

GENOME-WIDE SCAN REVEALS CANDIDATE GENES RELATED TO MILK PRODUCTION AND ADAPTIVE TRAITS IN SICILIAN CATTLE BREEDS

Serena Tumino¹, Donata Marletta¹, Giorgio Chessari¹, Santina Di Bella², Salvatore Mastrangelo³, Annalisa Guercio², Alberto Cesarani⁴, Andrea Criscione¹, Salvatore Bordonaro¹

¹University of Catania, Catania, Italy; ²Istituto Zooprofilattico Sperimentale della Sicilia “A. Mirri”, Palermo, Italy;
³University of Palermo, Palermo, Italy; ⁴University of Sassari, Sassari, Italy.

serena.tumino@unict.it

INTRODUCTION

Climate change is a pressing global issue that significantly impacts livestock systems. Selection towards heat-tolerant traits represents a major challenge for this sector. Preserving local breeds such as Cinisara (CIN) and Modicana (MOD), native to Sicily and adapted to its hot climate over centuries, is crucial for maintaining genetic diversity, enhancing resilience to climate change and supporting local economies. Cinisara and Modicana are endangered cattle breeds well-adapted to harsh environments. The Cinisara breed is primarily raised in the province of Palermo, while the Modicana breed is bred all over Sicily. These valuable breeds are renowned for producing traditional and high-quality cheeses: Caciocavallo Palermitano and Ragusano PDO, respectively.

This study aims to assess within-breed genetic diversity, detect runs of homozygosity (ROH) pattern and pairwise FST-outliers to identify genomic regions potentially associated with resilience and heat tolerance in these endangered breeds, by performing high-density genomic analysis.



