# The importance of using phenotypic and genomic data in unison in the SA Jersey Population

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**Key Message:** Genomic information does not replace phenotypic recording — it **enhances** it.

## SA Jersey Population



**450K+**

Cows Recorded

Under SA conditions

**10.3M**

Test-Day Records

Since 1989

- 1.9 million Lactation records (1970)
- 4.2 million SCC records (1990)

**15**

Pedigree Generations

Since 1930s

**7th**

Global Jersey Ranking

INTERBULL

INTERBULL participant since 2000 · SS-GBLUP introduced 2020 · Trait groups: Production, Udder Health, Fertility, Longevity, Conformation

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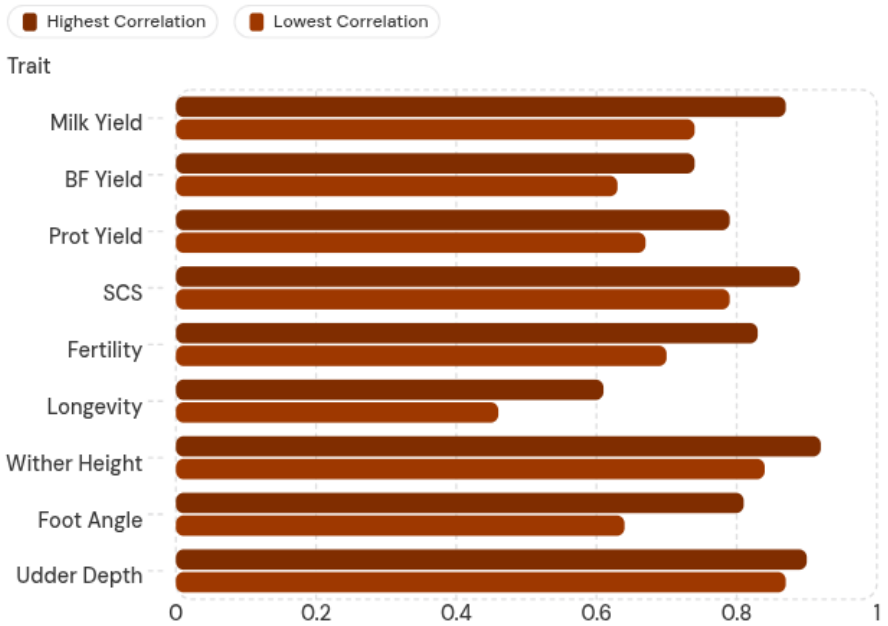
# Genetic Correlations with International Populations




## Strong International Links

SA Jersey EBVs are validated by INTERBULL. Highest correlations: Wither Height (0.92 GBR) and Udder Depth (0.90 NLD). Lowest: Longevity (0.46 NZL).

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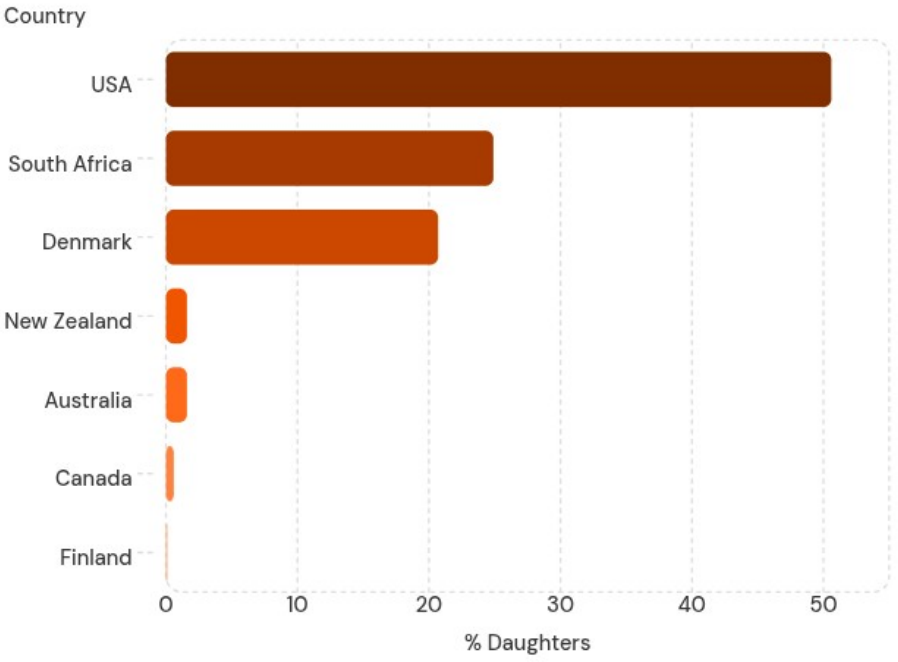
# Active Cow Origin — Daughters by Country of Birth




