



Animal Breeding and Genetics Group

College of Agricultural & Environmental Sciences

UNIVERSITY OF GEORGIA

Impact of genomic selection for growth on foot structure in Angus cattle

Zuleica Trujano¹, Jorge Hidalgo¹, Kelli Retallick², Andre Garcia²,
Daniela Lourenco¹, Ignacy Misztal¹

¹*Department of Animal and Dairy Science, University of Georgia, Athens, GA*

²*Angus Genetics Inc, American Angus Association, Saint Joseph, MO*

Zuleica Trujano

zuleica.trujano@uga.edu

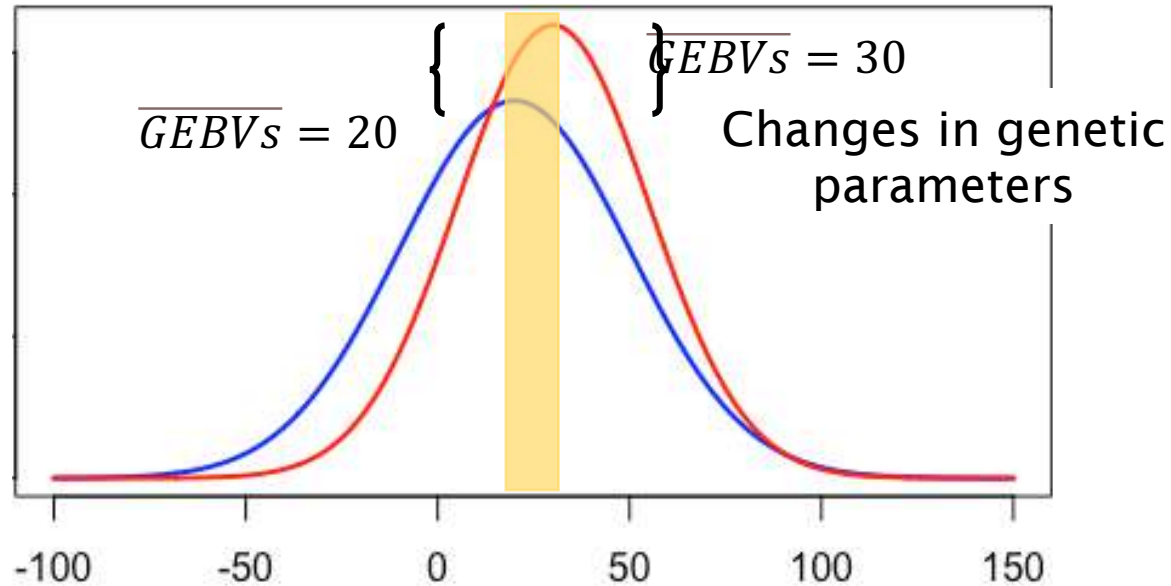
**2024 ASAS-CSAS-WSASAS
Annual Meeting**

07/2024



Introduction

After selection: Gen 1 → Gen 2



Genomic selection accelerates genetic progress



Accuracy



Generation interval

Response to selection:

$$\Delta G = h^2 S$$

Multi-trait selection:

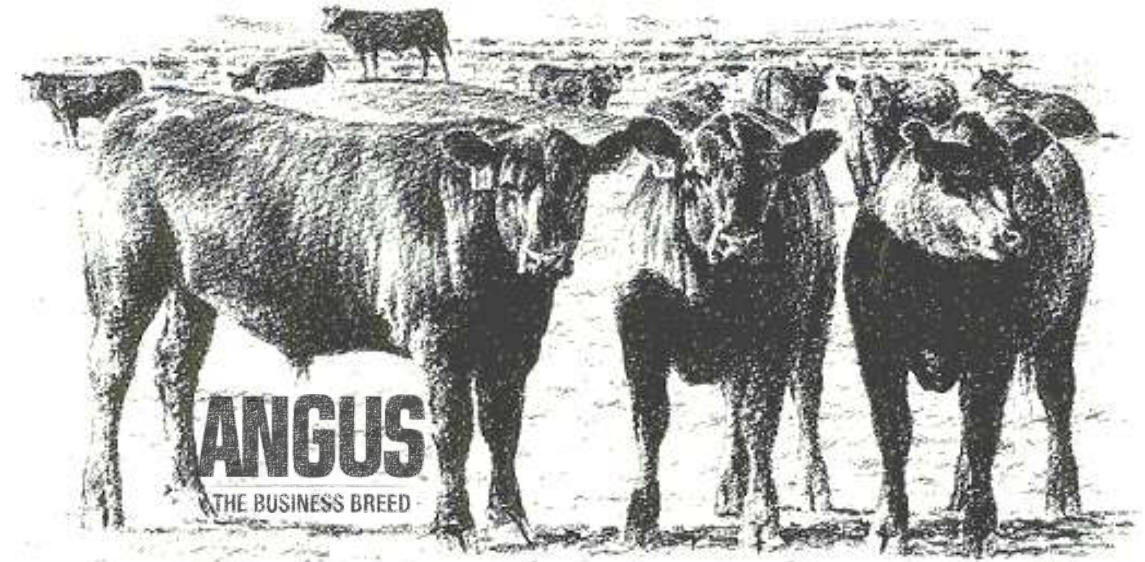
$$r_G = \frac{\sigma_{xy}}{\sqrt{\sigma_x^2 \sigma_y^2}}$$

Selection for Production and Fitness

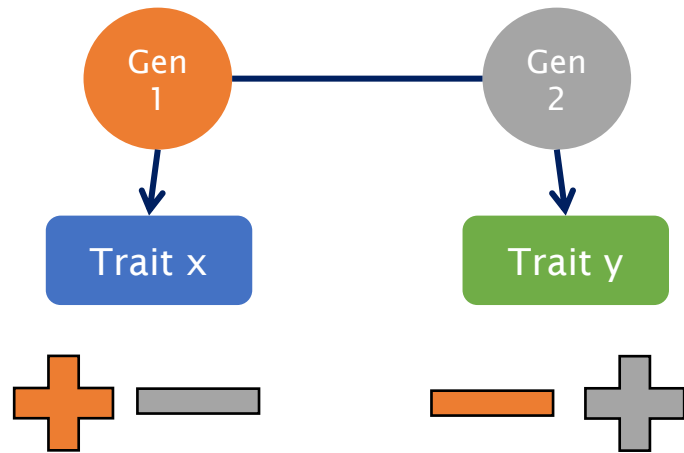


Introduction

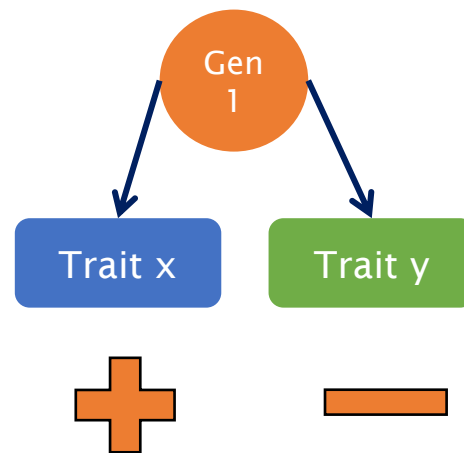
Fitness and production traits are often in antagonistic relationship (Rose, 1985):




Linkage disequilibrium



Pleiotropy



Genetics?

Animals become heavier
(growth traits) 

 Foot structure
(fitness traits) worsen

(Giess et al., 2021)