Cinisara
7259 Individuals (BDN – 2023)
Rick State (FAO): at risk

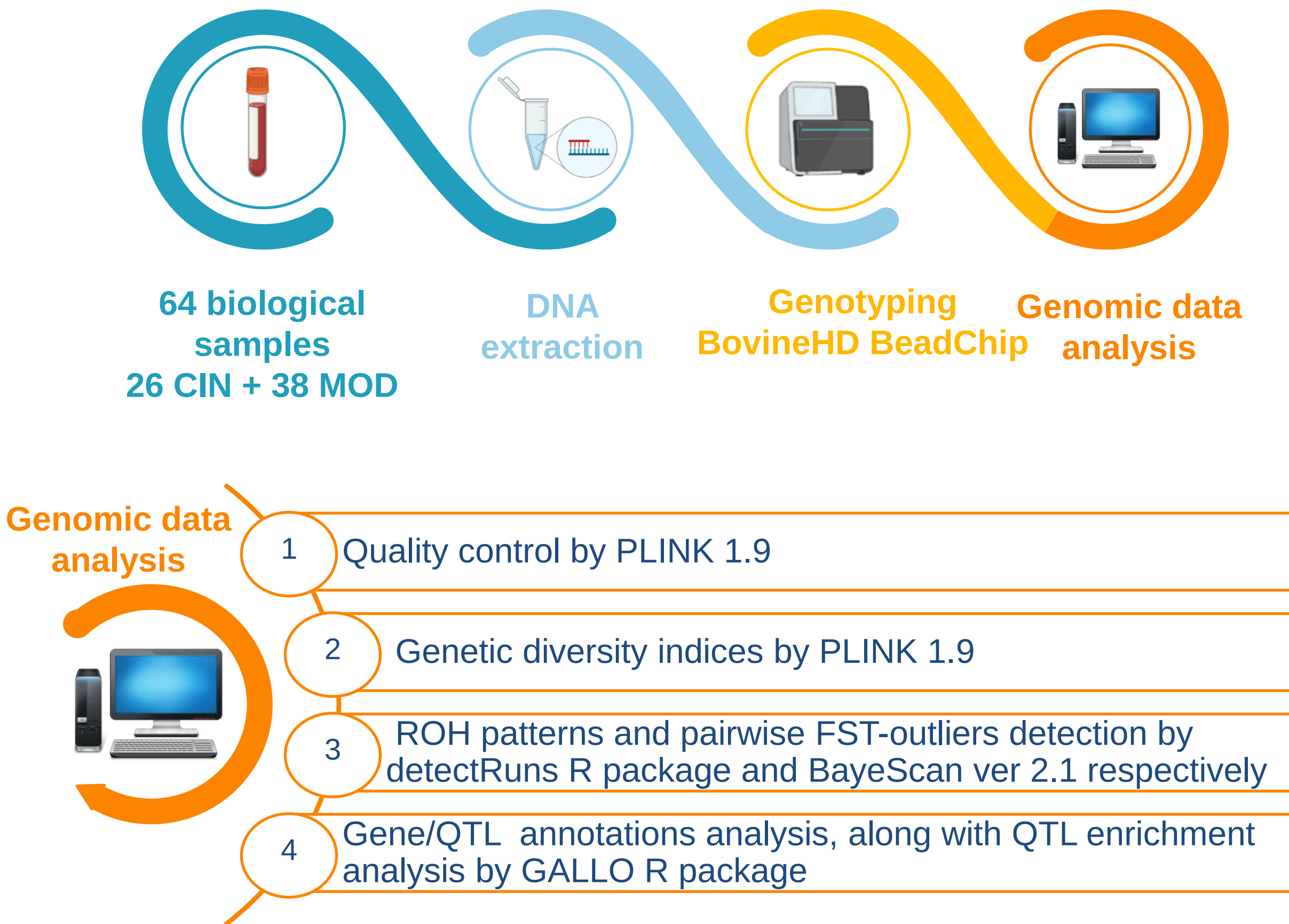


Modicana
6373 individuals (BDN – 2023)
Risk State (FAO): at risk

CONCLUSIONS

This preliminary study could be useful in defining relevant population genomic information and could reveal adaptation-related traits in CIN and MOD. These initial findings encourage further study to disentangle the genomic basis of the adaptation to hot climate in these Sicilian native cattle breeds.

MATERIAL AND METHODS



RESULTS

Analysis revealed a moderate within-breed level of variability in both breeds (Table 1). CIN exhibited half of the genomic inbreeding of MOD ($F_{ROH} = 0.06$ vs 0.12) (Table 2). In both breeds the high proportion of short ROH (82.6% and 74.9% were less than 2 Mbp long in CIN and MOD, respectively) highlighted the occurrence of old inbreeding events (Figure 1).

Table 1. Genetic diversity parameters

Breed	Ho	He
Cinisara	0.355	0.354
Modicana	0.374	0.367

Table 2. Parameters results of ROH analysis

Breed	Parameters	Mean	s.d.
Cinisara	S_{ROH}	207.07	90.93
	N_{ROH}	1.83	0.24
	L_{ROH}	290.26	145.07
	F_{ROH}	0.12	0.06
Modicana	S_{ROH}	90.41	40.70
	N_{ROH}	1.59	0.36
	L_{ROH}	153.99	155.25
	F_{ROH}	0.06	0.06

Seven ROH islands in CIN harboured 643 markers distributed in 7 chromosomes (BTA1, BTA6, BTA14, BTA15, BTA16, BTA21, BTA23), whereas a unique ROH island on BTA6 (783 SNPs) was identified in MOD.

ROH islands and FST-outliers approaches revealed QTLs involved in milk production, meat and carcass, reproduction, health, and local adaptation traits. In CIN the ROH hotspot on BTA14 (57 SNPs) harboured QTLs and genes (HSF1, DGAT1, ZNF34) related to milk production and heat tolerance. In particular, the HSF1 gene plays a key role in lactating dairy cows' cellular response to heat stress.

In the CIN breed, 95.02% of identified QTLs were related to milk production. In MOD QTL type for production, meat carcass, and milk traits were annotated and accounted for 60.02%, 24.84%, and 13.18%, respectively (Figure 2).

