

# The Genetic Transformation of the Italian Mediterranean Buffalo

*Five Years of Progress and New Frontiers*

**Mayra Gómez**, R. Cimmino, G. Di Vuolo, G. Neglia, G. Campanile & S. Biffani  
*Geneticist at the National Buffalo Breeders Association*



# Presentation Overview

1

Background & Population Overview

---

2

Genomic Evaluation

---

3

New Selection Indices

---

4

Key Results & Accuracy Gains

---

5

Conclusions & Future Directions

# A Globally Significant Breed

The Italian Mediterranean Buffalo represents over **90%** of Europe's buffalo population and about **95%** of its buffalo milk. Mainly used to produce *Mozzarella di Bufala Campana PDO*.



1,392,199

*Registered buffaloes*



326,089

*Live buffalo heads*



210,794

*Morphological evaluations*



74,914

*DNA-certified animals*



7,200

*SNP-genotyped animals*



182

*AI-authorized bulls*



# From Genetics to Genomics

01

---

Until 2022

## *Pedigree BLUP*

- *Pedigree and phenotypic*
- *Only family relationships*
- *No molecular information*
- *Limited accuracy for young animals*
- *Longer generation intervals*
- *Single-trait and multi-trait BLUP models*

03

---

## **IBMI genomic**

*This improved us to publish the genomic IBMI Index for the first time.*

02

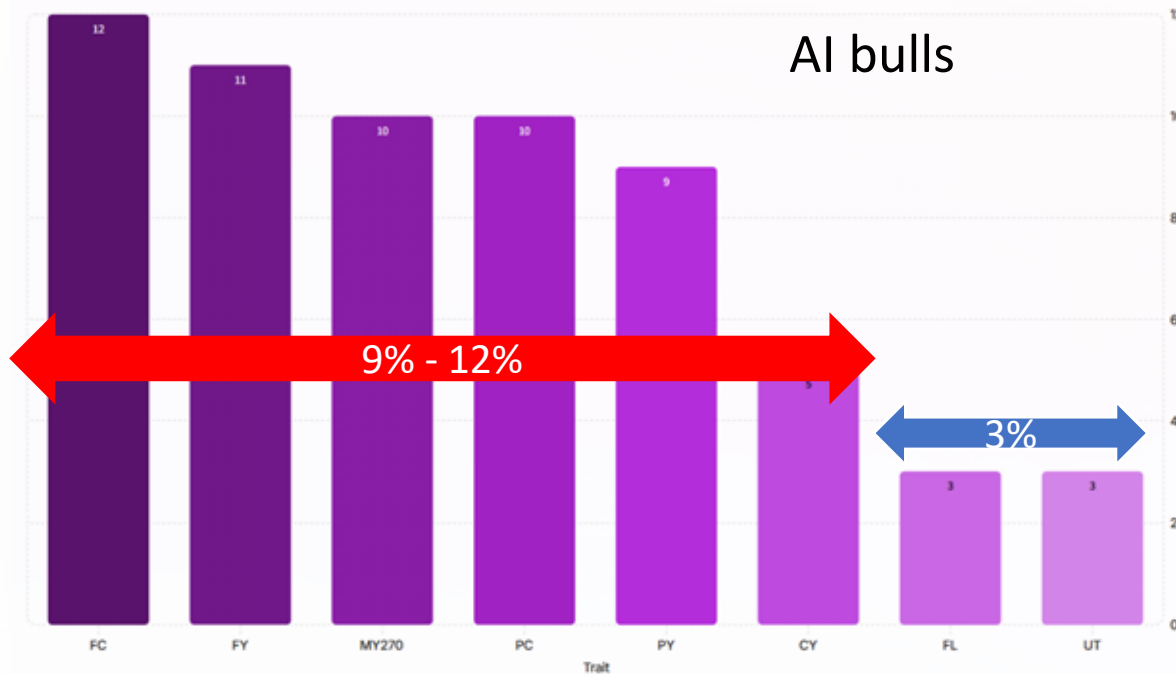
---

From 2023

## *ssGBLUP Integration*

- *Pedigree + phenotypic + genomic*
- *One unified model*
- *7,200 SNP-genotyped animals*
- *+40% improved EBV reliability*
- *It is more accurate and less biased.*

# Genomic Evaluation: Key Results



Accuracy Improvement: ssGBLUP vs BLUP (%)



J. Dairy Sci. 109:2771–2786

<https://doi.org/10.3168/jds.2025-27102>

© 2026, The Authors. Published by Elsevier Inc. on behalf of the American Dairy Science Association®. This is an open access article under the CC BY license (<https://creativecommons.org/licenses/by/4.0/>).

