

Towards more efficient and sustainable production in Egyptian buffalo: the clue lie in the genome



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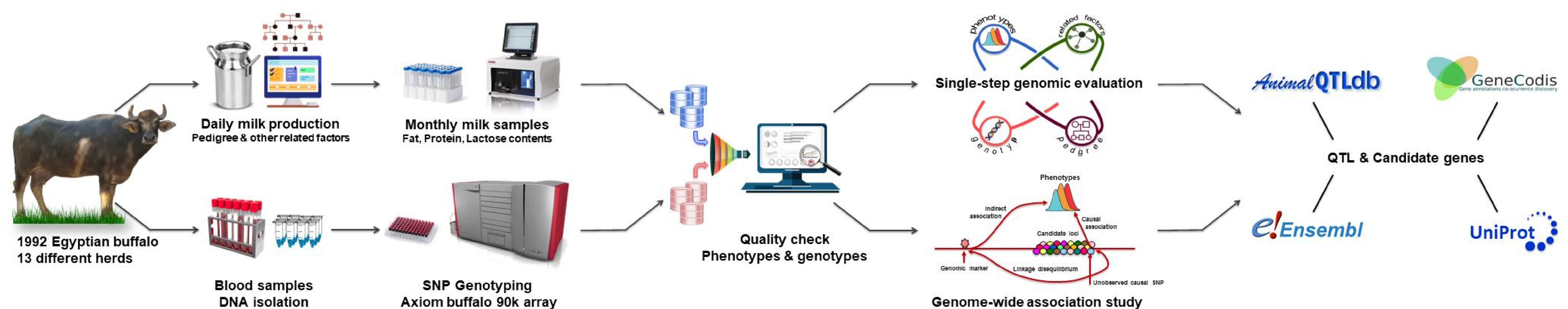
Background

Local livestock breeds such as Egyptian buffalo are crucial for supplying animal protein to local communities. The potential of this species is often underestimated and underutilized due to the lack of national recording systems and insufficient pedigree information, hindering traditional breeding efforts. The combination of uncontrolled insemination with foreign semen and economic crises has led to a 60% decline in their population in the last five years, putting their genetic potential at risk.

Objective

Explore the potential of integrating genomic information into breeding evaluations for Egyptian buffalo to achieve sustainable food production and preserve the genetic diversity.

Materials and Methods



Key Findings

Genome-wide association studies

- **SNP Discovery and QTL Mapping:** We identified 47 significant single nucleotide polymorphisms (SNPs) across 20 chromosomes (Figure 1), highlighting the polygenic nature of milk production traits.
- **Integration with Existing Knowledge:** The significant SNPs were mapped to 36 quantitative trait loci (QTL), with 11 regions overlapping known QTL. All genomic regions were located proximate to candidate genes with known biological functions linked to milk production traits. This integration of genomic and functional data strengthens the credibility of our findings.