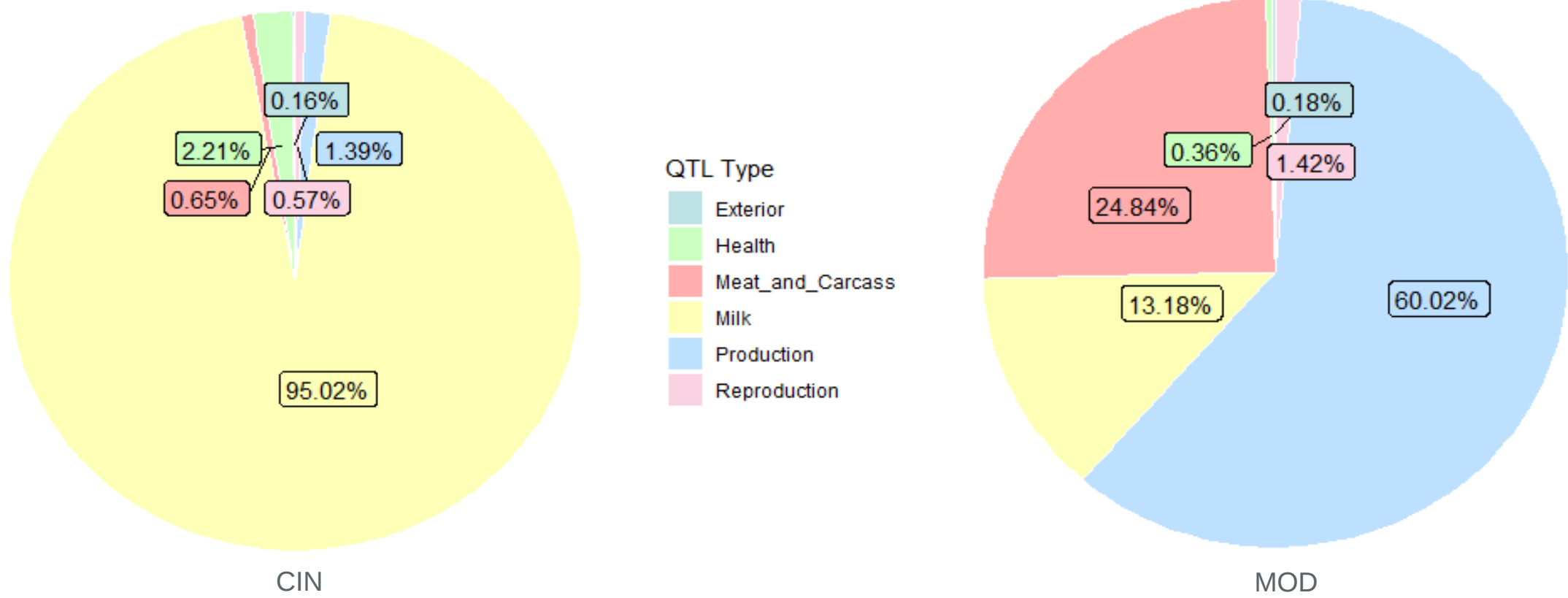


Figure 2. Mapping of QTLs in Cinisara and Modicana cattle breeds

The top most significant QTLs (Bonferroni-corrected p -value ≤ 0.05) identified by the QTL enrichment analysis were mapped on BTA14 in CIN and on BTA6 in MOD and are associated with milk, production and health traits (Figure 3).

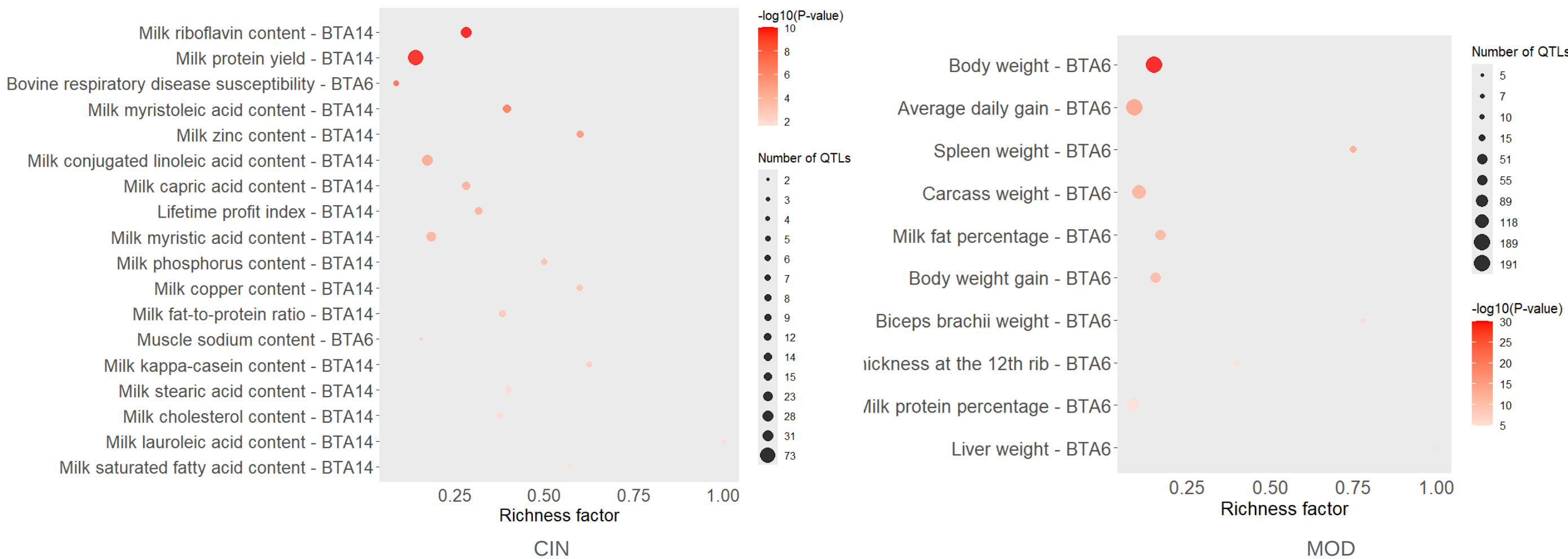


Figure 3. QTL enrichment analysis in Cinisara and Modicana cattle breeds

ACKNOWLEDGMENTS

This study was carried out within the Agritech National Research Center and received funding from the European Union Next-GenerationEU (PIANO NAZIONALE DI RIPRESA E RESILIENZA-PNRR-MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1,4 – D.D. 1032 17/06/2022, CN00000022).

This research was financed by Istituto Zooprofilattico Sperimentale della Sicilia – Project A.R.C.A.S. Azioni per il Recupero dei Caratteri Autoctoni in Sicilia. PSR Sicilia 14/20–Operazione 10.2b “Conservazione delle risorse genetiche animali in agricoltura”