta,[1] A. Legarra,[2] E. L. Nicolazzi,[3] P. M. VanRaden,[4] and I. Misztal[1]

- Plants


www.nature.com/hdy

the geneticssociety

ARTICLE

Single-step genomic prediction of *Eucalyptus dunnii* using different identity-by-descent and identity-by-state relationship matrices

Esteban J. Jurcic, Pamela V. Villalba, Pablo S. Pathauer, Dino A. Palazzini, Gustavo P. J. Oberschelp, Leonel Harrand, Martín N. García, Natalia C. Aguirre, Cintia V. Acuña, María C. Martínez, Juan G. Rivas, Esteban F. Cisneros, Juan A. López, Susana N. Marcucci Poltri, Sebastián Munilla and Eduardo P. Cappa

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The Plant Genome OPEN ACCESS

ORIGINAL RESEARCH | Open Access

Making the most of all data: Combining non-genotyped and genotyped potato individuals with HBLUP

Salej Sood, Zibei Lin, Brittney Caruana, Anthony T. Slater, Hans D. Daetwyler

First published: 29 September 2020 | https://doi.org/10.1002/tpg2.20056

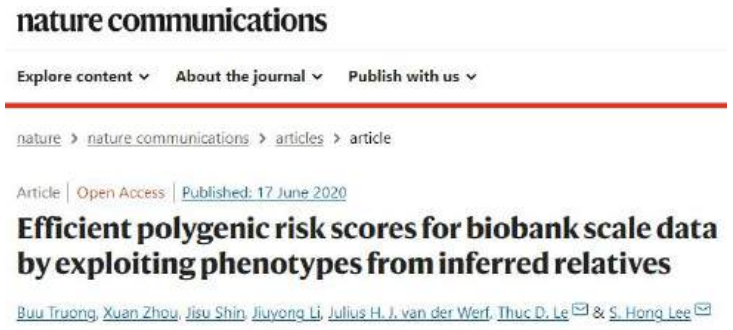

OXFORD G3 Genes | Genomes | Genetics

G3, 2021, 11(10), jkab253
DOI: 10.1093/g3journal/jkab253
Advance Access Publication Date: 16 July 2021
Multiparental Populations

**Single-step genomic BLUP enables joint analysis of disconnected breeding programs: an example with *Eucalyptus globulus* Labill.**

Andrew N. Callister, Ben P. Bradshaw, Stephen Elms, Ross A. W. Gillies, Joanna M. Sasse, and Jeremy T. Brawner

- Humans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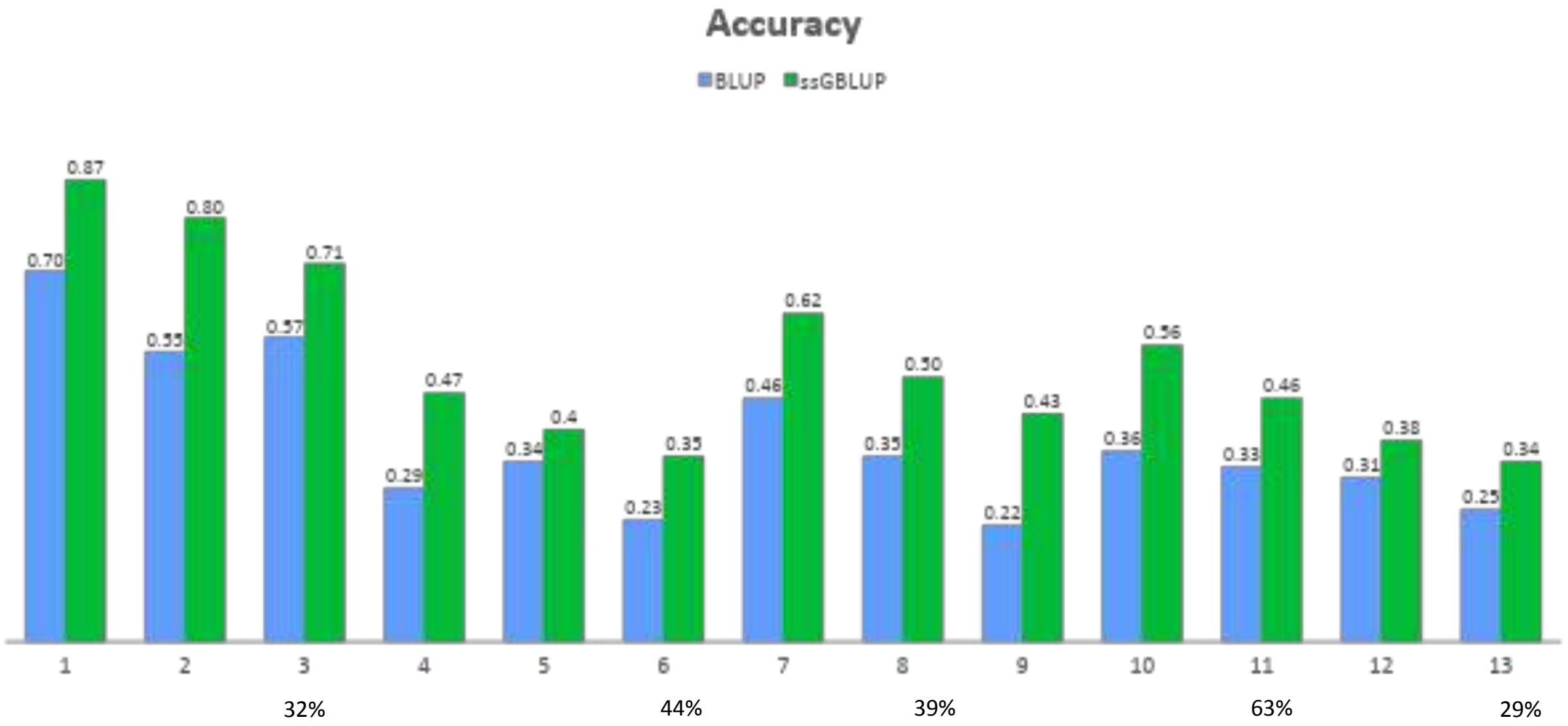
Article | Open Access | Published: 17 June 2020

**Efficient polygenic risk scores for biobank scale data by exploiting phenotypes from inferred relatives**

Buu Truong, Xuan Zhou, Jisu Shin, Jiuyong Li, Julius H. J. van der Werf, Thuc D. Le & S. Hong Lee

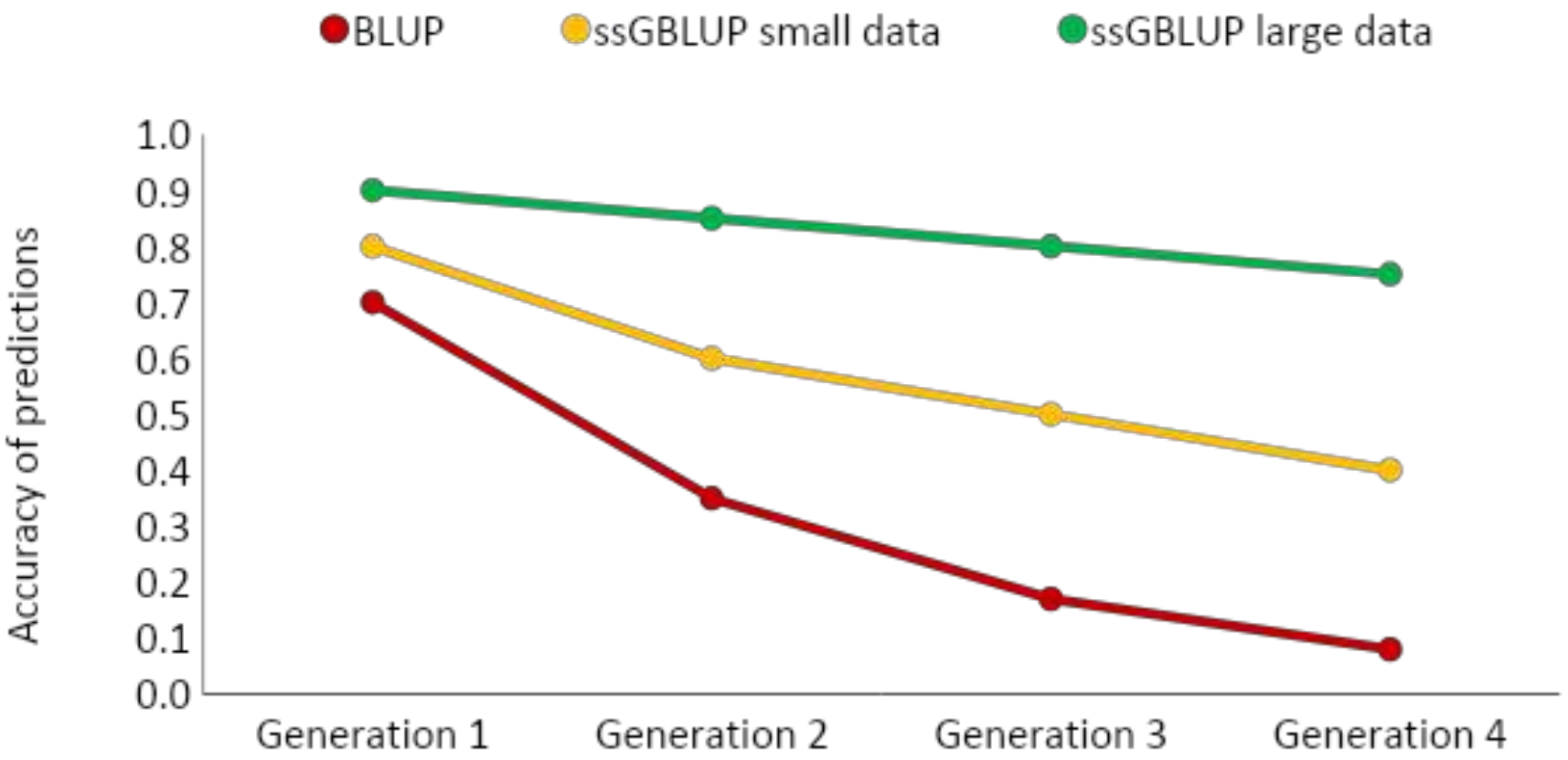
# Accuracy in ssGBLUP vs. BLUP




32% 44% 39% 63% 29%

Tsuruta et al. (2021) Lourenco et al. (2018) Lourenco et al. (2016) Lourenco et al. (2015) Garcia et al. (2018)

# Persistence of accuracy in broilers




JOURNAL ARTICLE

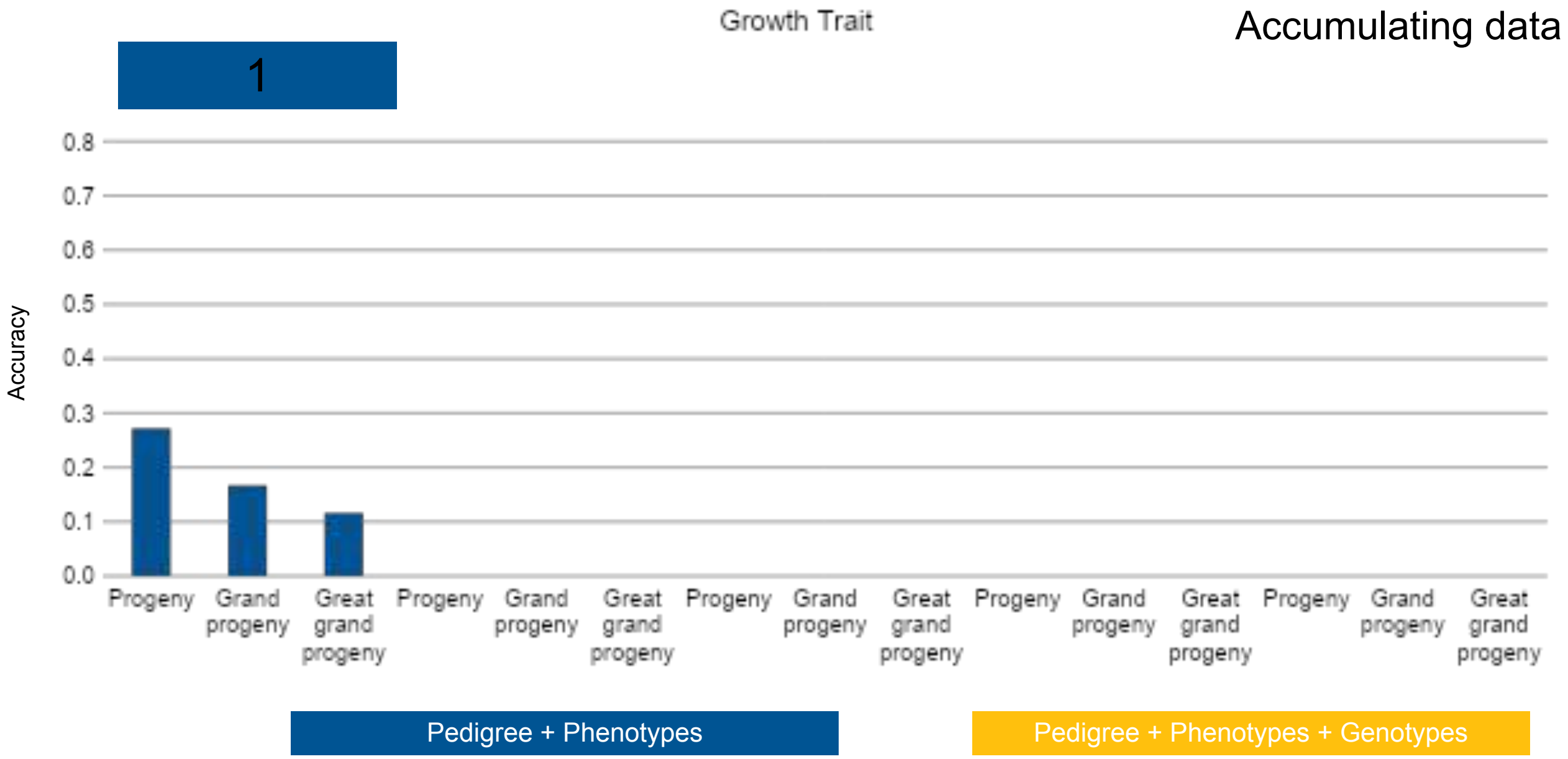
**Investigating the persistence of accuracy of genomic predictions over time in broilers**