## International Genetic Influence

USA genetics dominate (50.6%), with strong Danish (20.7%) and local SA (24.9%) contributions. NZL, AUS, CAN, and FIN represent minor shares.

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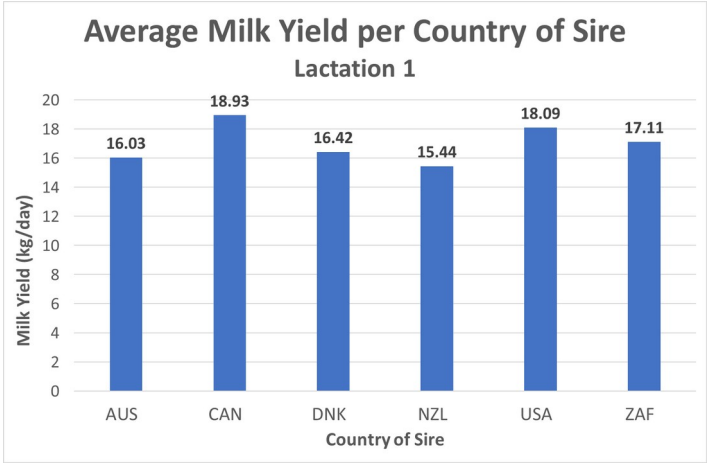
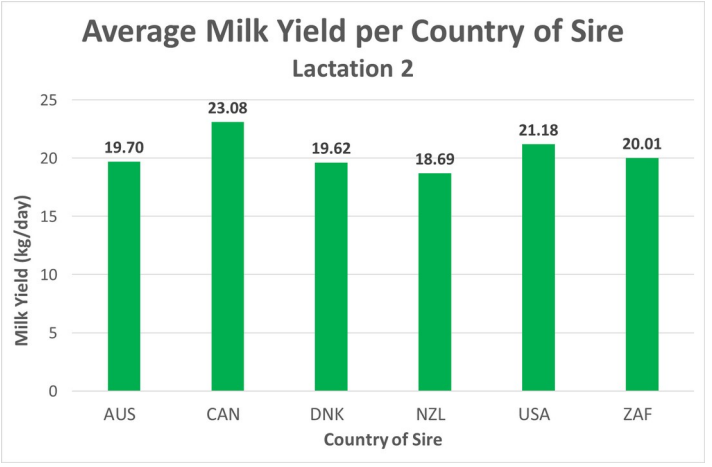
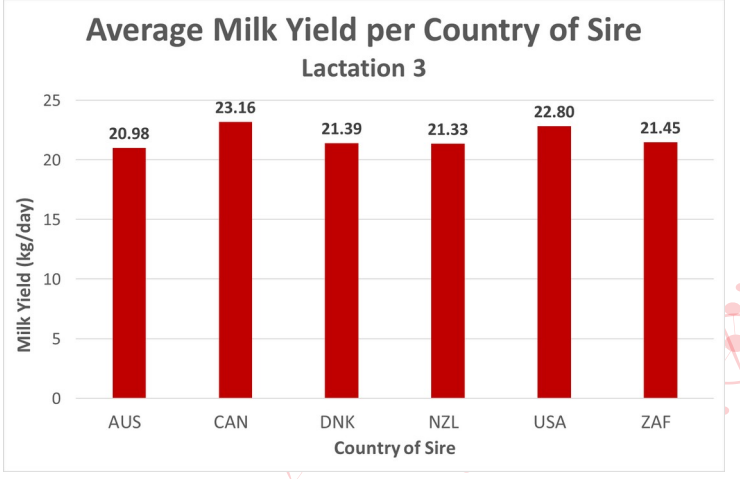
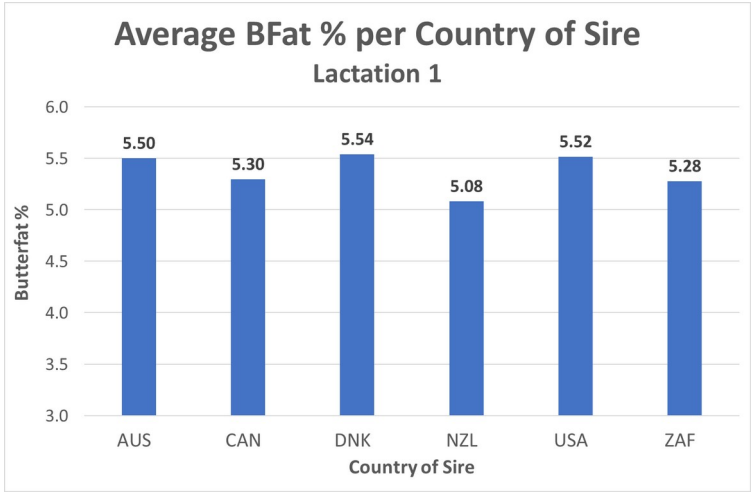
# MILK YIELD LEVELS PER COUNTRY OF SIRE