## Single-step genomic evaluation for production and type traits in the Italian Mediterranean buffalo

M. Gómez-Carpio,<sup>1</sup> A. Cesarani,<sup>2,3</sup> L. Zullo,<sup>1</sup> R. Cimmino,<sup>1</sup> D. Rossi,<sup>1</sup> L. Gubitosi,<sup>1</sup> Y. Gombia,<sup>1</sup> G. Di Vuolo,<sup>1</sup> G. Campanile,<sup>4</sup> S. Biffani,<sup>5,6</sup> and L. Neglia<sup>4</sup>

### Why ssGBLUP Wins

**Reduced bias**  
Breeding values move closer to unity.

**Better validation**  
Higher correlations for production traits.

**Works with sparse data**  
Performs well with incomplete pedigree depth.

**Earlier selection**  
Enables more confident decisions sooner.

*ssGBLUP gives more reliable EBV across all traits*

# Genomic Selection Advantage

*Accuracy the most important result of genomic selection for our program - Genomic information provides detailed genetic insights beyond pedigree alone, enabling more accurate breeding value estimates.*

0.29

**Accuracy Without Genotyping**

*Bulls without daughters/ phenotypic showed accuracy.*

0.60

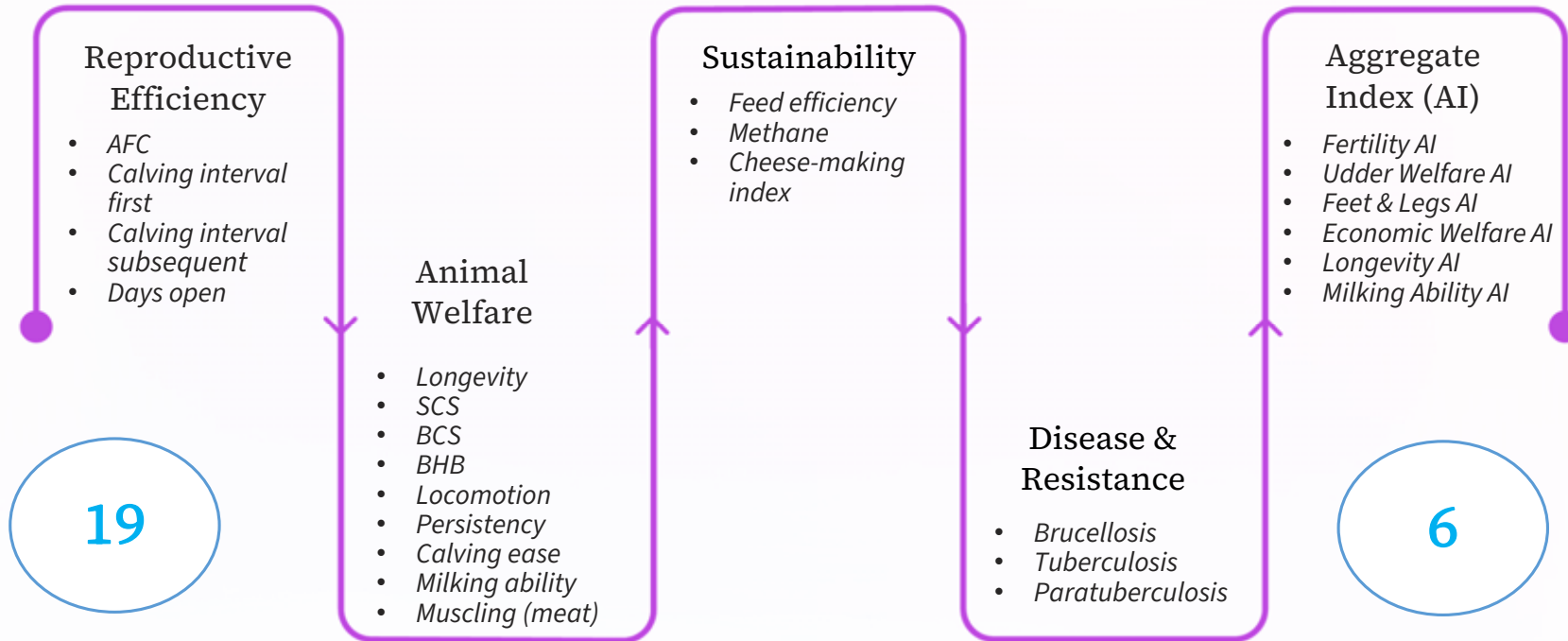
**Accuracy With Genotyping**

*Accuracy after genotyping - more than double the precision for breeding decisions.*