Jorge Hidalgo ✉, Daniela Lourenco, Shogo Tsuruta, Yutaka Masuda, Vivian Breen, Rachel Hawken, Matias Bermann, Ignacy Misztal

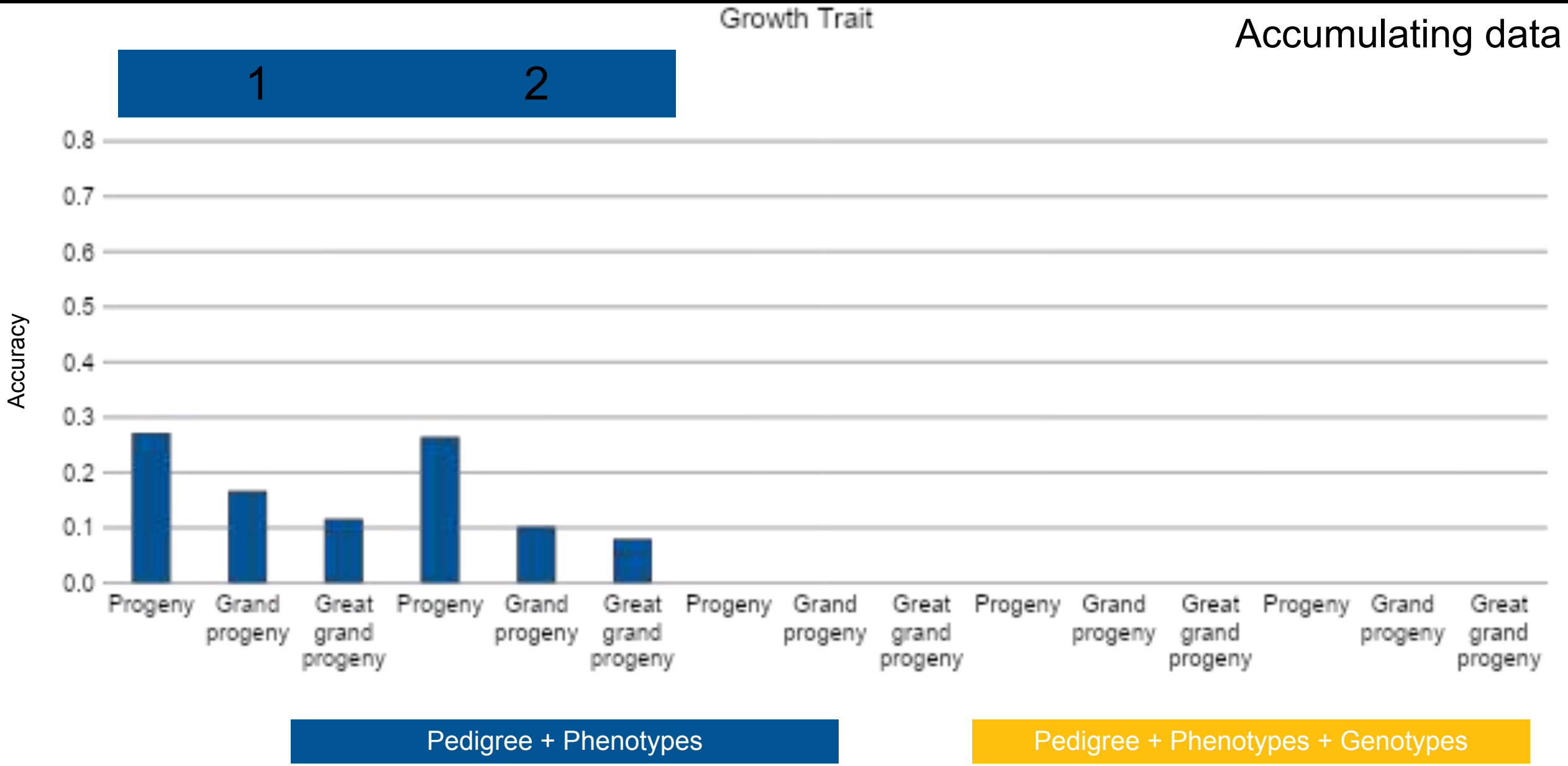
*Journal of Animal Science*, Volume 99, Issue 9, September 2021, skab239, https://doi.org/10.1093/jas/skab239