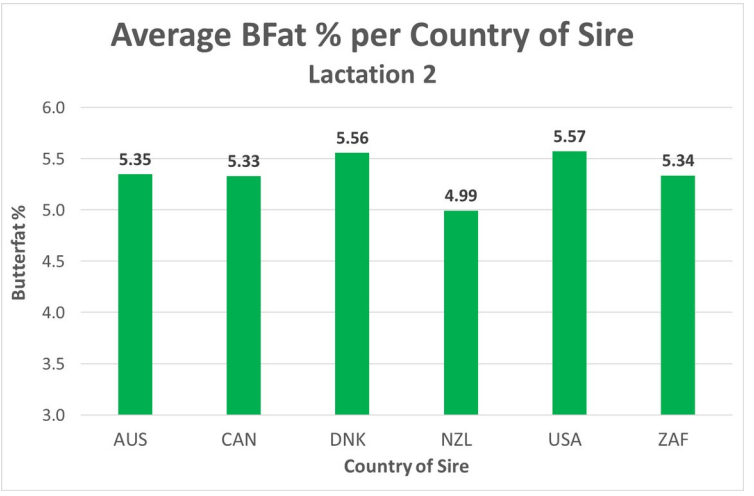


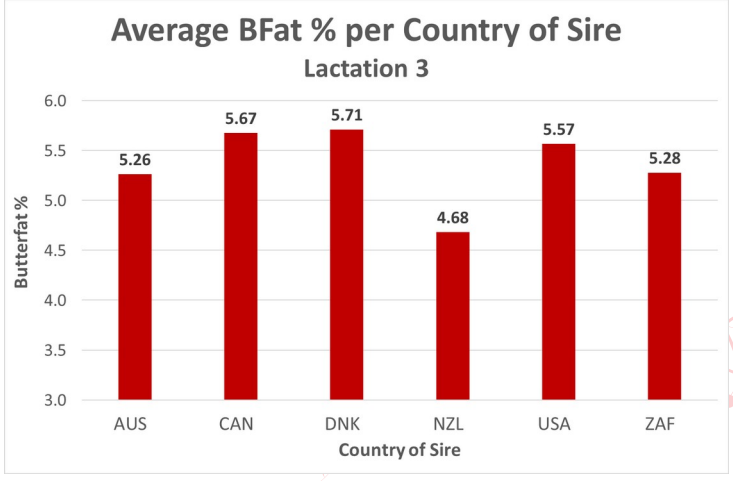



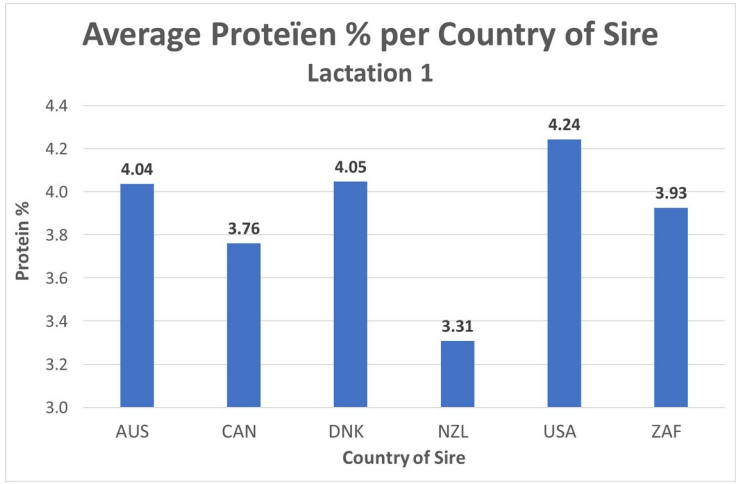
# BFAT % LEVELS PER COUNTRY OF SIRE

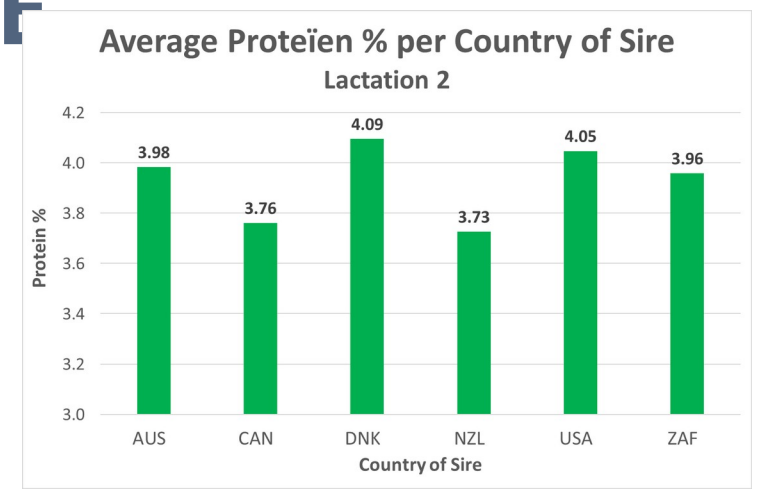


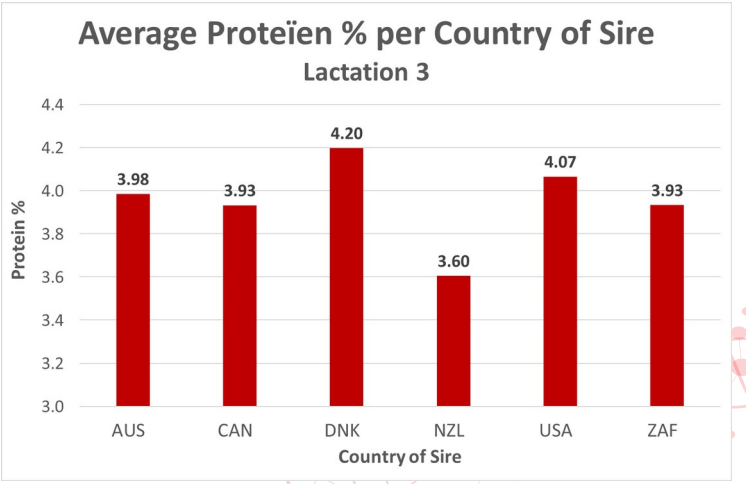



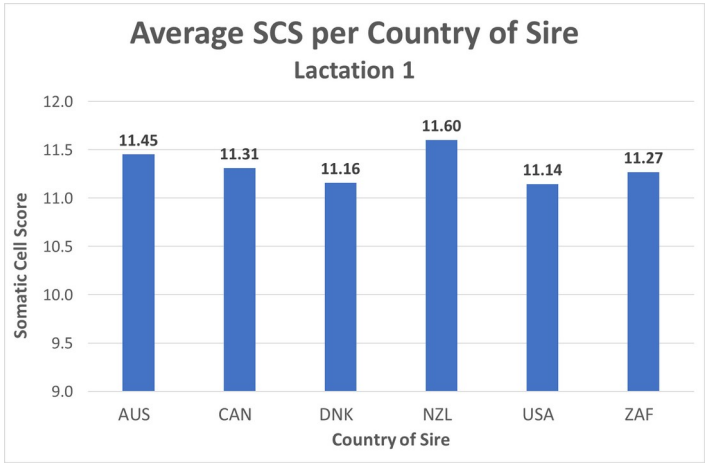
# PROTEIN % LEVELS PER COUNTRY OF SIRE

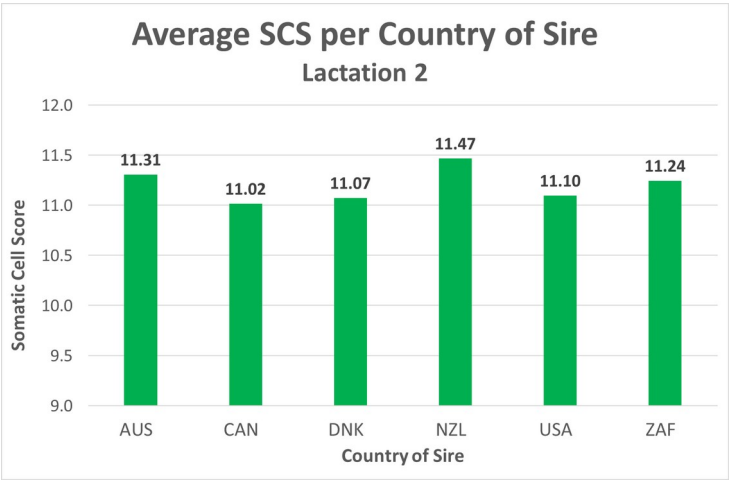


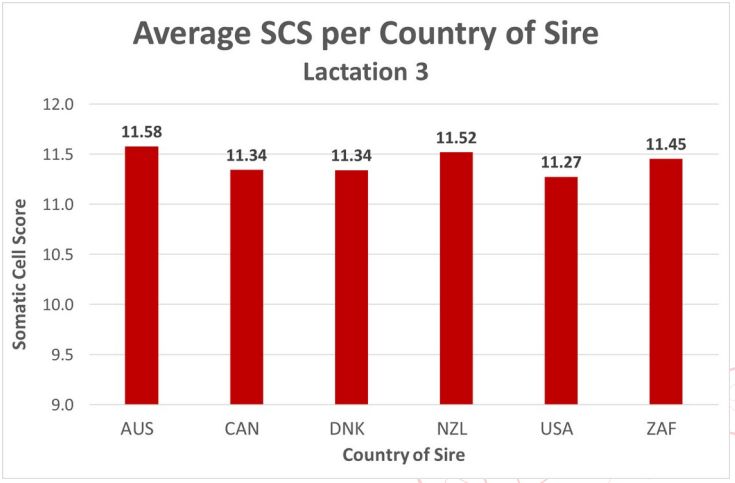



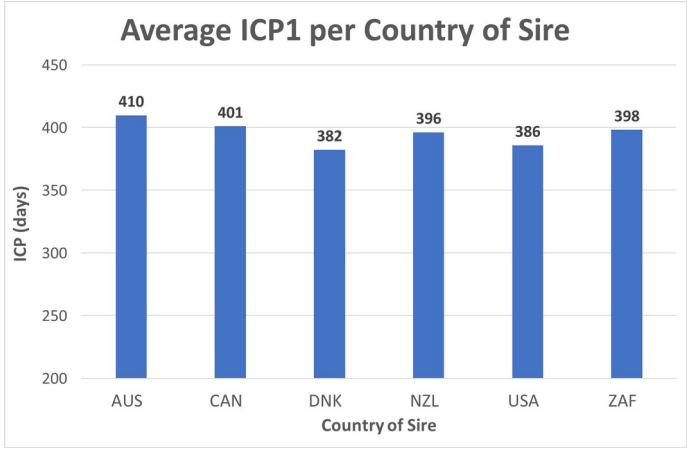
# SCS LEVELS PER COUNTRY OF SIRE

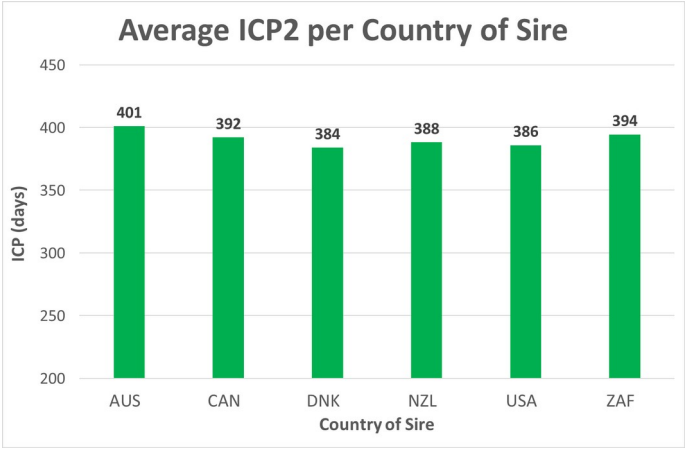


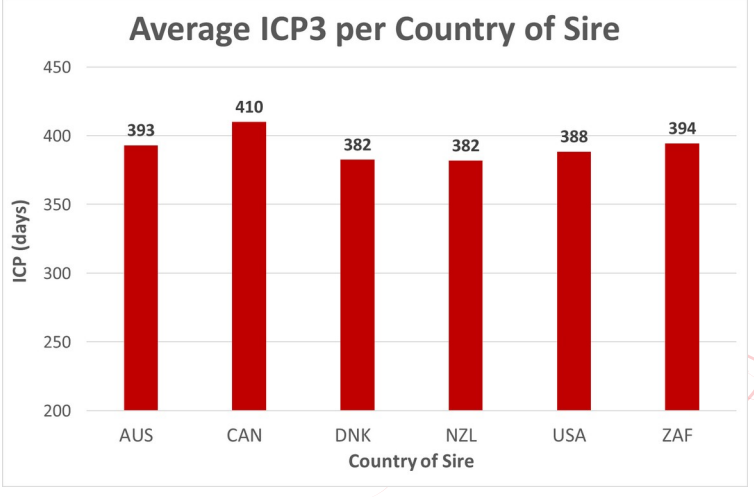



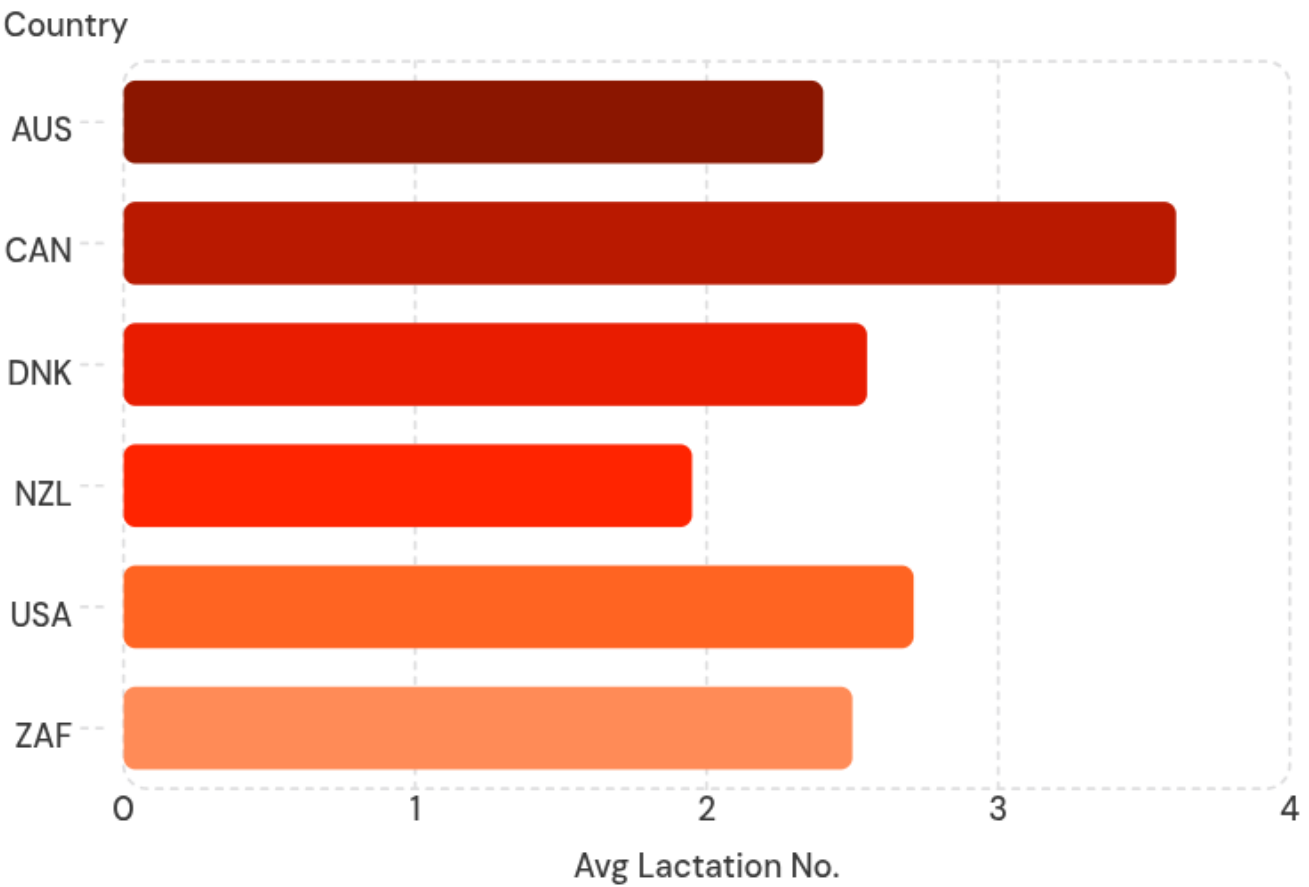