*Before, we had to wait 6 years, after progeny testing. Now, with genomic information at 1 year of age or less.*

*Real benefit is the time - this reduction in generation interval accelerates genetic progress*

# New Selection Indices (2021–2025)

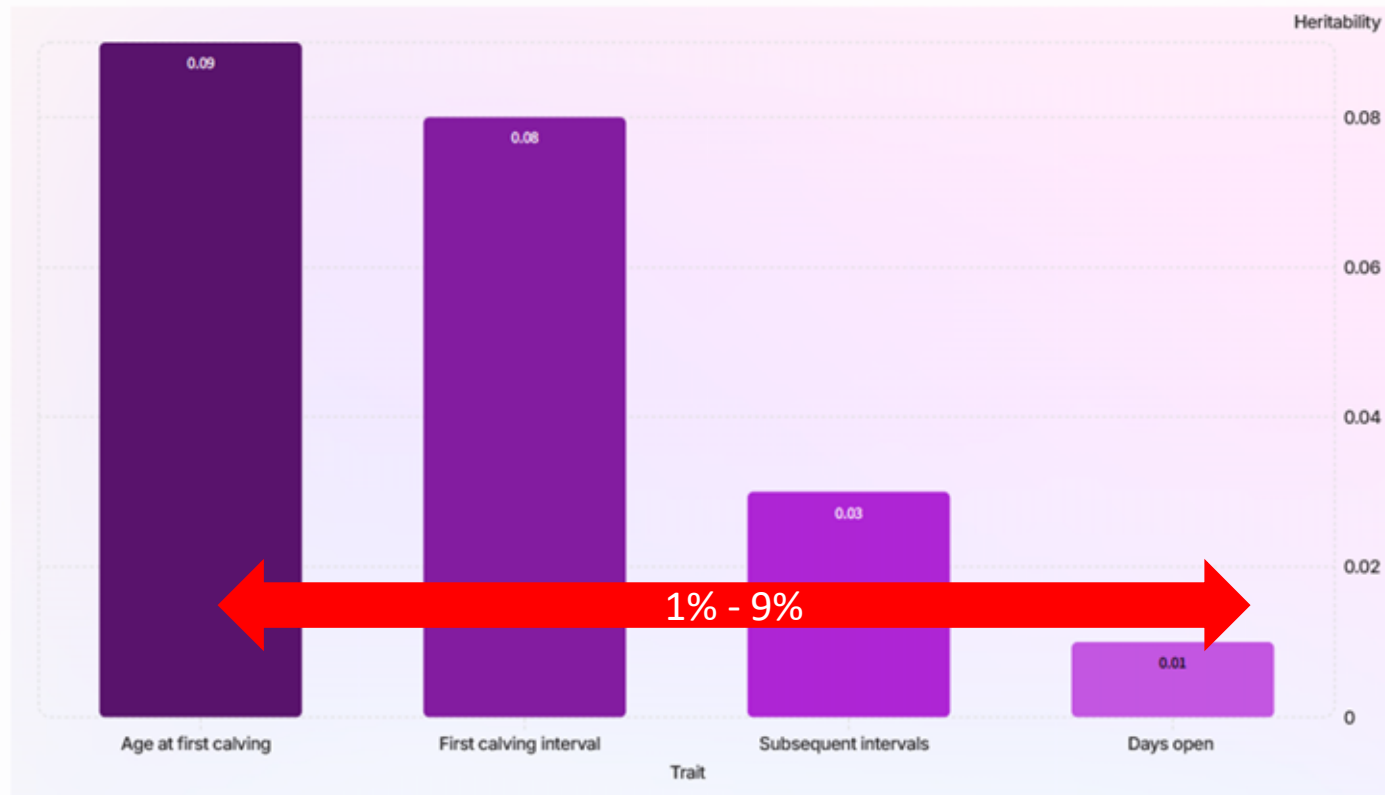


The breeding objective was structurally redefined across **five functional categories**, reflecting a paradigm shift from production-centered selection to a **multidimensional genomic framework**.