- 1.2M birds from 7 years
- 150K genotyped

# Trends for accuracy – validation per generation

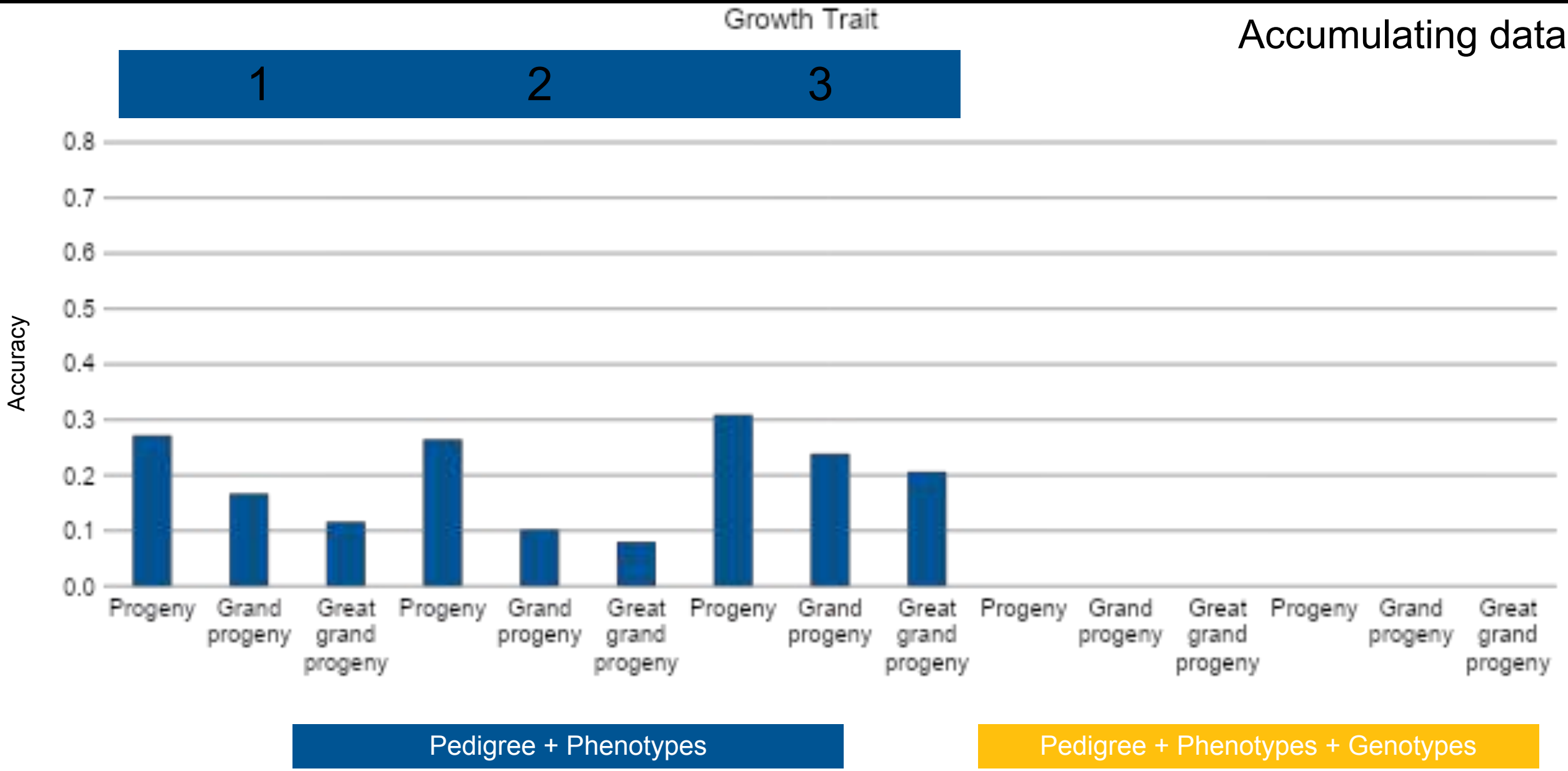


# Trends for accuracy – validation per generation

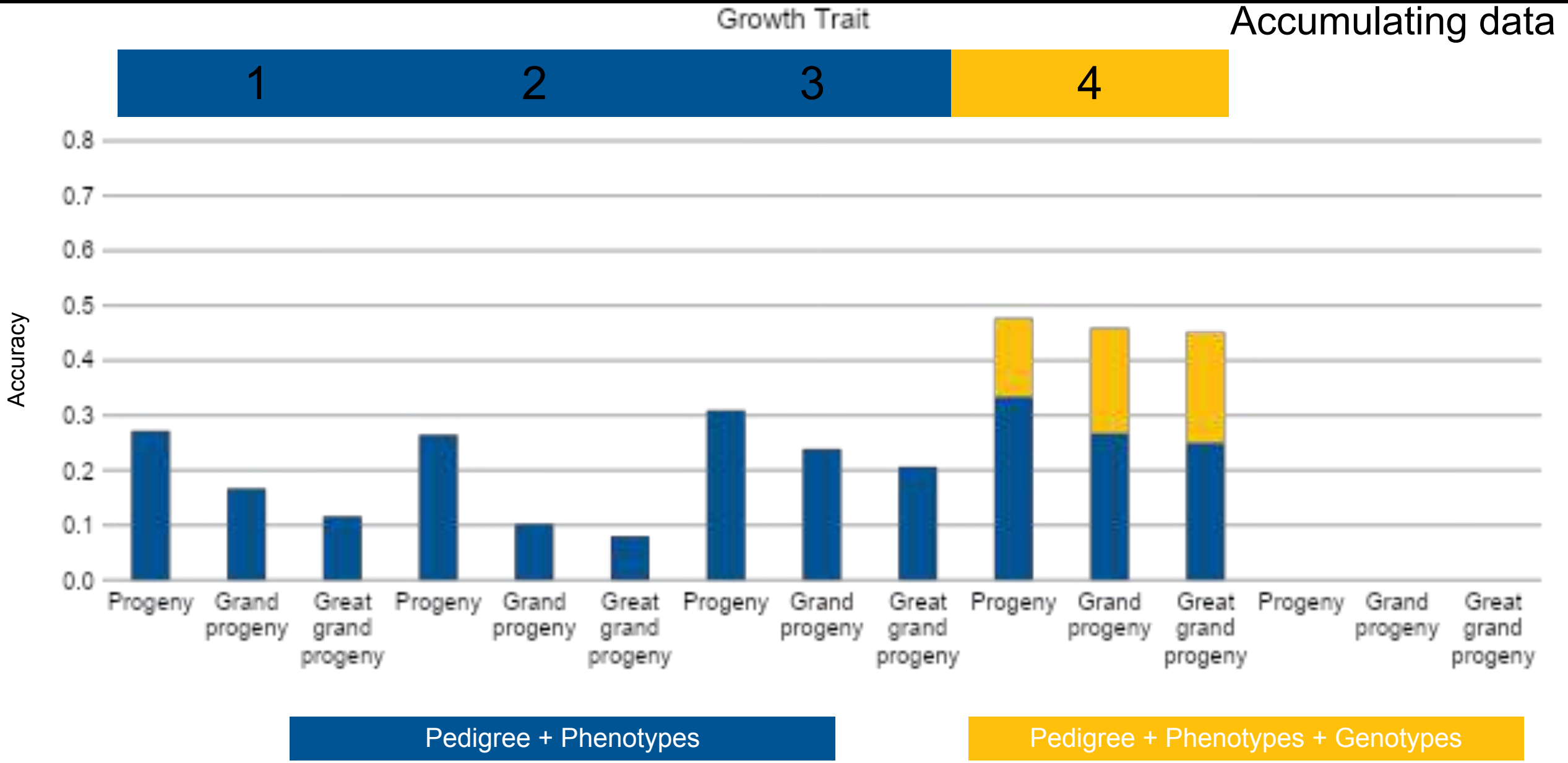


# Trends for accuracy – validation per generation

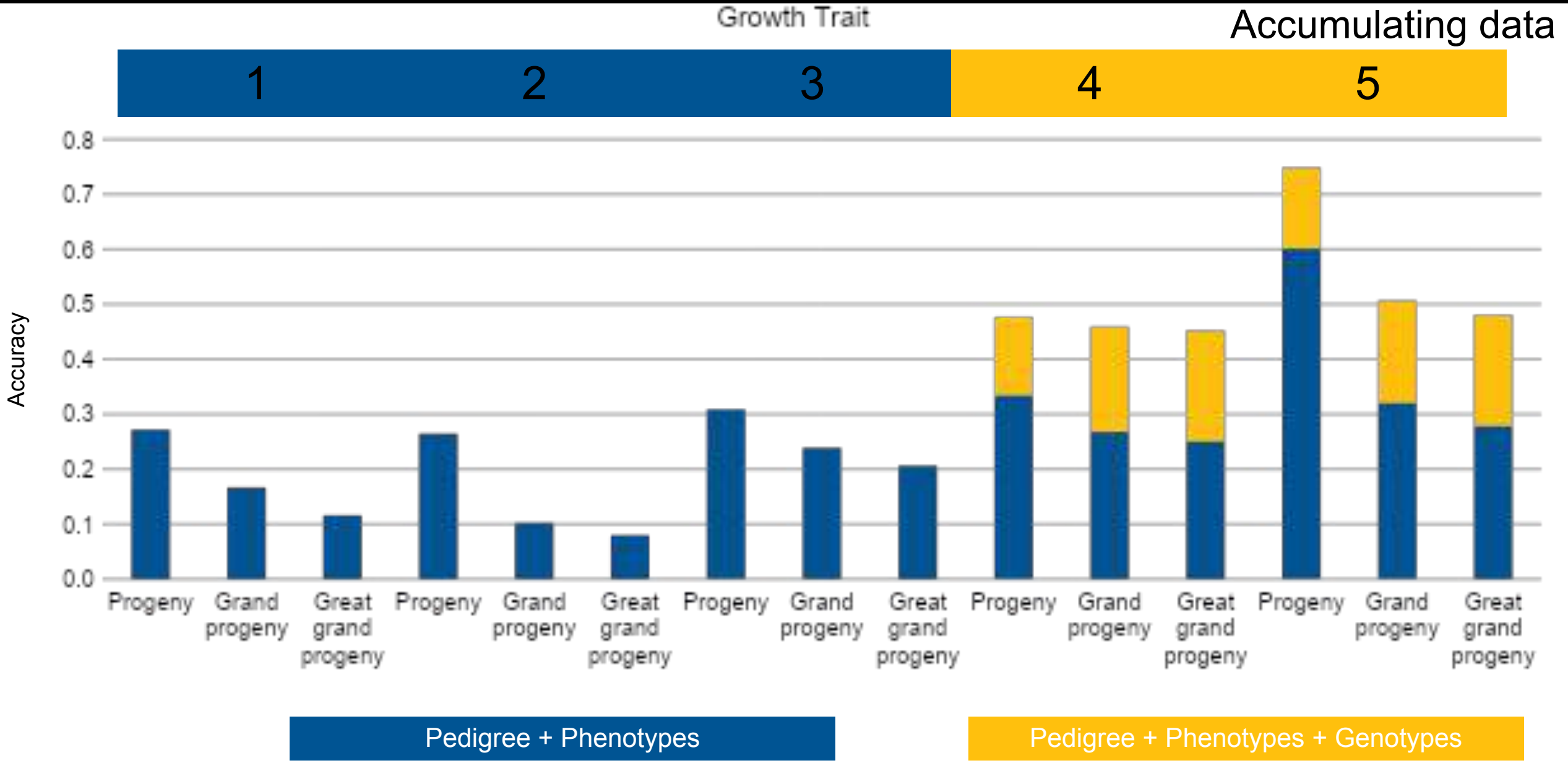
Accumulating data



# Trends for accuracy – validation per generation

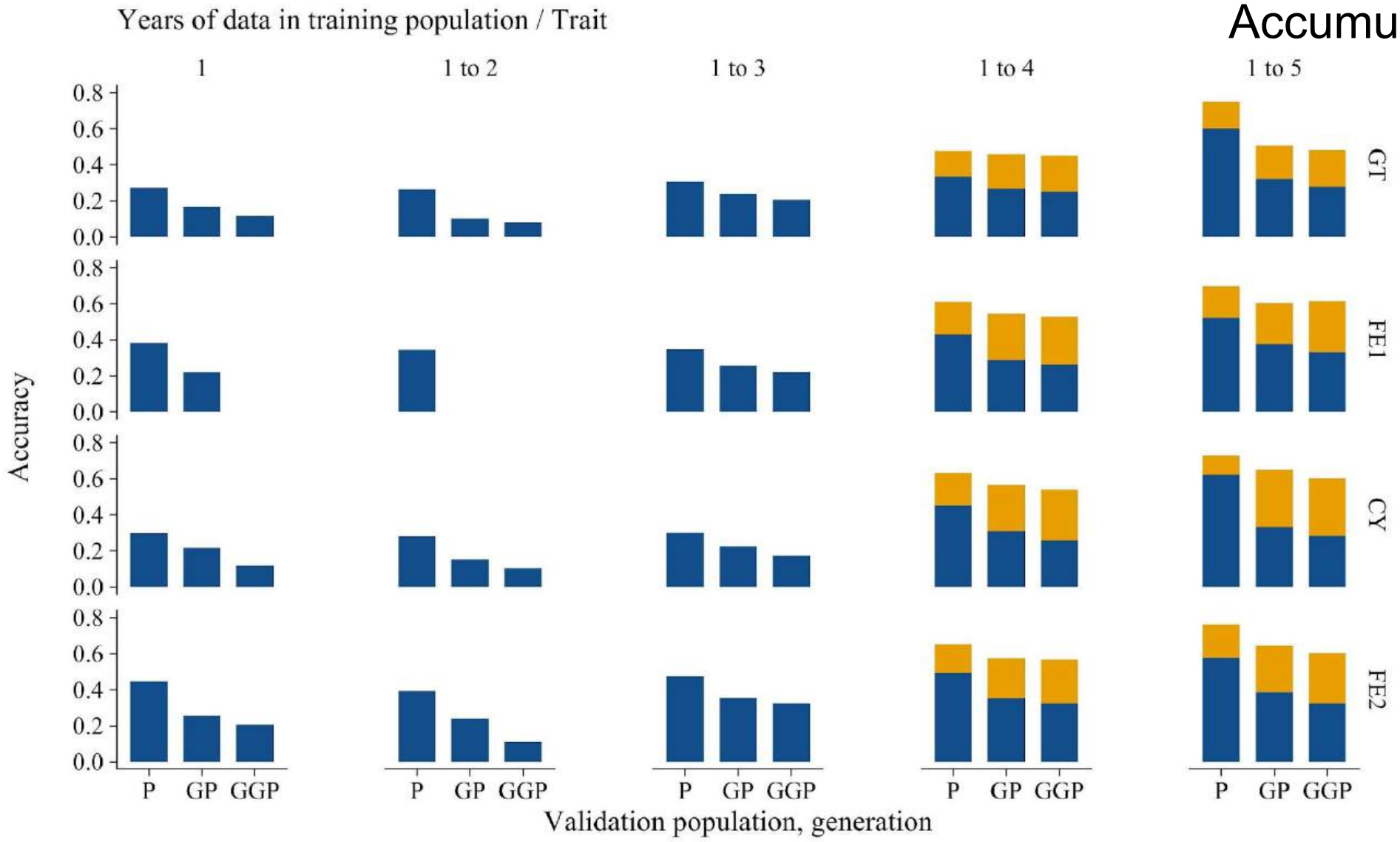


# Trends for accuracy – validation per generation



# Trends for accuracy – validation per generation

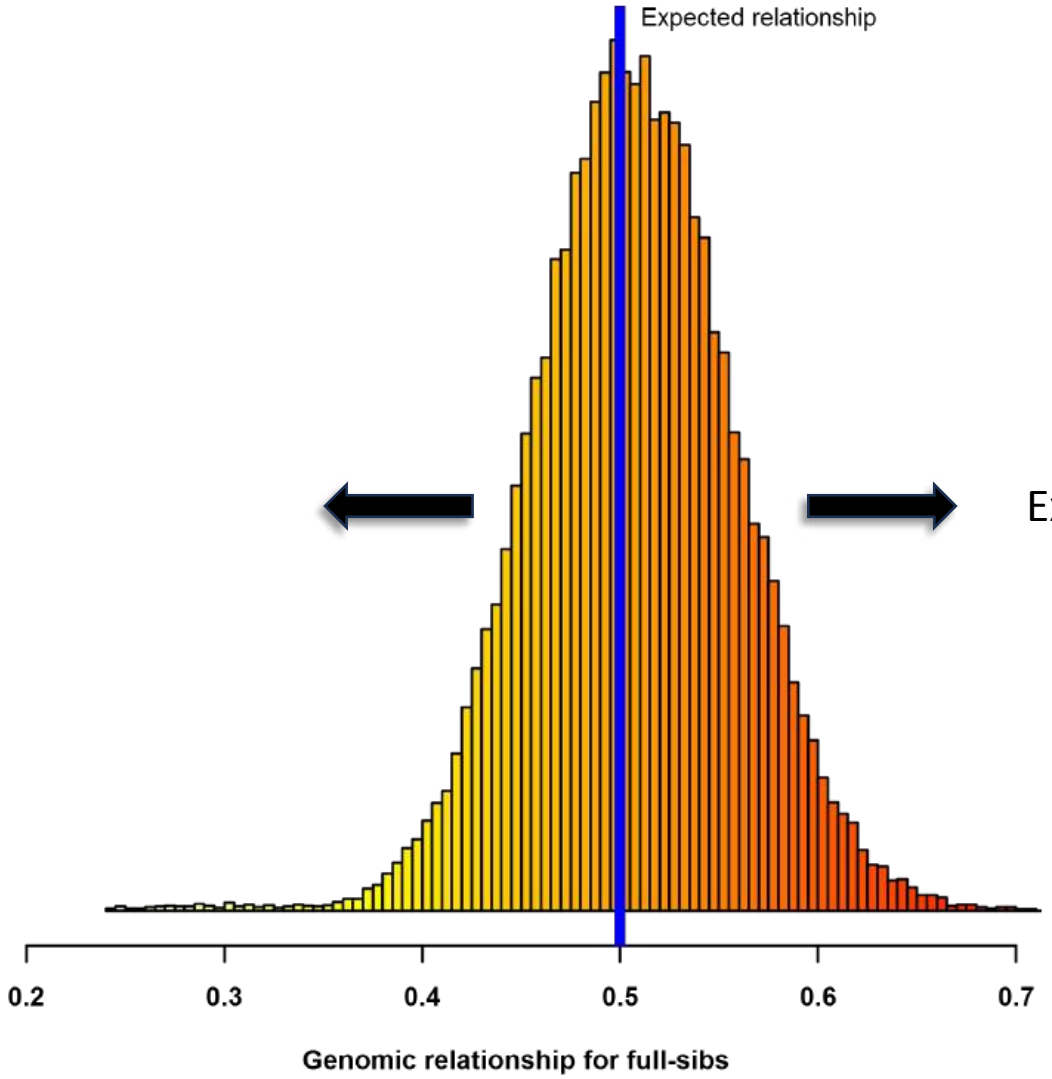
Accumulating data




Pedigree + Phenotypes

Pedigree + Phenotypes + Genotypes

# Why greater gain for poultry?




- Several factors
  - Large full-sib groups
  - Pedigree relationships = 0.5
  - Genomic relationships = 0.25 to 0.72

Extra information

Adapted from Lourenco et al. (2015)

# Why greater gain for poultry?

$$\Delta G = \frac{i\, r\, \sigma_a}{L} \times \delta$$

**Are we loosing anything by using genomics?**

# Are we loosing anything with genomics?

- Is genetic variability decreasing?