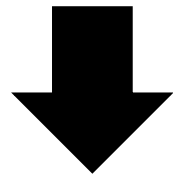
Complementary

Pleiotropic-based

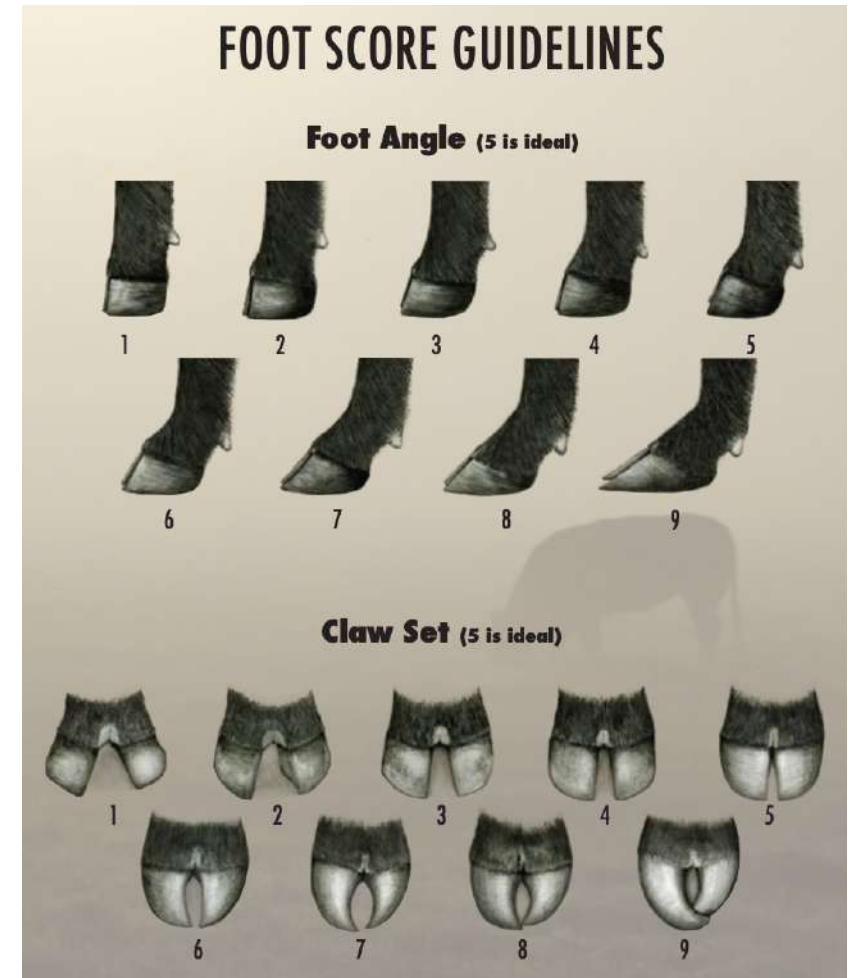


Objective

Evaluate the impact of genomic selection for growth traits on foot structure traits in Angus cattle



Changes over time in genetic parameters



Data and analyses



St Joseph,
MO, USA

Data from 2011 to 2022

Growth Traits (GT): 270,256

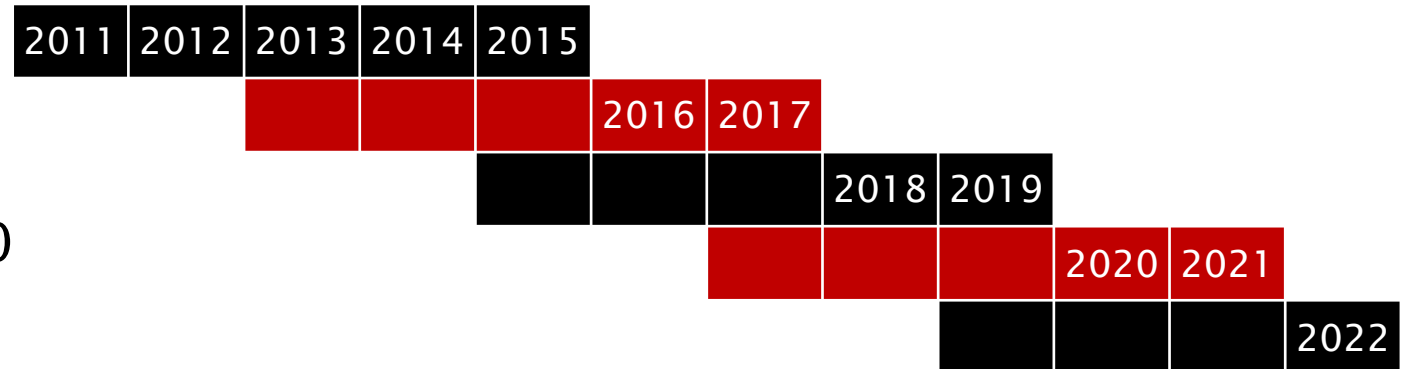
- Birth Weight (BW)
- Weaning Weight (WW)
- Post-Weaning Weight (PWG)