Statistical models included single-trait linear, multi-trait, repeatability, and threshold models. Variance components estimated via REML or Bayesian Gibbs sampling.

# Reproductive Efficiency

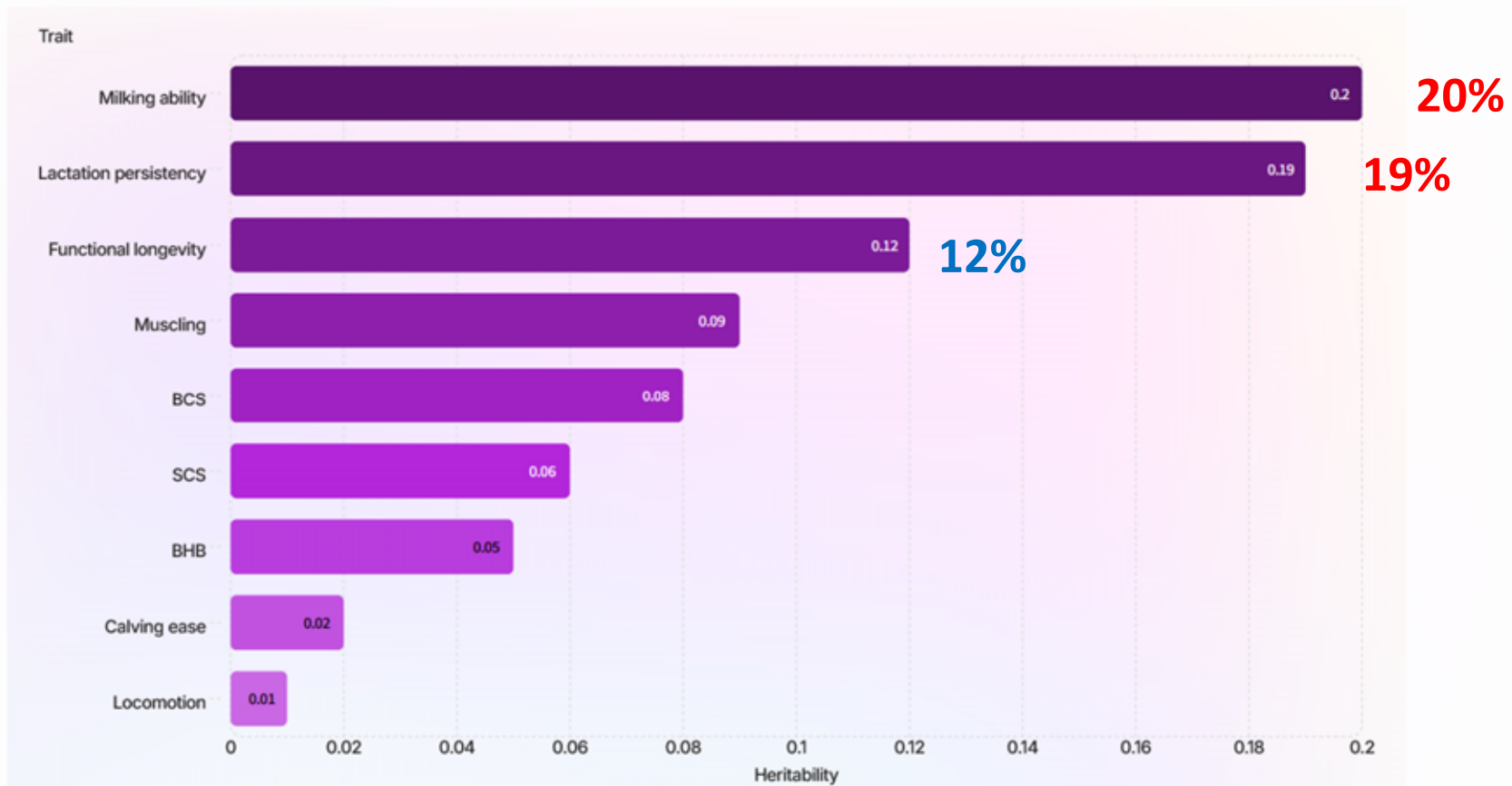


Influenced by farm management decisions and thus have large environmental component

*Heritability estimates are low to moderate, 0.09 (AFC), 0.08 (first calving interval), 0.03 (subsequent intervals), 0.01 (DO).*

*However, even at these low levels, is possible to improve fertility. We can use multi-trait models and aggregated reproductive indices, reducing calving intervals and increasing farm profitability.*