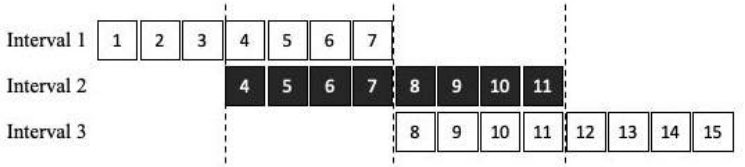
JOURNAL ARTICLE

**Temporal dynamics of genetic parameters and SNP effects for performance and disorder traits in poultry undergoing genomic selection**

Jennifer Richter ✉, Jorge Hidalgo, Fernando Bussiman, Vivian Breen, Ignacy Misztal, Daniela Lourenco

*Journal of Animal Science*, Volume 102, 2024, skae097, https://doi.org/10.1093/jas/skae097

- 55 mating groups



# Are we loosing anything with genomics?

- Is heritability decreasing?

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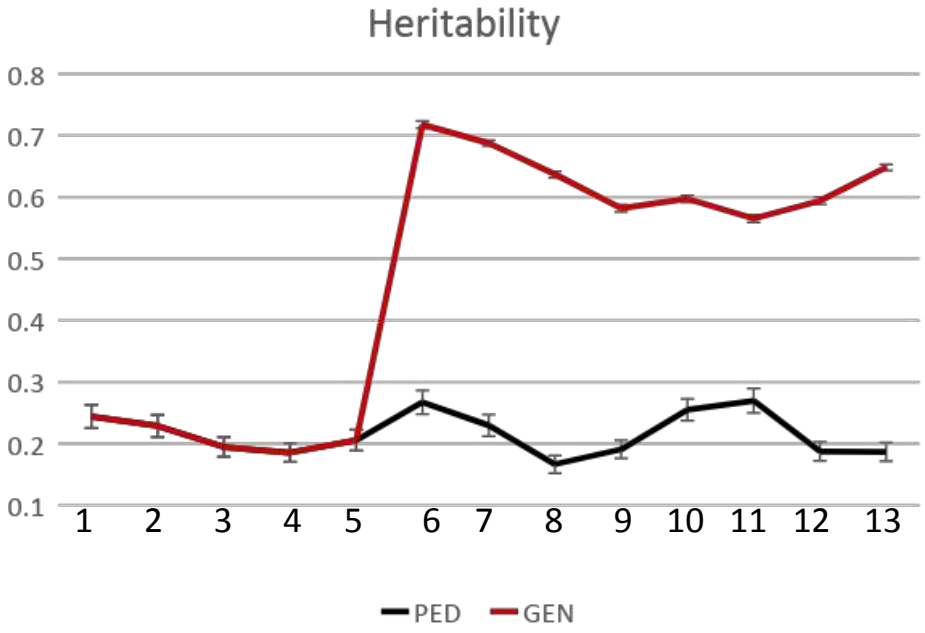
*Journal of Animal Science*, Volume 102, 2024, skae097, https://doi.org/10.1093/jas/skae097

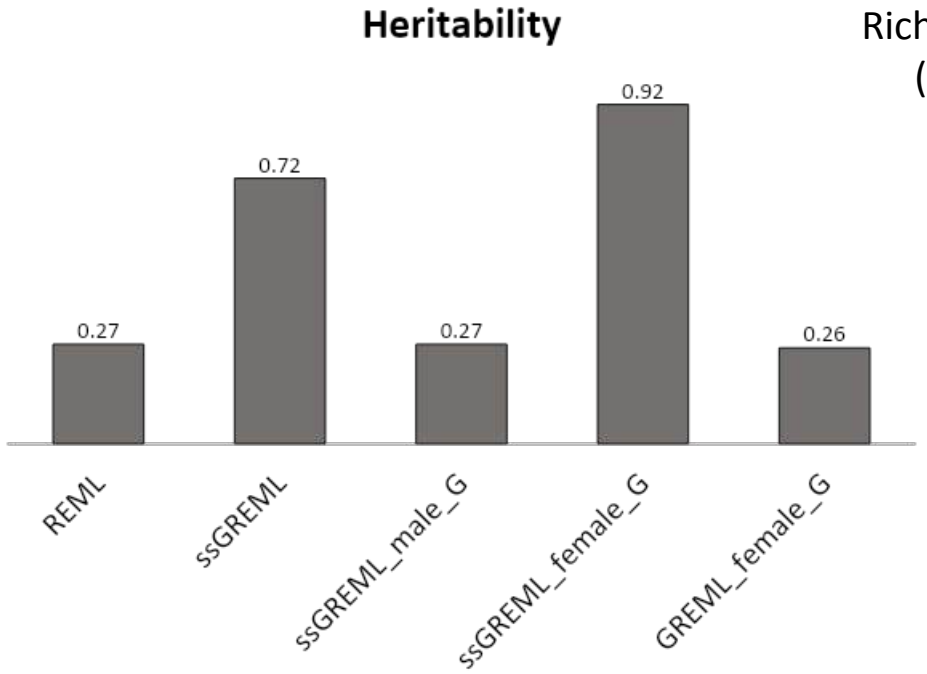
- Really different
- Selective genotyping

# $h^2$ with and without genomics

- Heritability for body weight




Richter et al. (2024)




- Selection of females to genotype

| Group | SD |
|---|---|
| Non-genotyped females | 1.00 |
| Genotyped females | 0.63 |
| Non-genotyped males | 1.00 |
| Genotyped males | 0.89 |

# Are we loosing anything with genomics?

- Are genetic correlations changing?

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# Correlation of SNP effects

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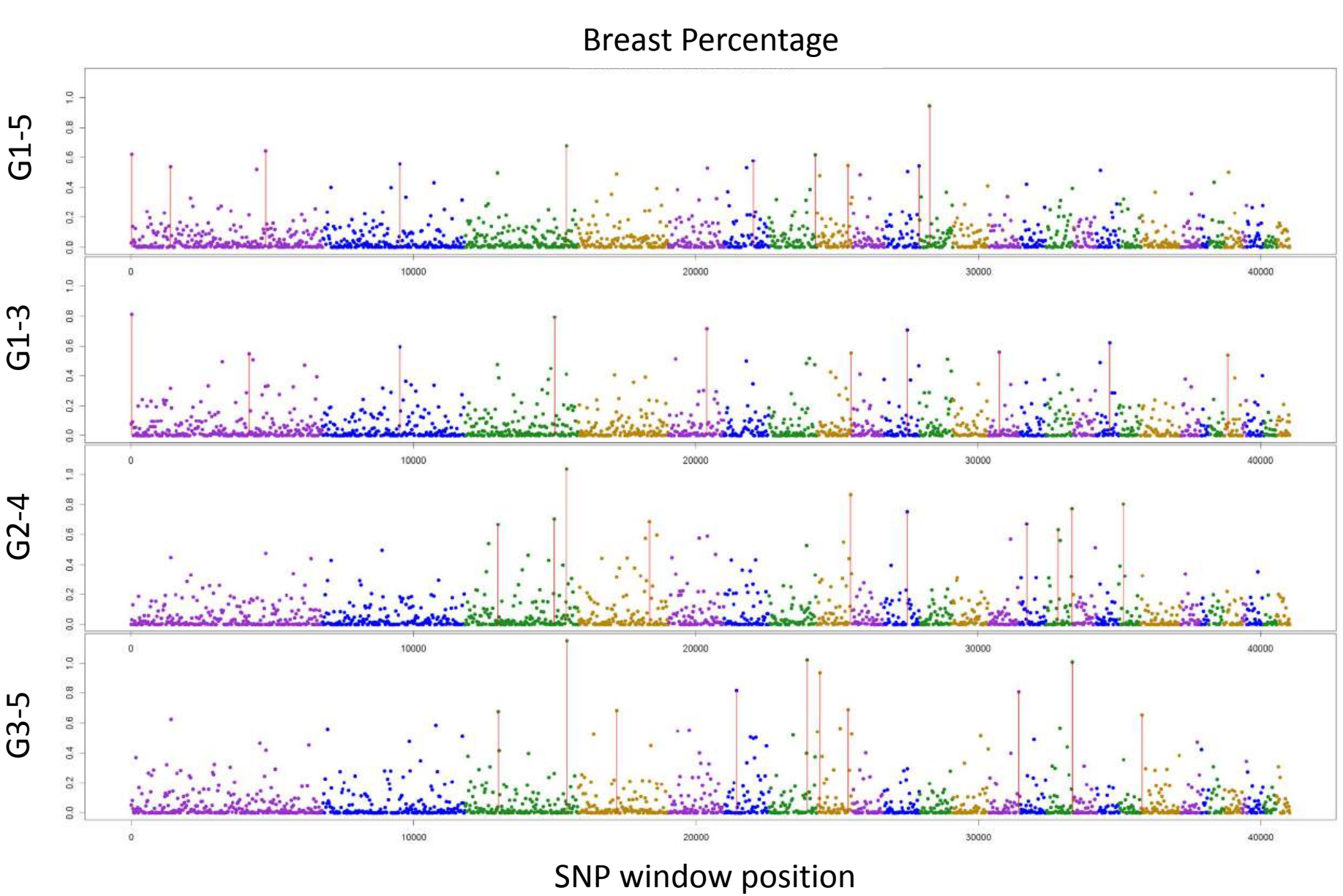
*Journal of Animal Science*, Volume 102, 2024, skae097,
https://doi.org/10.1093/jas/skae097

- Lower correlations
  - Genetic distance
  - Magnitude of genetic interactions
  - Distribution of allele frequencies

# Variance explained by SNP

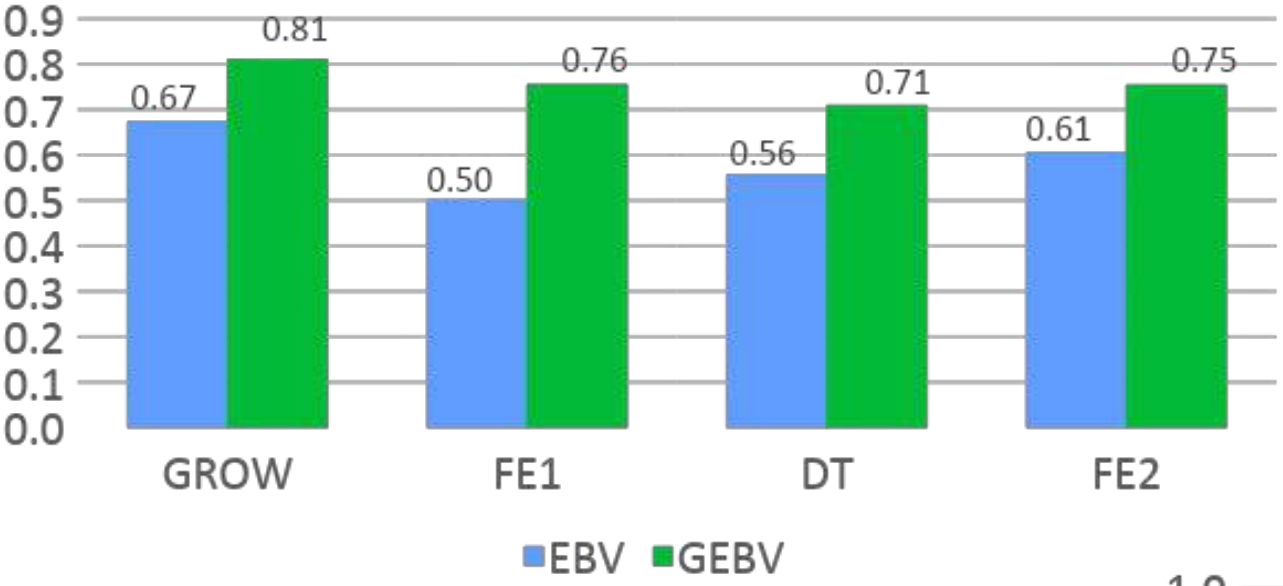



frontiers in GENETICS
ORIGINAL RESEARCH ARTICLE

Changes in variance explained by top SNP windows over generations for three traits in broiler chicken