Foot structure Traits (FT): ~80,000

- Claw Set (CS)
- Foot Angle (FA)

Variance Components Estimation

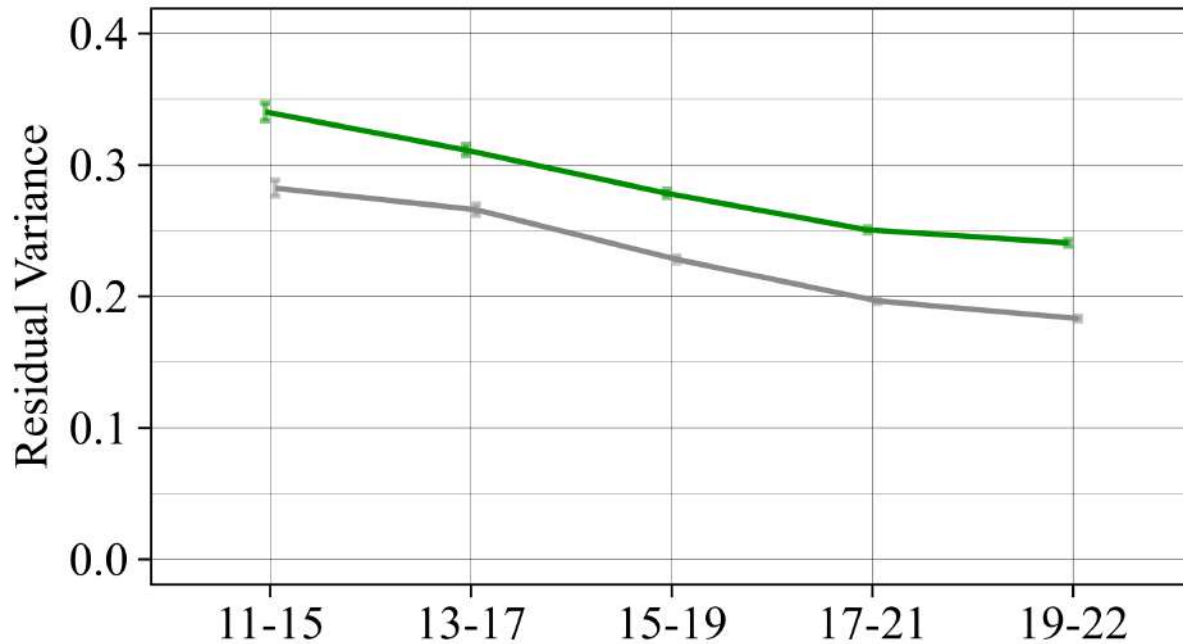
- Five-trait model, ssGBLUP
- Bayesian Approach
- GIBBSF90+ program (Misztal et al., 2014)