# ICP LEVELS PER COUNTRY OF SIRE



# Average Lactation Number — Active Cows

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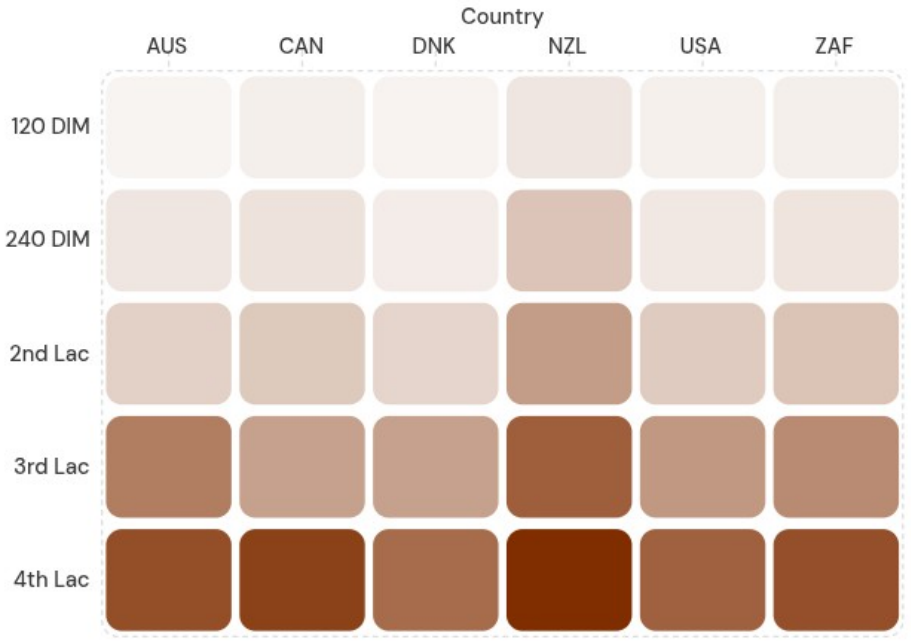
# Erosion Levels per Sire Country (Cows Born Since 2020)




## Greatest Erosion Occurrence

NZL sires show highest total erosion at 4th lactation (97.1%), with greatest loss between 2nd–3rd lactation (30.4%). CAN shows highest erosion between 3rd–4th lactation (46.4%).

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# Phenotypes + Genomics = Most Accurate Breeding Values