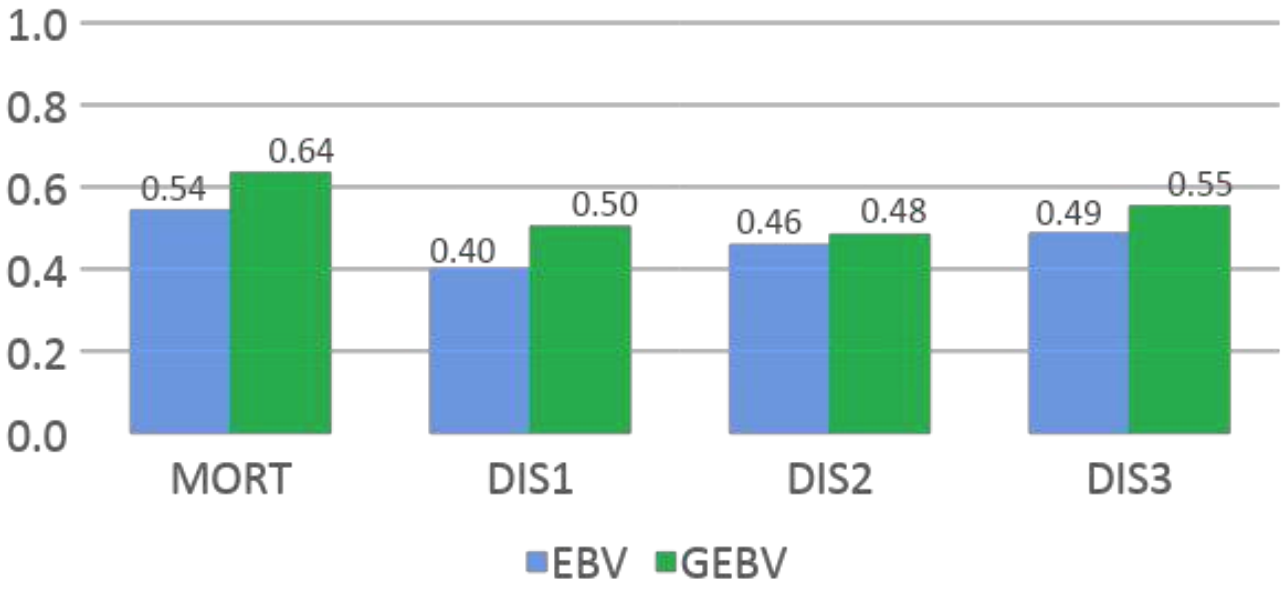
Breno de Oliveira Fragomeni[1]*, Ignacy Misztal[1], Daniela Lino Lourenco[1], Ignacio Aguilar[2], Ronald Okimoto[3] and William M. Muir[4]

# Accuracy of production and health




Zhang et al. (2018)

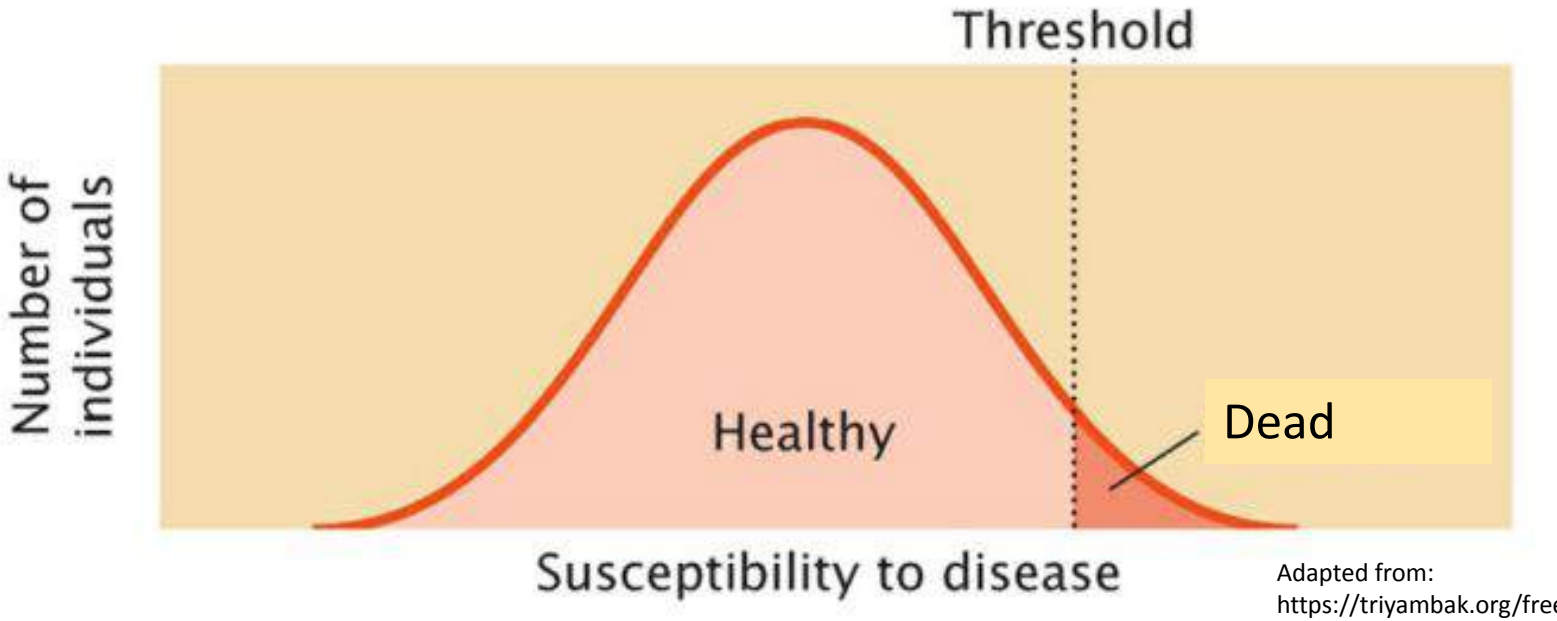
+ 17 points with genomics




+ 7 points with genomics

# Reviewing the definition of mortality

- Mortality is a complex trait
  - Different genetic and biological factors in different life stages




Adapted from:
https://triyambak.org/free-resources/csir-net-life-sciences/pointer/2065

JOURNAL ARTICLE

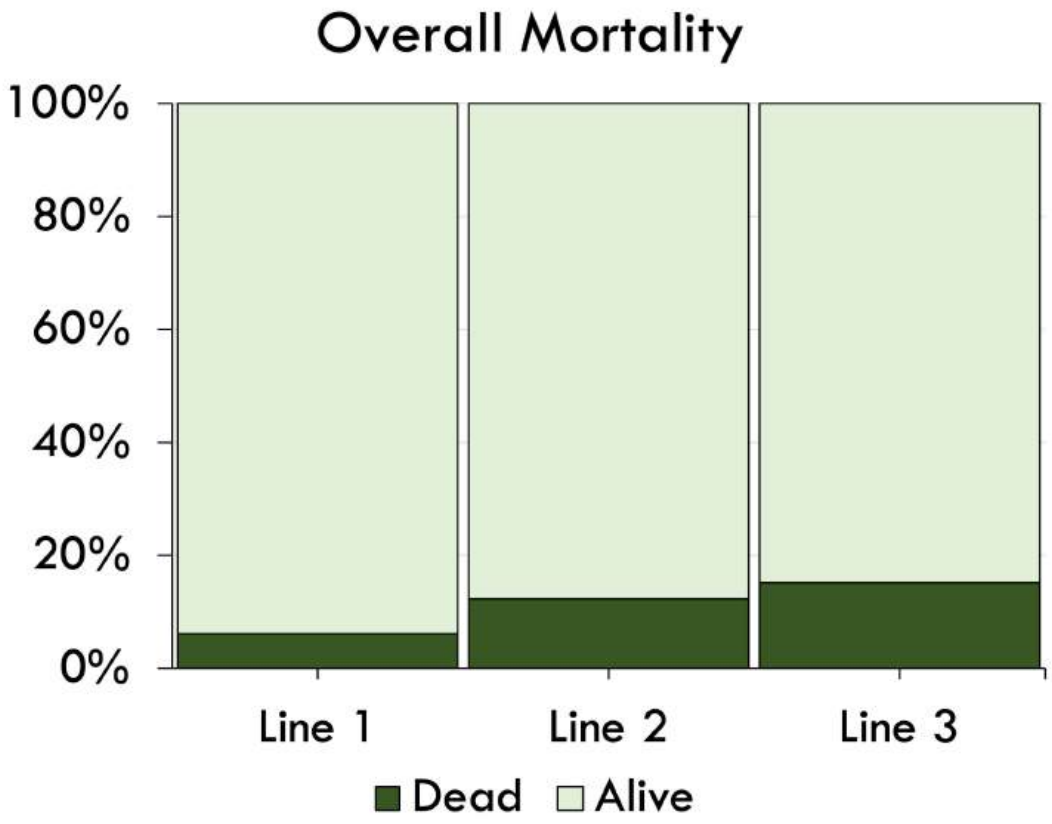
**Reviewing the definition of mortality in broiler chickens and its implications in genomic evaluations**

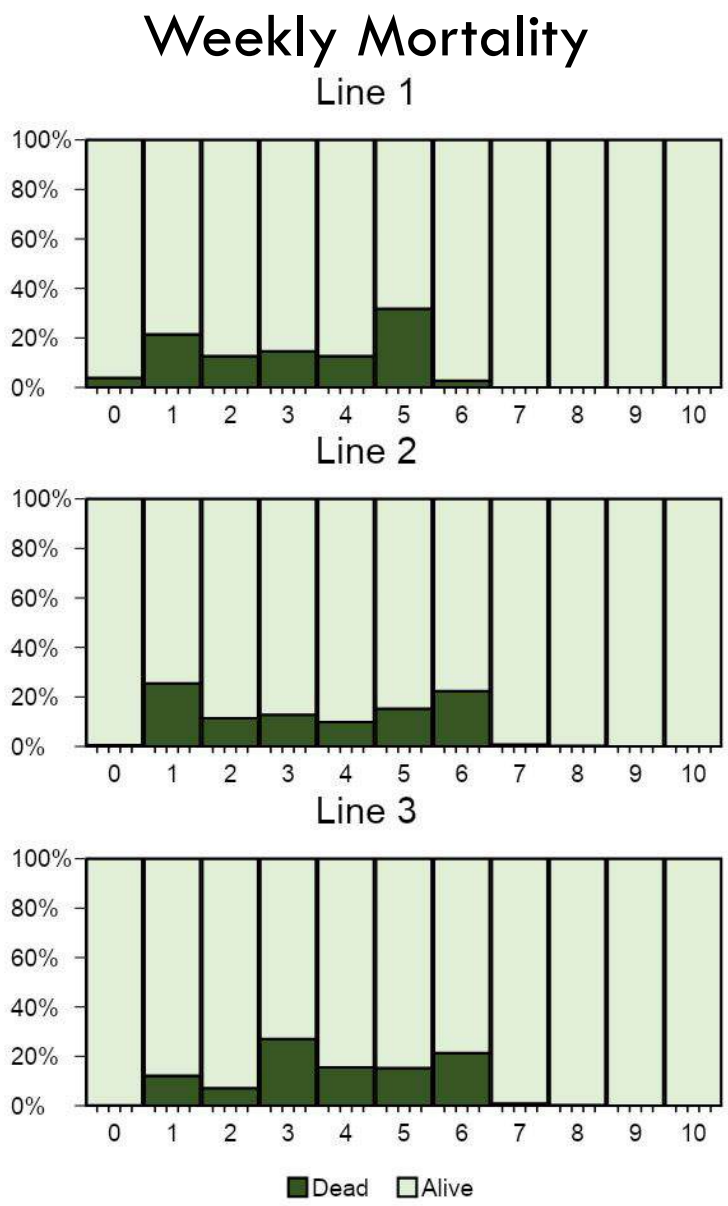
Jennifer Richter ✉, Fernando Bussiman, Jorge Hidalgo, Vivian Breen, Ignacy Misztal, Daniela Lourenco

*Journal of Animal Science*, Volume 102, 2024, skae190,
https://doi.org/10.1093/jas/skae190