Variance

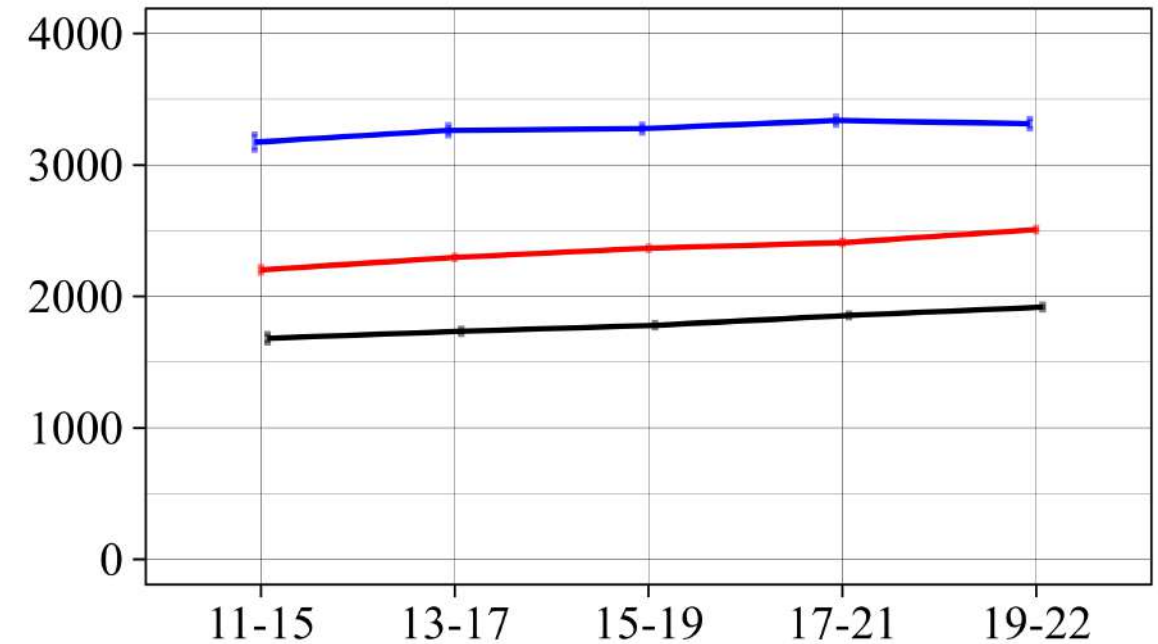
Foot structure

Trait — CS — FA



Growth

Trait — BW10 — PWG — WW

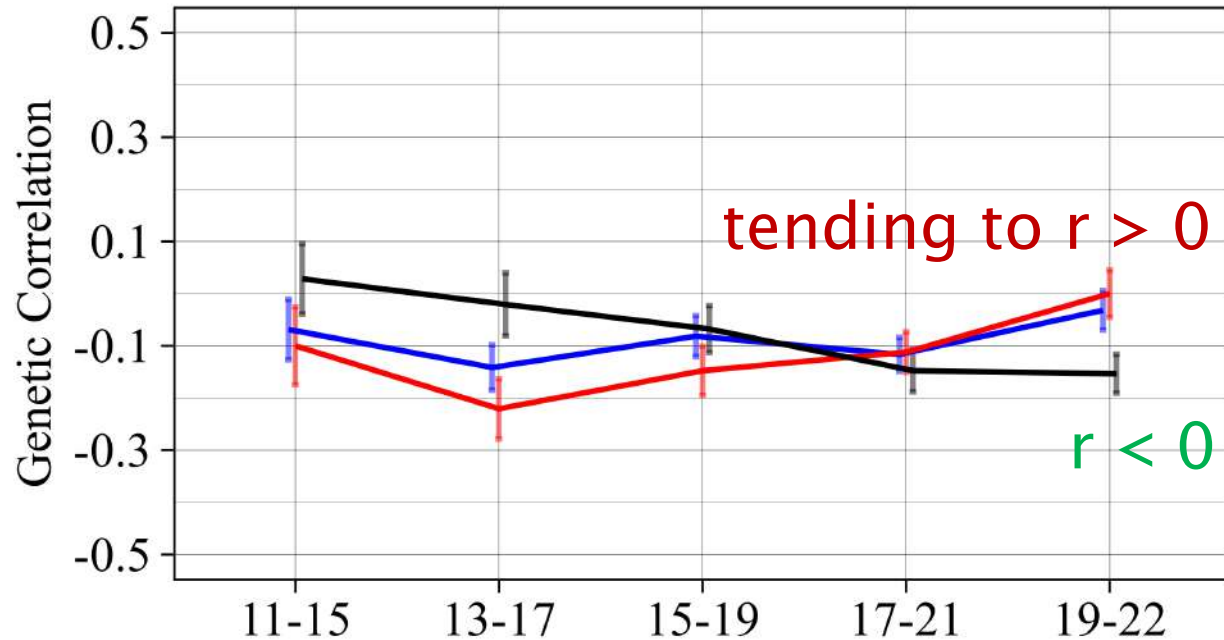


Genetic parameters

GT   FT: 5-9 $r < 0$

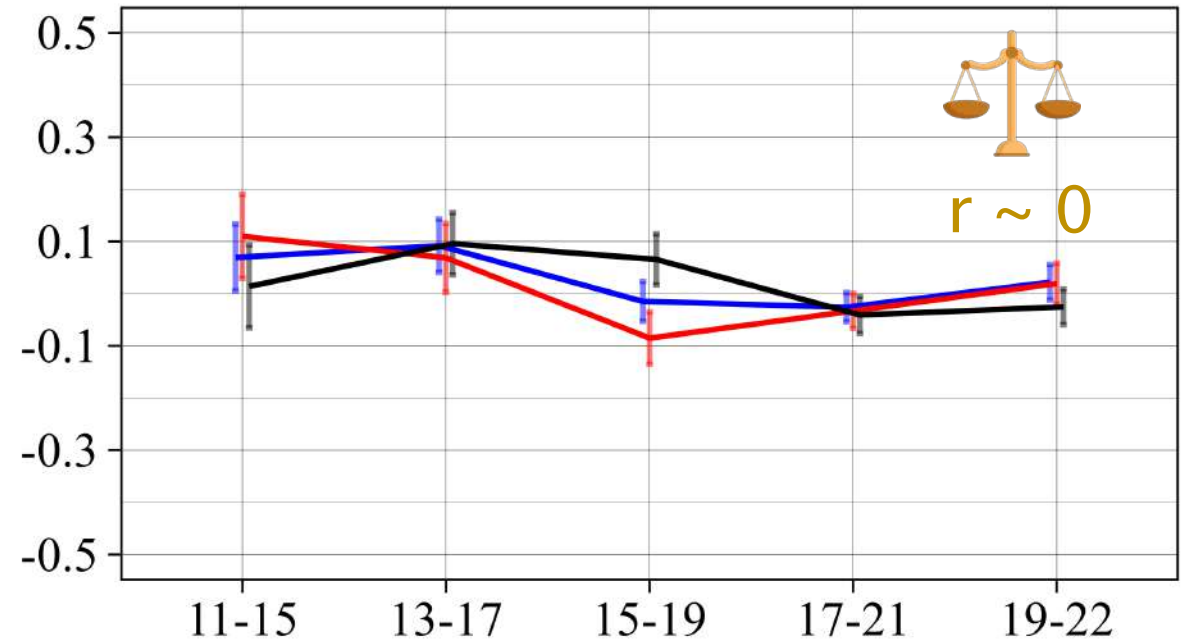
Foot Angle - Growth

Trait — FA-BW — FA-PWG — FA-WW



Claw Set - Growth

Trait — CS-BW — CS-PWG — CS-WW



Bonus

- VCE limitations