**Phenotype + Pedigree + Genomics = Most Accurate Breeding Values**

## Why Phenotypes Are Essential

### Foundation of Evaluation

No phenotypes = no genetic parameters = no breeding values

### Population Monitoring

Essential for heritability and genetic correlation estimation

### Genomic Training

Phenotypes train genomic prediction equations

## Why Phenotypes Alone Are Not Enough

### Young Animals

No own performance records available

### Bulls

No milk records; low heritability traits require many daughters

### Progeny Testing Delay

5–7 years before reliable EBVs become available

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# What Genomics Adds

### Available at Birth

DNA never changes; predicts inherited genetic merit

### Earlier Selection

Shorter generation interval; faster genetic gain

### Increased Accuracy

Real genomic relationships vs. theoretical pedigree

## Single-Step GBLUP

SS-GBLUP replaces $A^{-1}$ with $H^{-1}$, combining pedigree, phenotypes, and genomics into one unified evaluation:

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

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + \lambda H^{-1} \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X'Y \\ Z'Y \end{bmatrix}$$

$$P = G + E \quad V_P = V_A + V_{D+I} + V_E$$

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# Challenges & Benefits

## Challenges

- Cost of genotyping
- Maintaining milk recording
- Data quality & farmer participation
- Computational requirements

## Benefits to Breeders

- Earlier identification of elite heifers
- More accurate mating decisions
- Reduced generation interval
- Greater profitability & sustainability

## Future Traits Requiring New Phenotypes

Methane & Feed Efficiency

Heat Tolerance & Resilience

Disease Resistance & Hoof Health

A2A2, Cheese Yield & Milk Composition

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# To Remember

- Genomics **complements** — not replaces — phenotypic recording
- Every phenotype improves future genomic predictions
- Greatest genetic gain achieved when **pedigree, phenotype, and genomics** are used together
- Continued investment in recording today ensures more accurate breeding decisions tomorrow

**DNA tells us what potential an animal has received; Phenotypes reveal how that potential is expressed.** Together they provide the most accurate picture of genetic merit and the greatest opportunity for sustainable genetic improvement in the South African Jersey population.

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Baie Dankie !!

Thank you !!

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