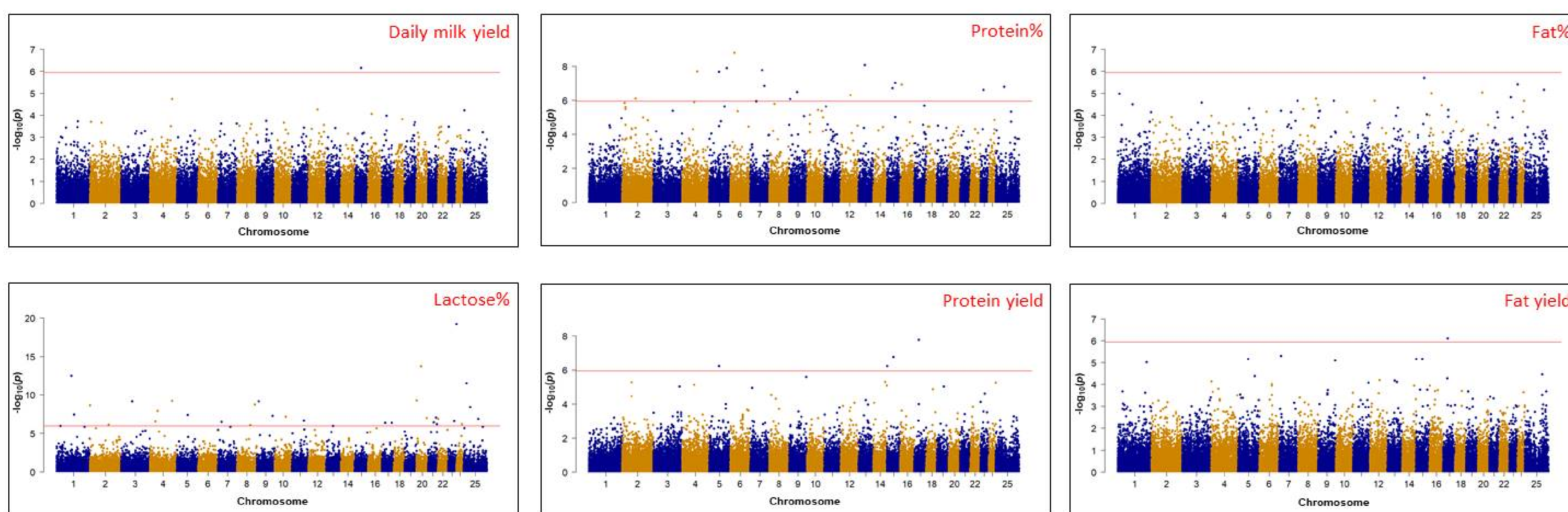


Figure 1: Genome-wide association analyses for milk production traits in Egyptian buffalo. The Horizontal lines indicate significant threshold level after Bonferroni correction

Single-step genomic evaluation

- **Heritability Insights:** Daily milk yield exhibited a heritability estimate of 0.20 ± 0.03 , indicating potential for production improvement.
- **Enhanced Prediction Accuracy:** Single-step yields a marginal 0.01 improvement in prediction accuracy, accompanied by a reduction in SE compared to pedigree-only.
- **Wide-reaching Genetic Influence:** Top ten segments across chromosomes 1, 2, 3, 4, 6, 9, 11, 12, and 16 explain 6% additive genetic variance. Adding another set raises this to 10% (Figure 2).