- Large data sets
- Time demanding



Predictivity based formulas

$$c = \text{corr}(y_i - Xb_i, \hat{u}_i)$$

$$\hat{h}_i^2 = \frac{c^2 + \sqrt{c^4 + 4c^2(Me/N)}}{2} \pm \frac{3c}{\sqrt{n}}$$

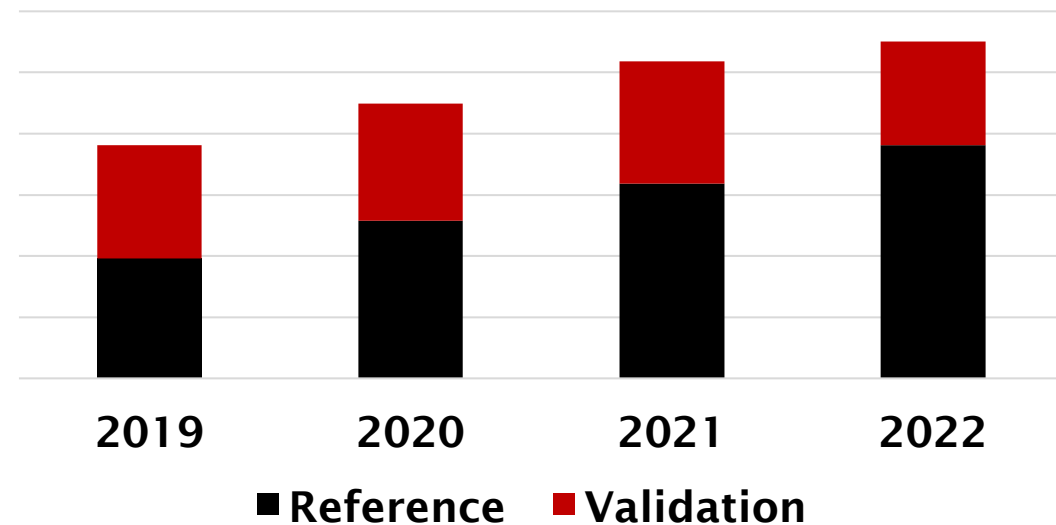
$$\text{corr}_{ij} = \frac{\text{corr}(y_i - Xb_i, \hat{u}_j)}{\hat{h}_{i\text{acc}_j}} \pm \frac{1}{\hat{h}_{i\text{acc}_j}\sqrt{n}}$$