- Overall mortality as a binary trait
  - Alive = 1
  - Dead = 2

# Incidence of mortality



# Redefining mortality

## Trait Definition



BMORT

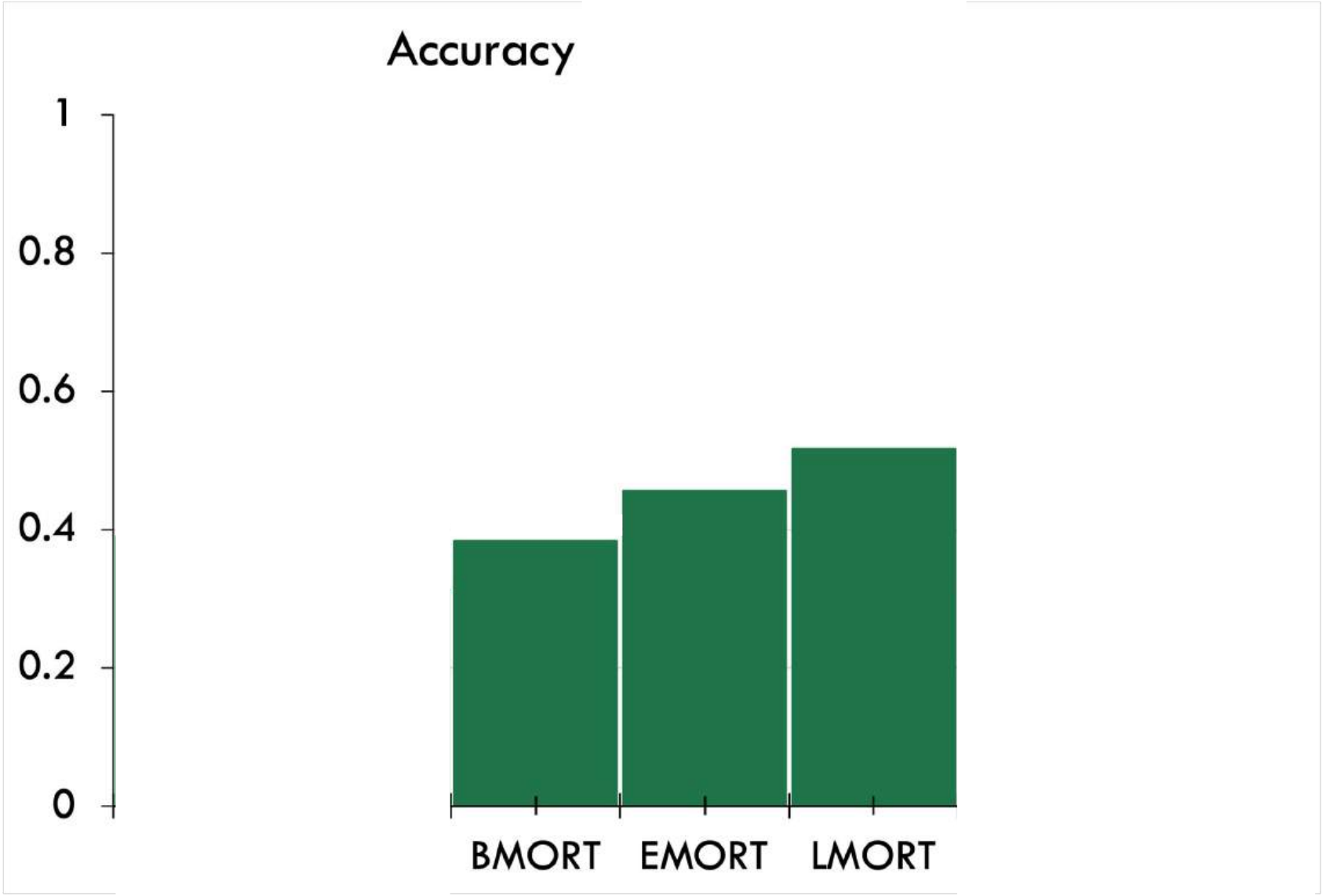
Died within first 6 weeks (1,2)


EMORT LMORT

Died within first 3 weeks (1,2)

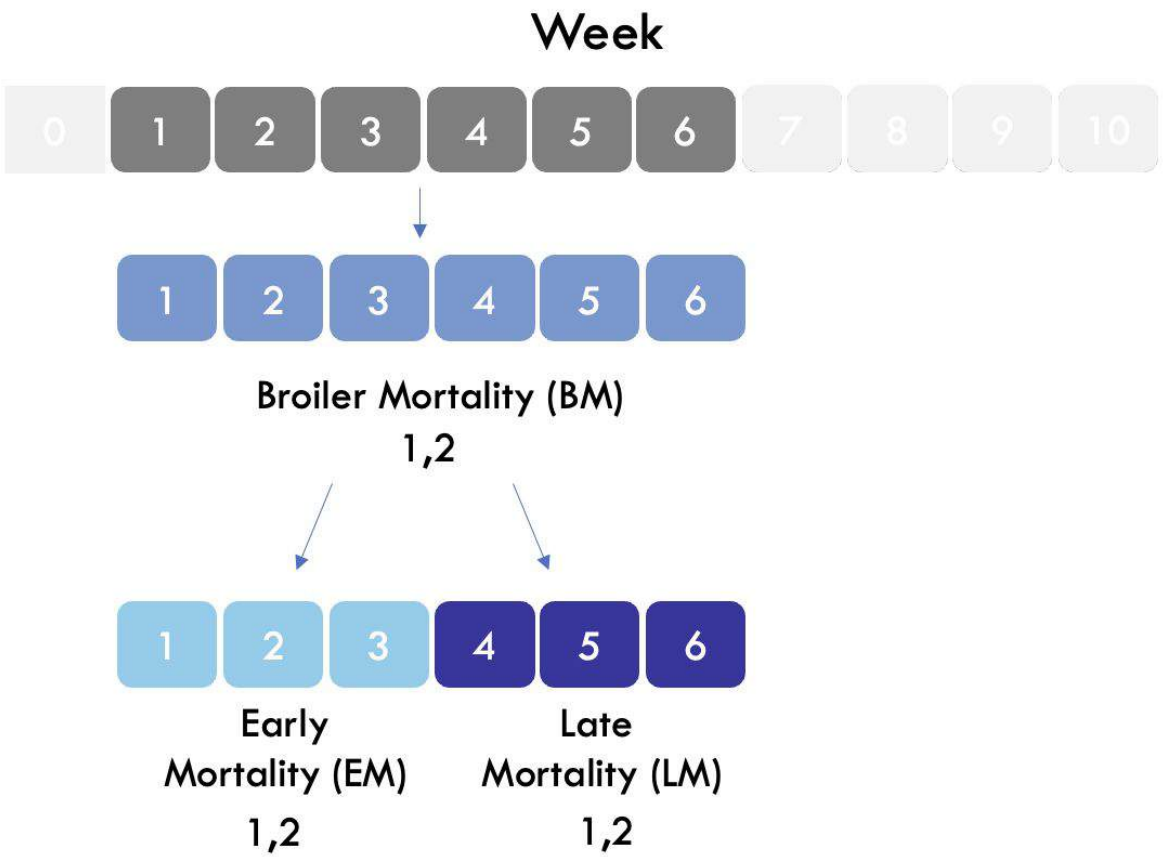
Died within last 3 weeks (1,2)

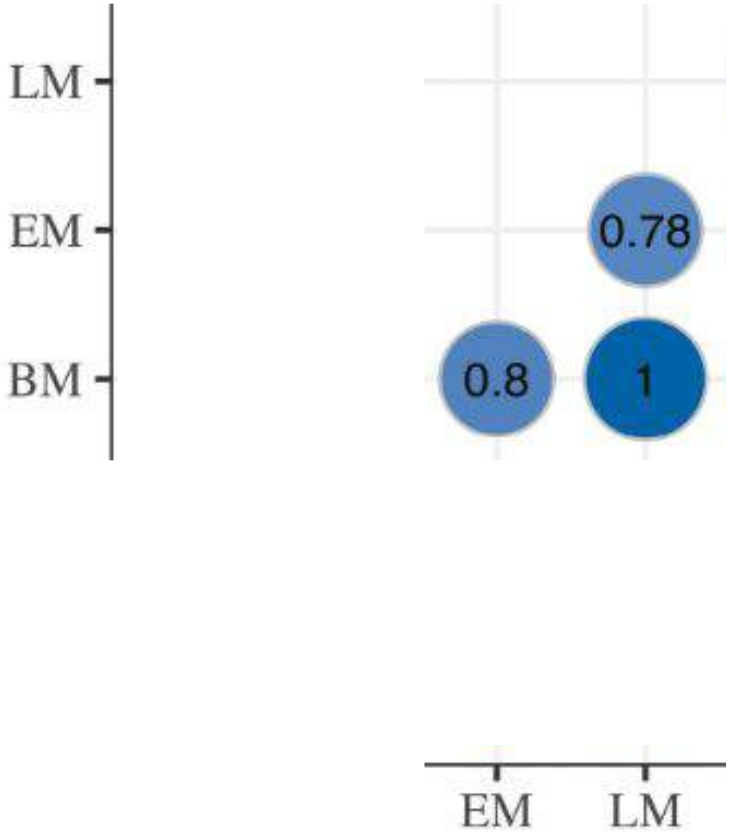
# Redefining mortality



# Early and late mortality

- Genetic correlations



# Early and late mortality

JOURNAL ARTICLE

**Reviewing the definition of mortality in broiler chickens and its implications in genomic evaluations**

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*Journal of Animal Science*, Volume 102, 2024, skae190, https://doi.org/10.1093/jas/skae190

- Having early and late mortality may lead to better selection against mortality

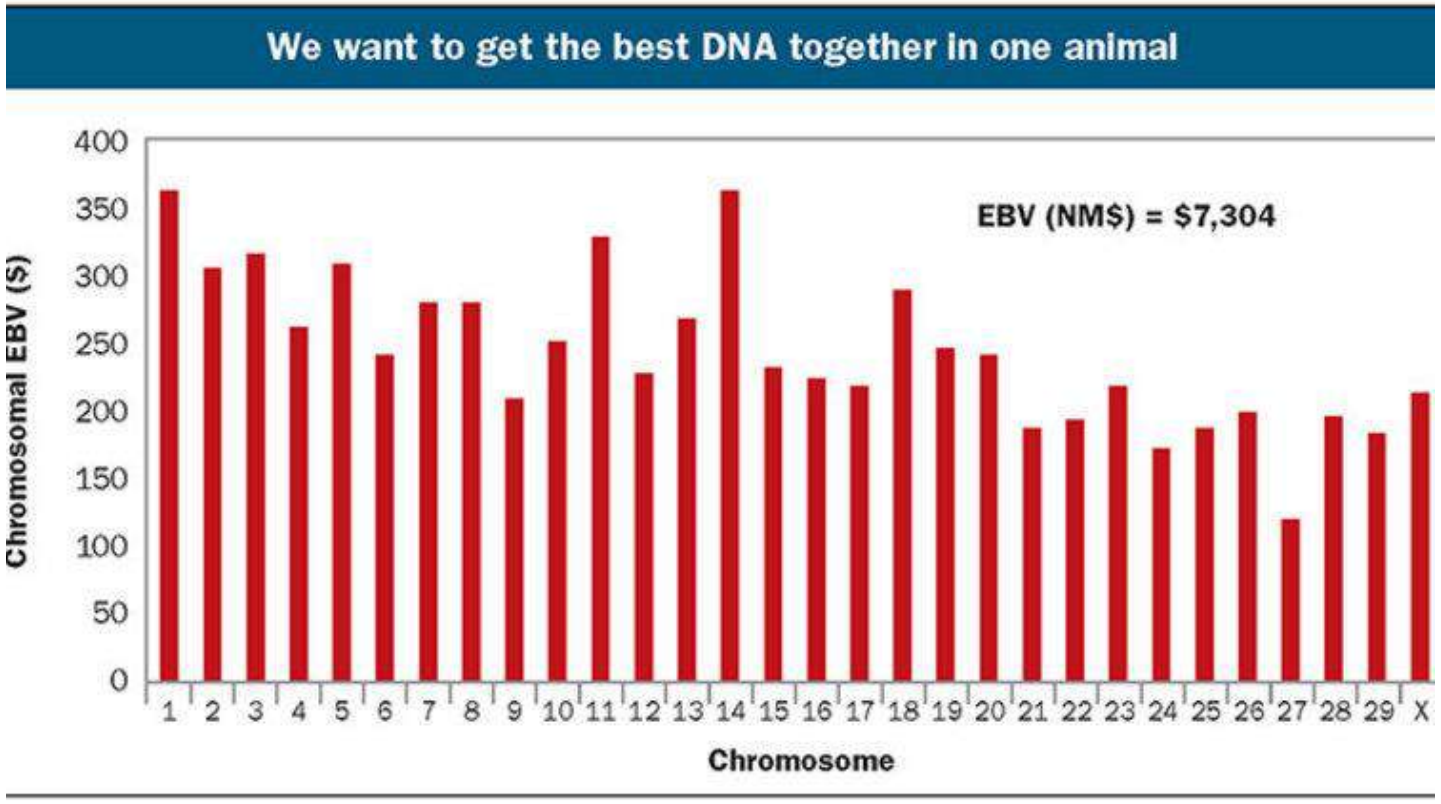
# Always looking for improvements

$$\Delta G = \frac{i\, r\, \sigma_a}{L}$$

- Redefining traits
- Refining selection indexes
- Using genomic information
  - Increase in accuracy and genetic gain
  - Success stories in poultry
  - Have we reached the limit of genomic selection?