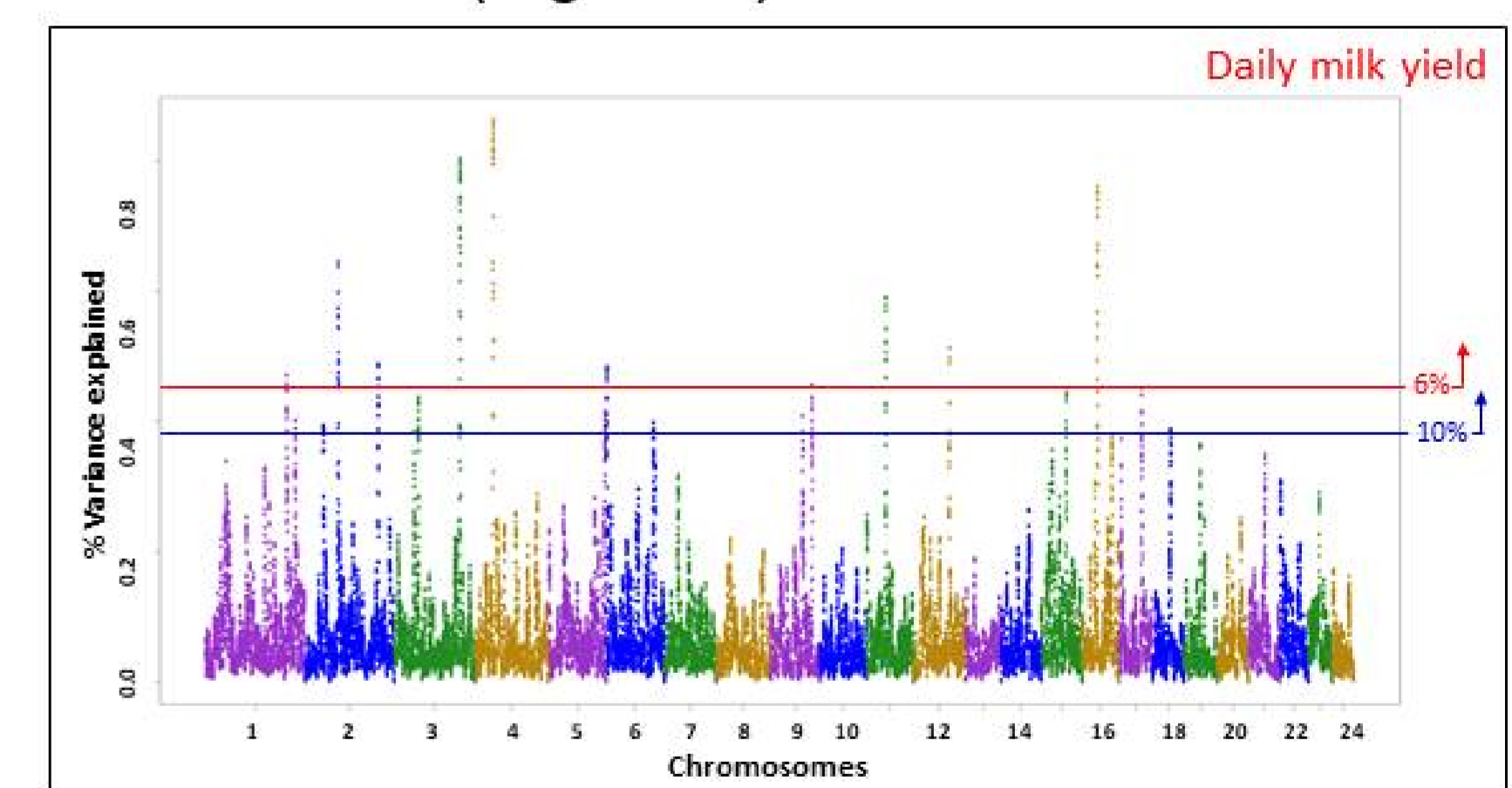
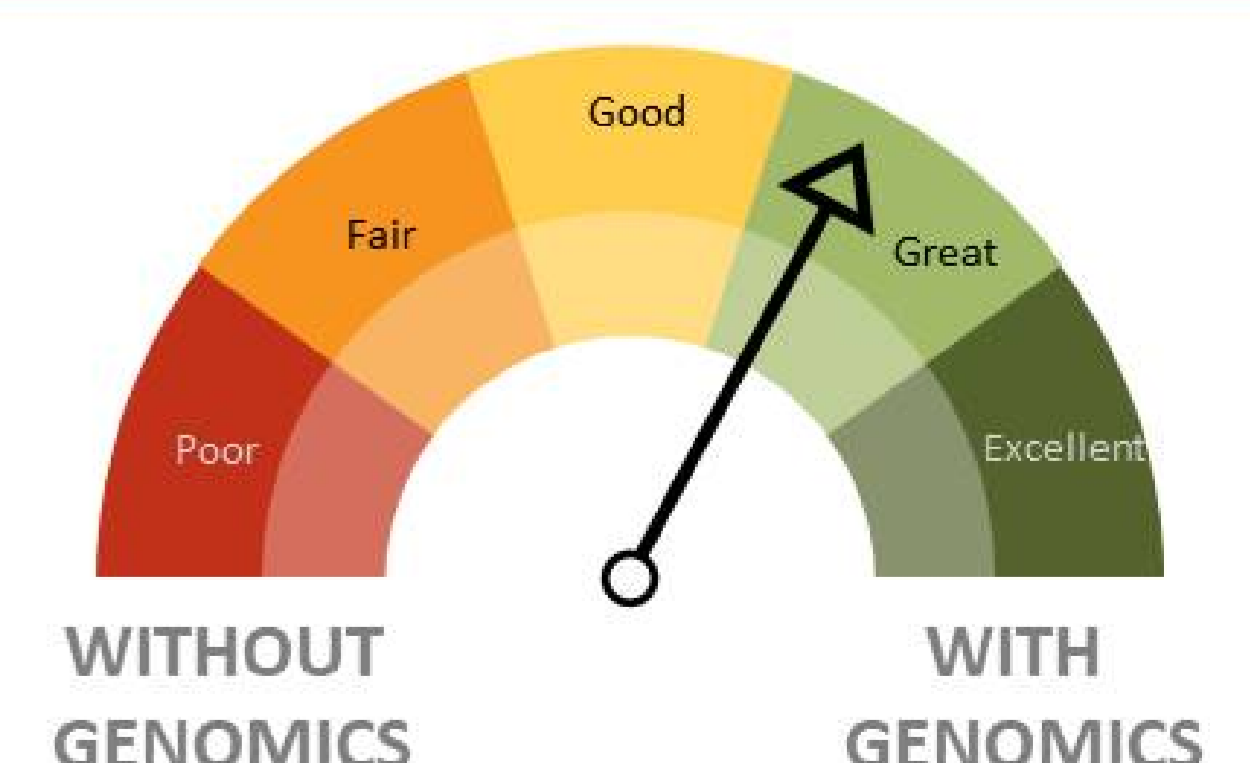


Figure 2: Additive genetic variance explained by each SNP for daily milk yield in Egyptian buffalo.

Conclusions

- Genomics plays a pivotal role in unlocking the production potential of Egyptian buffalo.
- Integrating genomics enhances accuracy despite limited pedigree and small samples.
- This advancement supports food security and genetic diversity preservation.
- Our work facilitates sustainable breeding, fostering a resilient future.



Further Reading



Acknowledgments



Technology
Arts Sciences
TH Köln

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