(Misztal, 2023)

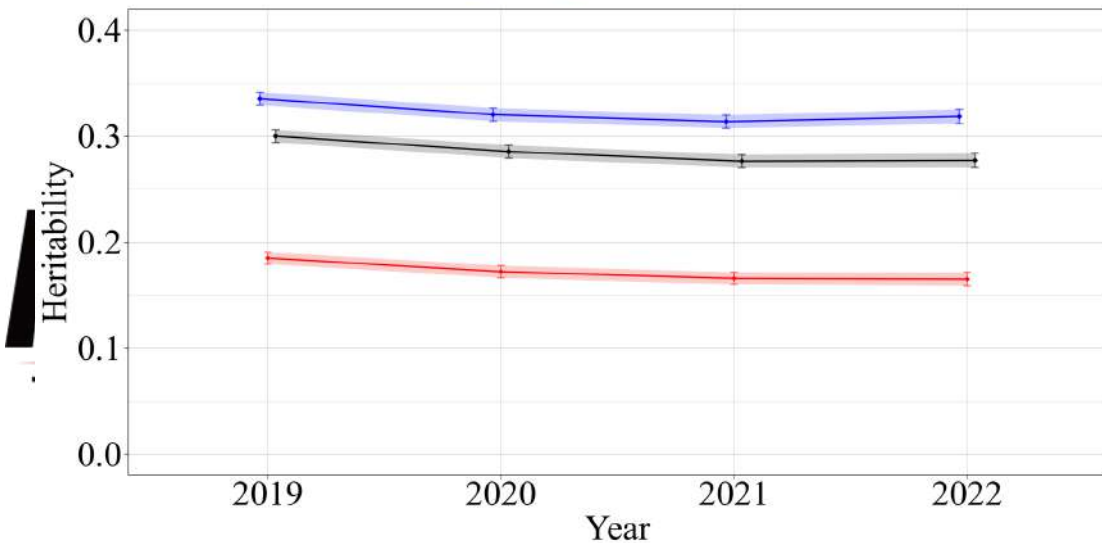
Time slices

ref →	2000	...	2018	2019	2020	2021	2022
val →	2000	...	2018	2019	2020		
	2000	...	2018	2019			
	2000	...	2018				
				
	2000	...					