# Animal Welfare

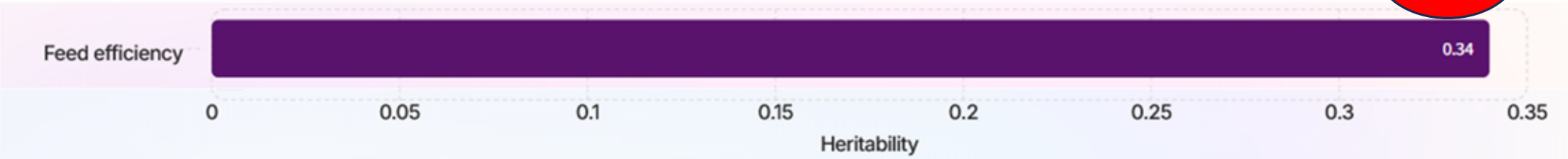


The welfare traits show moderate variation in heritability, with **milking ability (0.20)** and **lactation persistency (0.19)** leading the group. These estimates suggest meaningful selection opportunities for improving functional traits tied to health, productivity, and animal well-being. Even traits with lower heritability, still offer useful selection opportunities in a multi-trait index



# Sustainability

34%



- *Feed efficiency  $h^2 = 0.34$  — highest — meaning greater potential for direct selection*
- *Methane production is inversely related to feed efficiency*  
***More efficient animals tend to produce less methane***



Selecting for feed efficiency could also help reduce greenhouse gas emissions, linking genetic improvement with environmental goals

matter intake (DMI)

$$DMI = (91 \text{ g} * \text{Metabolic Weight}) + (0.27 \text{ kg} * \text{kg ECM})$$

Neglia, G., Cotticelli, A., Vasseti, A. *et al.* Buffalo milk and rumen fluid metabolome are significantly affected by green feed. *Sci Rep* **13**, 1381 (2023). <https://doi.org/10.1038/s41598-022-25491-w>

Height / Width / Body Length, Stature, Width of Ilium / Ischium, BCS

→ Body weight

# 🛡️ Disease Resistance & Resilience



## Exploitable Genetic Variability

Including these traits in the breeding program allows us to:

- select animals that are genetically more resilient,
- reducing the need for veterinary treatments and antibiotic use

IMB is currently the **only** breed and species in Italy with developed indices for these diseases

### Brucellosis

Heritability: **0.15**

### Paratuberculosis

Heritability: **0.15**

### Tuberculosis

Heritability: **0.07**

# Five Years of Transformation – Key Achievements

---

## Genomic Integration

*ssGBLUP operational since 2023*

*Pedigree + phenotype + genotype*

---

## STR-to-SNP Imputation

*Novel imputation pipeline*

*From STR markers to SNP arrays*

---

## Accuracy Gains

*+3% to +12% across production and morphological traits*

*40% of the accuracy in young animals*

---

## 19 New Indices + 6 Aggregate Index

*Reproductive, animal welfare, climate change and farm sustainability*

---

## Global Leadership

*One of the most advanced buffalo genetic programs worldwide*

---

## ~8,000 Genotyped

*Largest buffalo genomic dataset  
Making the IMB genetic program the most advanced for this species*

# Conclusions

*IMB program has undergone a true genetic revolution*

1. **Cost-effective and efficient genotyping - combining genomic tools**

*STR-from-SNP imputation ensuring parentage verification and reducing genotyping costs.*

2. **Faster genetic gain**

*Genomic selection reduced the generation interval from 6 to 1 year in young bulls, accelerating annual genetic progress.*

3. **More reliable EBV**

*The result is a more efficient, reliable, and sustainable breeding program.*

4. **Modern breeding leadership**

*Disease resistance, feed efficiency, and methane indices place the IMB program at the forefront of modern breeding.*

*It addresses climate change, sustainability, and animal welfare challenges.*

5. **Replicable model**

*Buffalo genomics model that can be replicated for other local dairy breeds around the world.*



thank  
you

Contact:

[m.gomezcarpio@anasb.it](mailto:m.gomezcarpio@anasb.it)

*Research supported by ITALIAN MINISTRY OF AGRICULTURE (MIPAAF – DISR07). Project: “BIG” Prot. N. 0215513 11/05/2021 and by Programma di ricerca per la Biosicurezza delle Aziende Bufaline- articolo 4 bis dell’OPCM n. 3634 del 21/12/2007*