# Have we reached the limit of GS?

**Best chromosomes in the Us Holstein population**



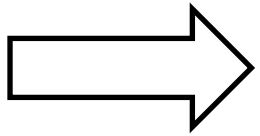

John Cole
(2019)

Sum of the effects of SNP
in each chromosome
for each animal

- Hypothetical animal based on chromosomal EBV: NM$ 7,304
- The top bull available for sale in 08/2024: NM$ 1,509 (born in 4/23)

# What is next?

- Whole-genome sequence
- Enviromics
- Metabolites
- Gut microbiome
- Phenomics
  - Self-tracking sensors and cameras



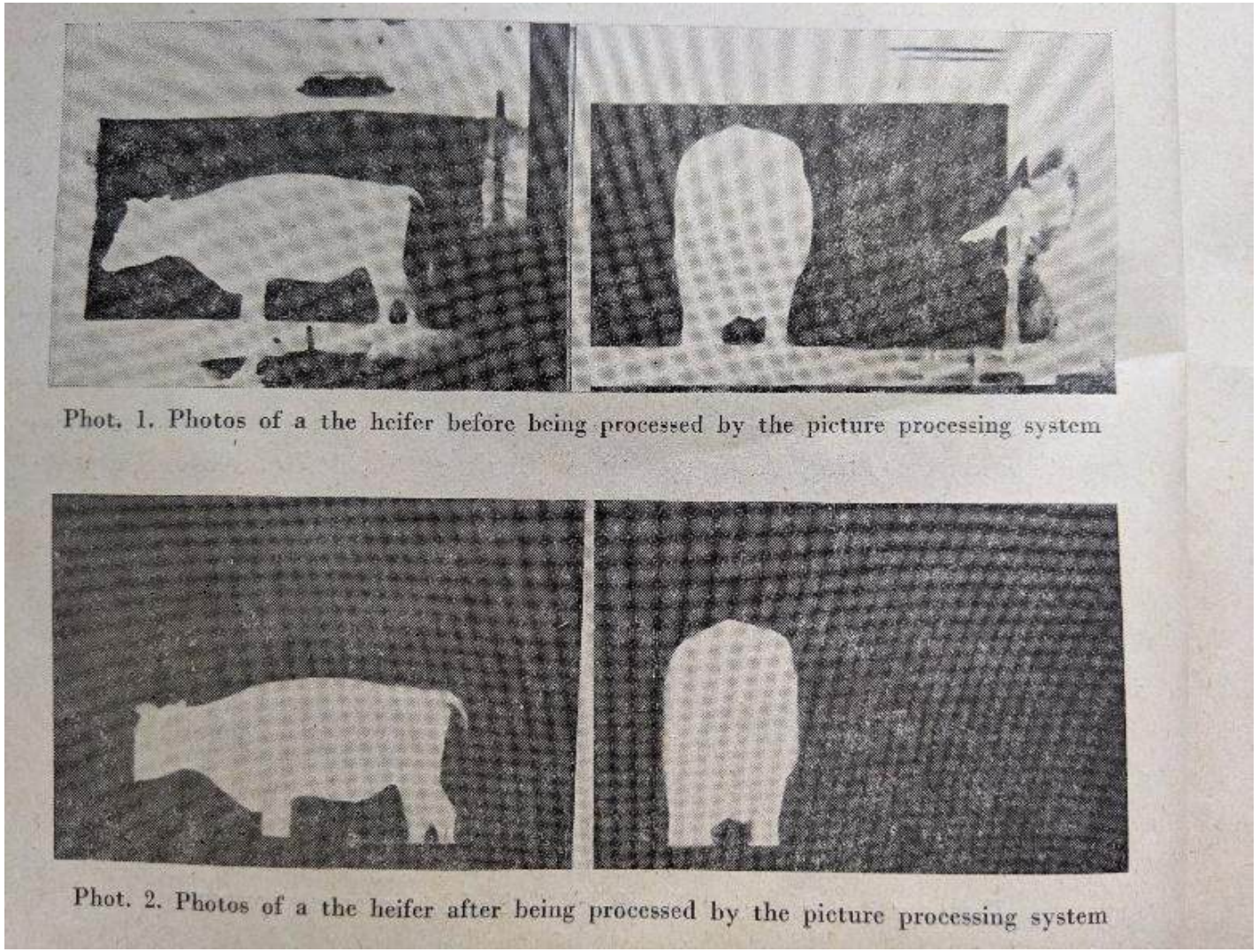
- More accurate EBV for many traits
- Improve farm animal populations

# Phenomics - are phenotypes important?

**Genomics**


**Phenotypes**

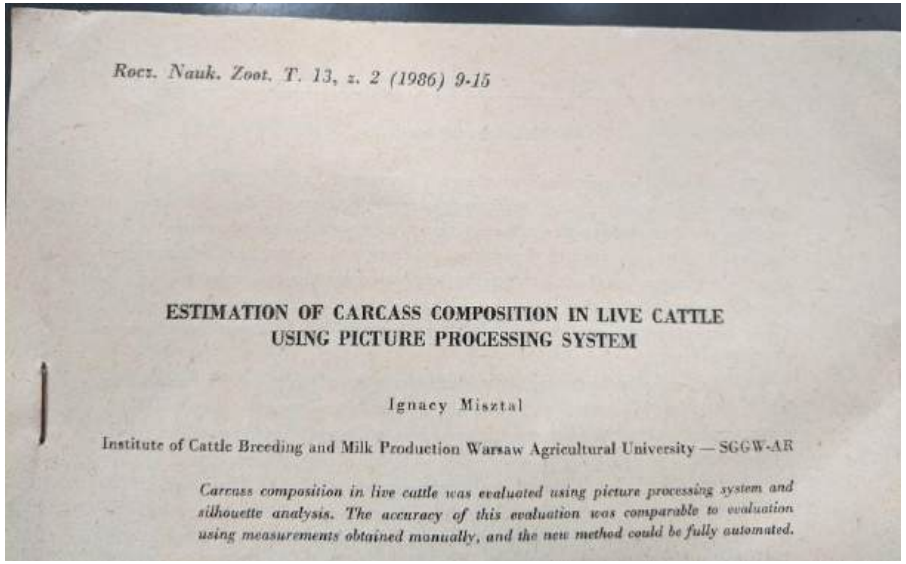
# Digital phenotypes – are they new?



Phot. 1. Photos of a the heifer before being processed by the picture processing system

Phot. 2. Photos of a the heifer after being processed by the picture processing system

Misztal (1986)



*Rocz. Nauk. Zoot. T. 13, z. 2 (1986) 9-15*

**ESTIMATION OF CARCASS COMPOSITION IN LIVE CATTLE USING PICTURE PROCESSING SYSTEM**

Ignacy Misztal

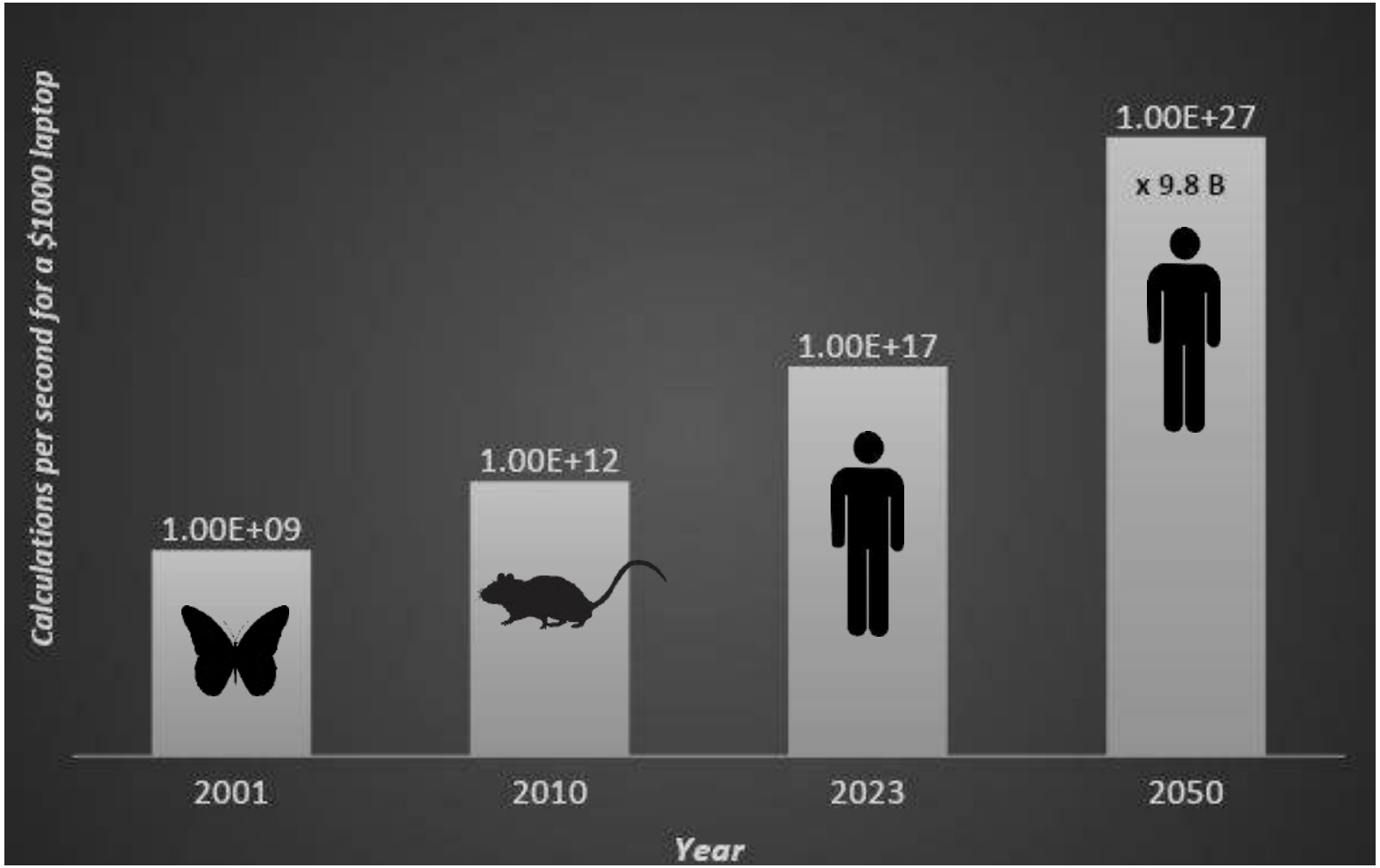
Institute of Cattle Breeding and Milk Production Warsaw Agricultural University — SGGW-AR

*Carcass composition in live cattle was evaluated using picture processing system and silhouette analysis. The accuracy of this evaluation was comparable to evaluation using measurements obtained manually, and the new method could be fully automated.*

# Digital phenotyping - decades apart

- Cameras and sensors
  - High-throughput phenotyping (phenomics): 24/7 collecting data
  - Feed intake, grazing behavior, temperature, gas emission, fertility, weight, size, …
- Machine learning (artificial intelligence)
  - Algorithms to automatically learn from the data and make predictions
  - Expensive to teach a machine (computing resources and time)
  - Image recognition comes with an appetite for computing power

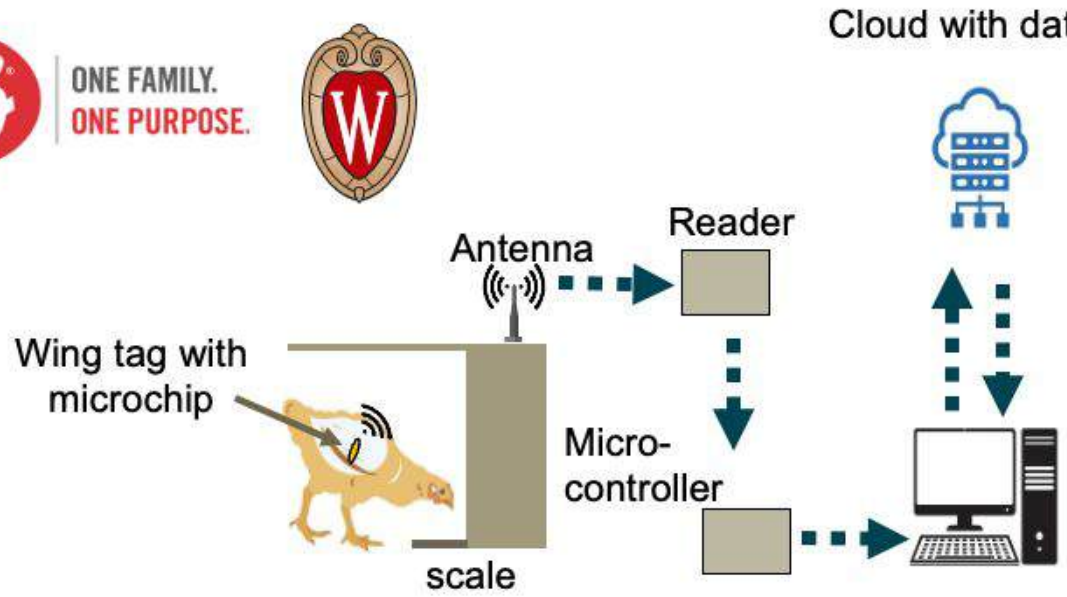
# $1000 of computing power

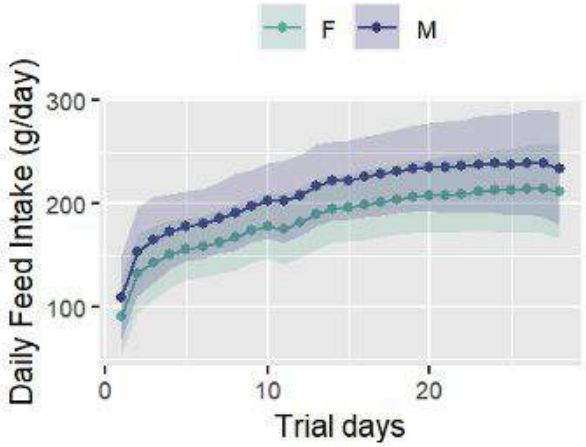



Adapted from: Peter Diamandis https://www.youtube.com/watch?v=7XrbzlR9QmI

# Feed efficiency in broilers

## Measuring Feed-Efficiency in Broilers using RFID Systems




| Trait | $h^2 \pm$ s.e |
|---|---|
| Feed Conversion Rate | 0.25 ± 0.01 |
| Residual Feed Intake | 0.32 ± 0.02 |
| Daily Feed Intake | 0.31 ± 0.01 |