Reference and validation (gen+phen) animals up to year



■ BW ■ PWG ■ WW

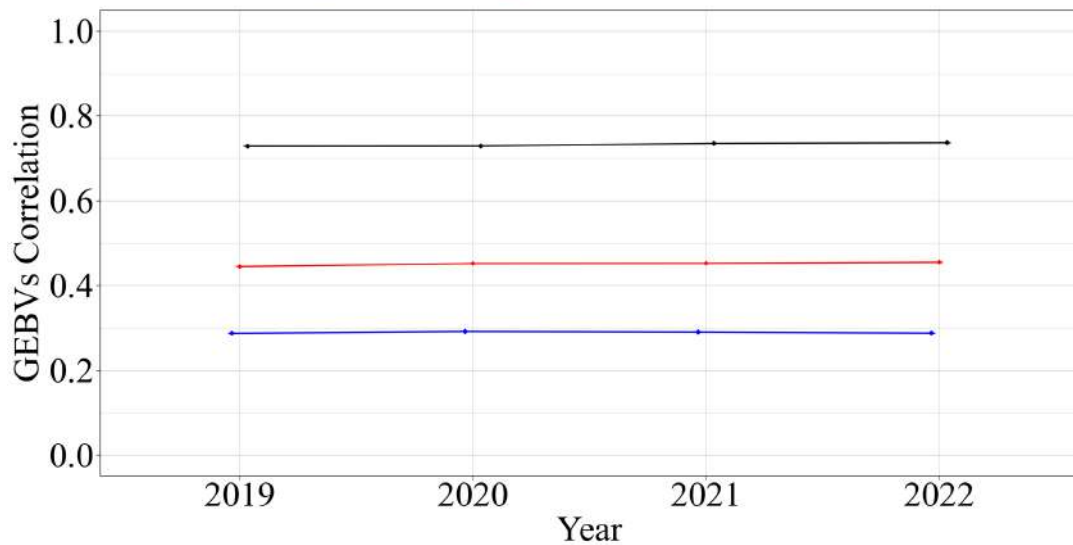


Time for Genetic correlations and h^2

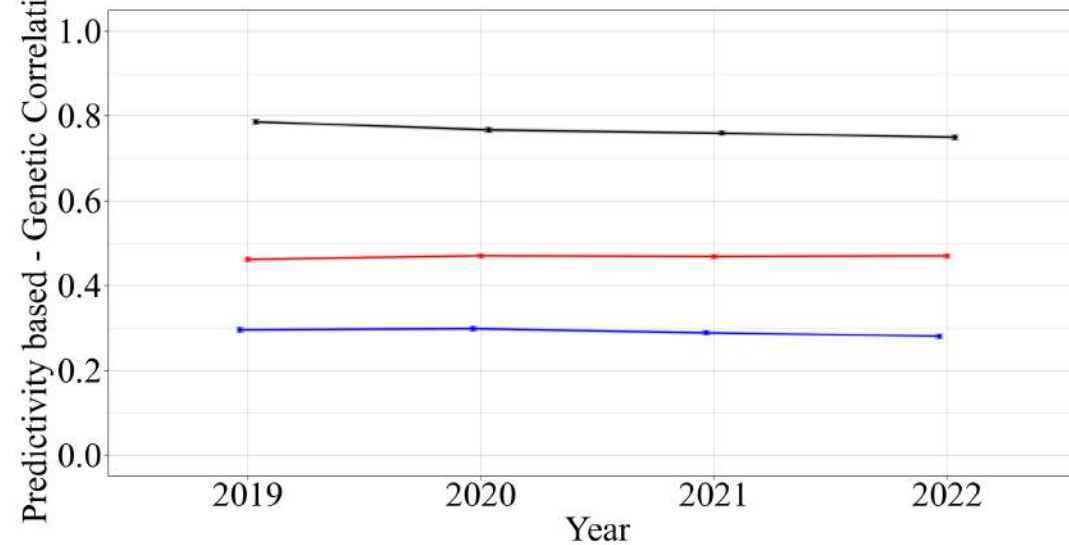


Data from 2000 to 2022

■ BW_PWG ■ BW_WW ■ WW_PWG



■ BW_PWG ■ BW_WW ■ WW_PWG



Conclusions

- Acceptable (CS-GT), desirable (FA-WW) and negative (FA-PWG) outcomes
- Early FT genetic selection implementation
- Need of multi-trait genetic selection approach to mitigate genetic antagonism
- Adopting predictivity-based formulas reduces the time for
genetic parameter estimation
- Allows the use of complete data

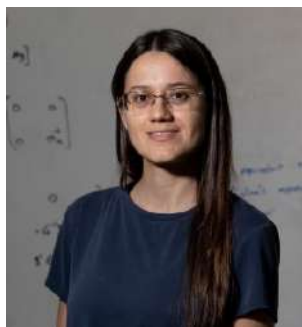




Animal Breeding and Genetics Group

College of Agricultural & Environmental Sciences

UNIVERSITY OF GEORGIA



Zuleica Trujano
zuleica.trujano@uga.edu