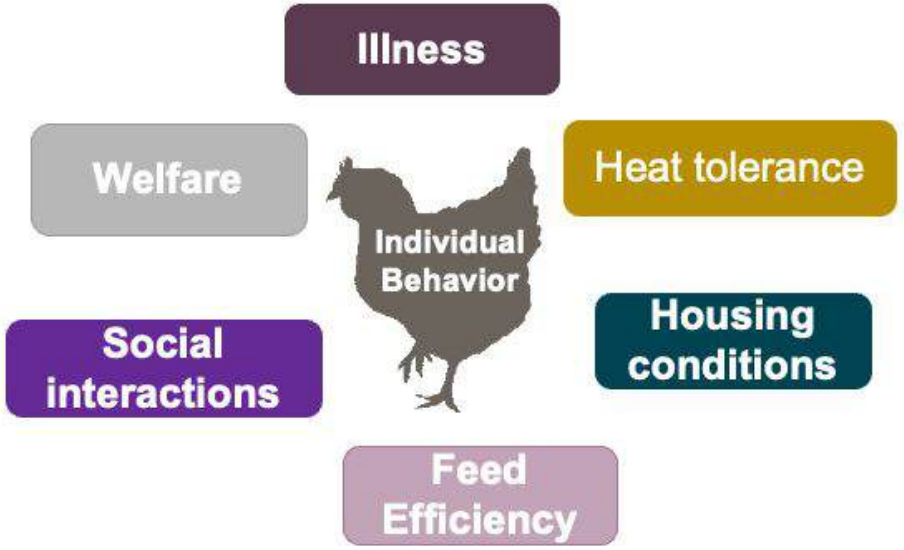
Anderson Alves
Assist. Professor
UGA

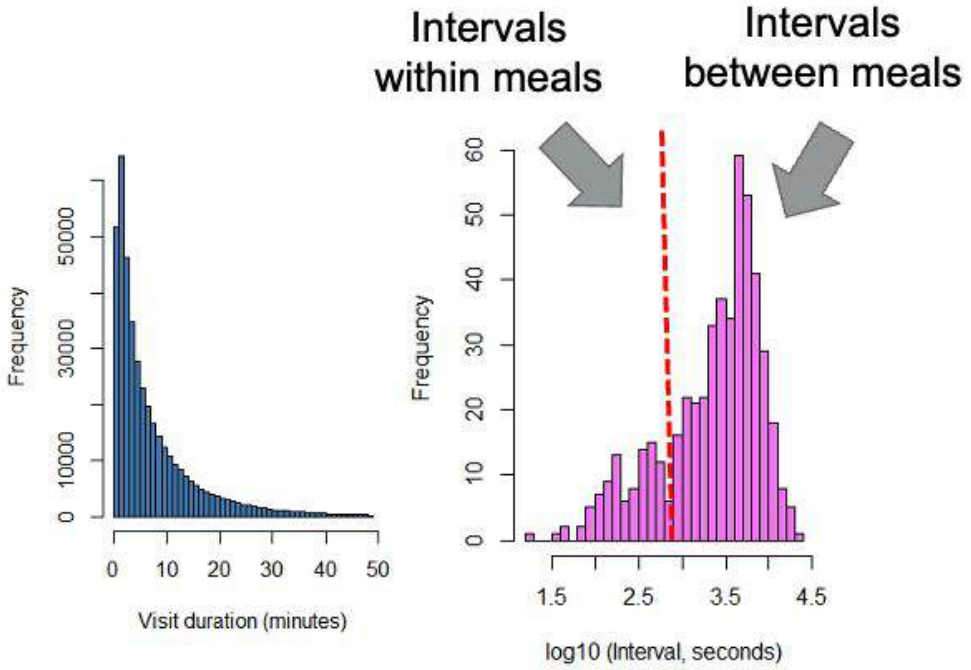
- 100M visits
- 96K birds

# Behavior in broilers

Anderson Alves
Assist. Professor
UGA

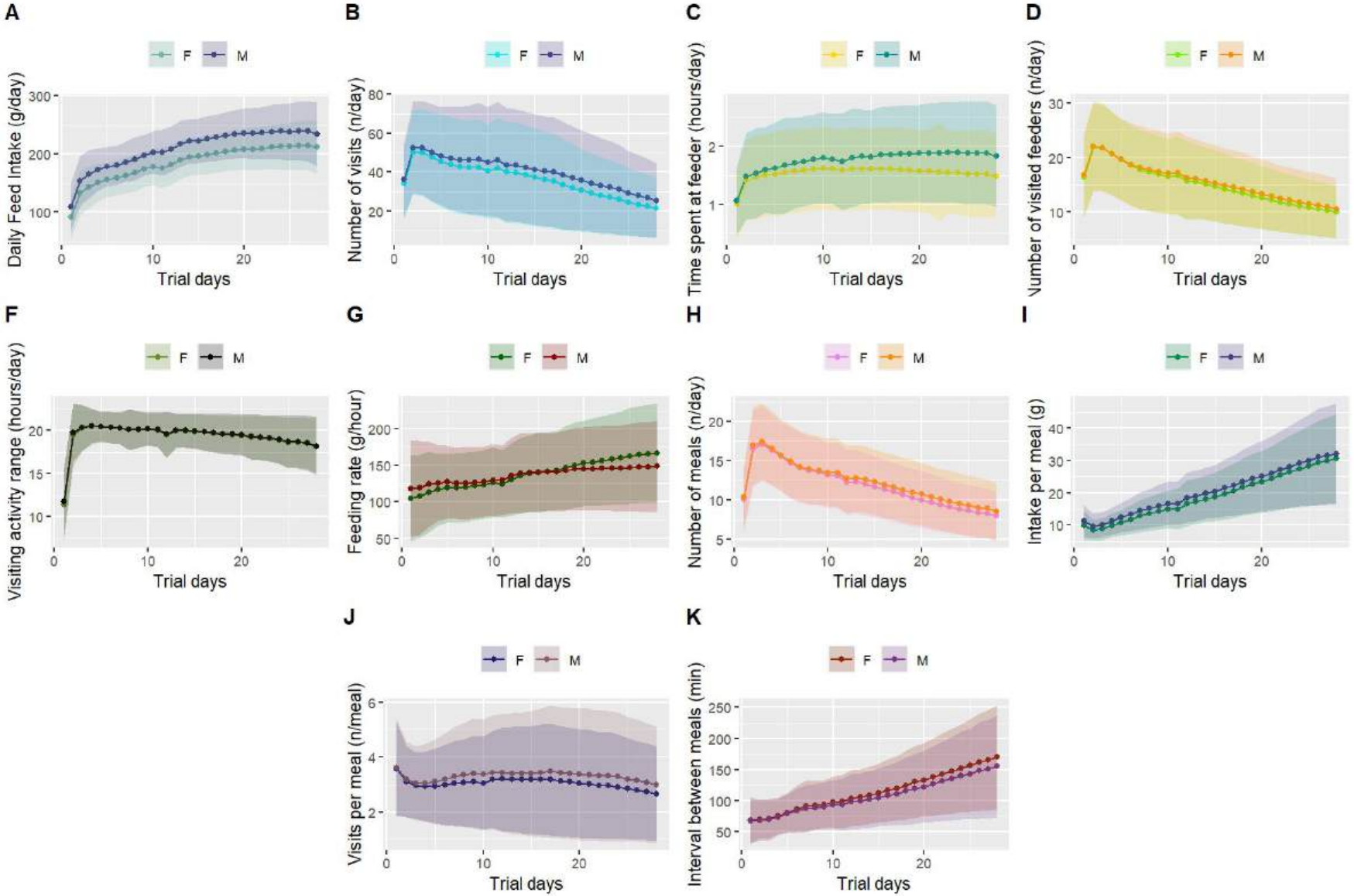
## Going Beyond Feed Efficiency…




Computing feeding or drinking behavior from raw RFID data can be done using a combination of appropriate visit criteria

# Behavior in broilers

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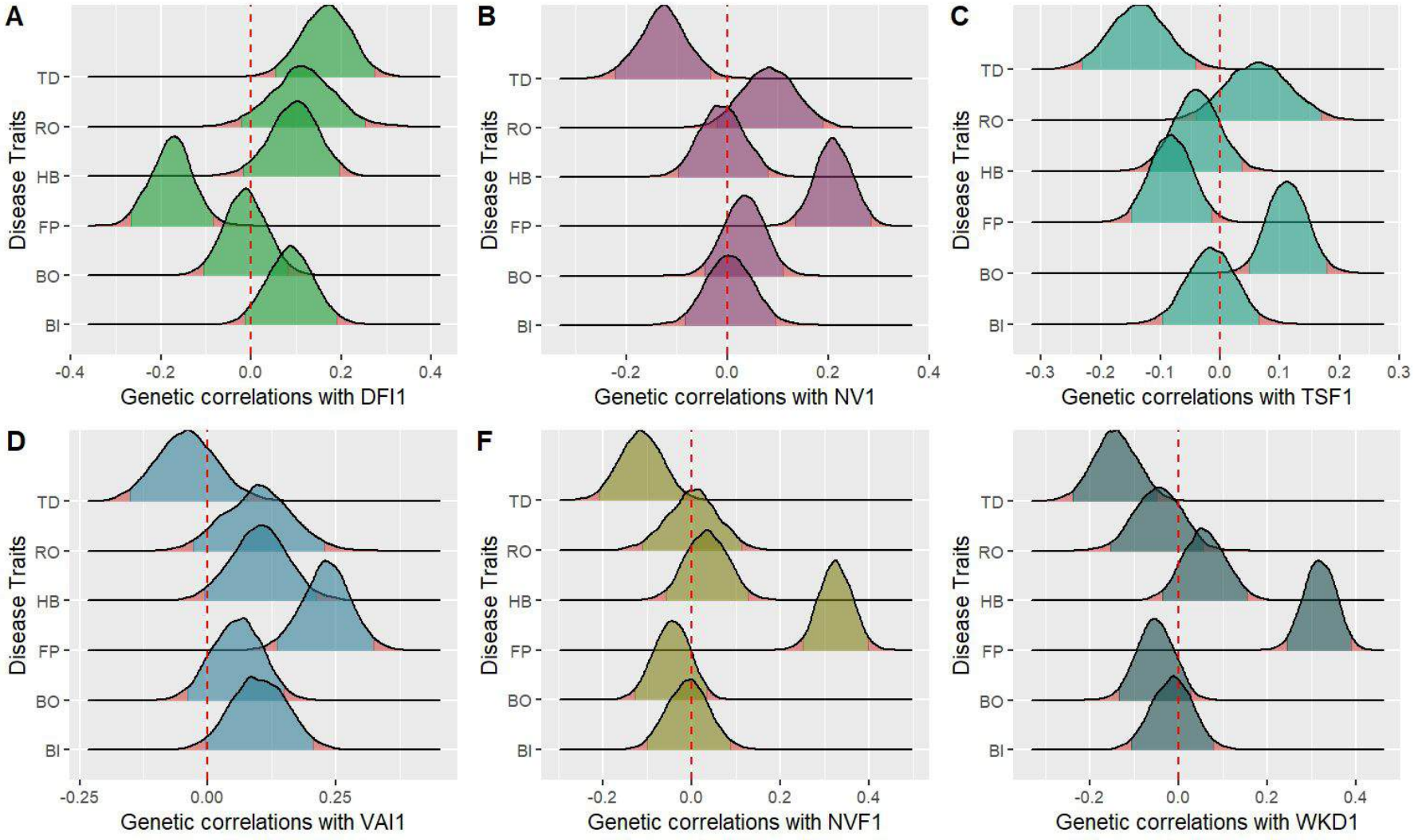
# Feeding behavior as welfare indicators

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Reduced number of visits
Tibial dyschondroplasia

Distance walked
footpad dermatitis

# Take home messages

- Genomic selection
  - Important factor in poultry breeding programs
  - Contributes to the increased genetic gain
  - Higher accuracy
  - More genotyped animals with phenotypes = higher accuracy
- Opportunities for increased genetic gain
  - Digital phenotyping => more precise phenotyping
  - Removes subjectivity
  - Define new traits
- Current status: GS is entering the digital phenotyping era

# UGA AB&G team

USDA NIFA ANGUS THE BUSINESS BREED AGI PIC

USDA United States Department of Agriculture Agricultural Research Service

Warmwater Aquaculture Research Unit

zoetis Smithfield

Cobb ABCZ CDCB COUNCIL ON DAIRY CATTLE BREEDING DNA GENETICS Greater gains. Improved performance.

Rural Development Administration National Institute of Animal Science

WAGYU AMERICAN WAGYU ASSOCIATION BAYER Crop Science

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