

A MULTI-BREED GENOME-WIDE ASSOCIATION STUDY FOR TEMPERAMENT IN THREE ITALIAN BEEF CATTLE BREEDS

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Fig. 1: Marchigiana



Fig. 2: Chianina



Fig. 3: Romagnola

Introduction

Marchigiana (Fig. 1), Chianina (Fig. 2), and Romagnola (Fig. 3) are local Italian beef cattle breeds characterized by their large size, posing a real risk of injury the personnel and damage to properties during management. The temperament trait plays indeed an important and increasingly role in breeding plans due to the benefits it can bring to farm productivity, animal welfare, and safety. A genetic component in the manifestation of temperament is also well documented and could be related to various biochemical, hormonal, and neurological factors. The aim of this study was to detect potential genomic associations for the temperament phenotype within three Italian beef cattle breeds in a multi-breed dataset of young bulls in performance test.

Materials and methods

A total of 228 animals (84 Marchigiana, 78 Chianina, 63 Romagnola) were phenotyped for temperament and genotyped using the GeneSeek Genomic Profiler Bovine HDv3 150K chip (Illumina Inc., San Diego, CA, USA). Temperament was recorded as a linear score during 12 different stages and manipulations by assessors during the performance test, and the final values were rank-based transformed with GenABEL package in R. Genotypes were quality controlled with BITE package in R (id.cr<0.95; snp.cr<0.95; MAF<0.05; hweq<10⁻⁶), resulting in 117,662 SNPs for genome-wide association study. Breed, year, and month of birth were included in the models. Variance components and heritability (Tab. 1) were estimated by Gibbs sampling with Gibbsf90+ software (100,000 cycles, 1,000 burnin, 10 thinning interval). GWAS was performed with GEMMA software, employing a univariate linear mixed model.

Temperament

σ^2_a	0.44 (0.26)
σ^2_e	0.60 (0.21)
h^2	0.41 (0.22)

Tab. 1: Posterior means and standard deviations of additive genetic variance (σ^2_a), residual variance (σ^2_e), and heritability (h^2).

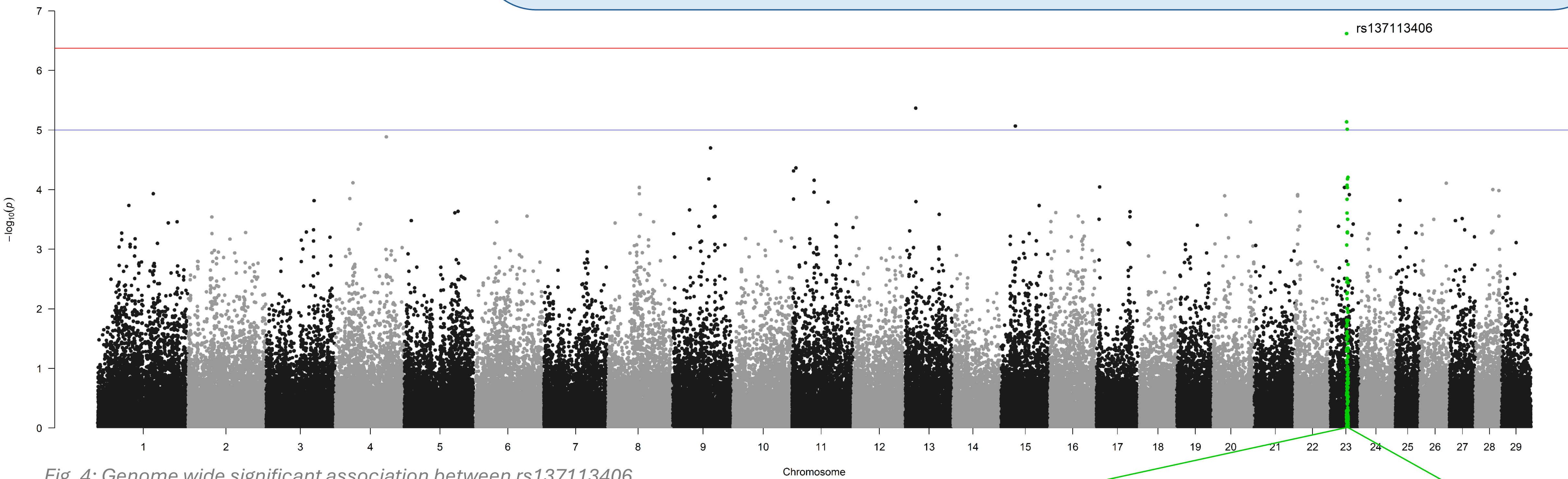


Fig. 4: Genome wide significant association between rs137113406 and temperament in Italian beef cattle breeds. The red line represents the Bonferroni-corrected threshold of significance.

Results & conclusions

The results highlighted a significant SNP (rs137113406) on BTA23 associated with temperament (P -value 1.30×10^{-7}) (Fig. 4). This SNP mapped inside the largest cluster of olfactory receptor genes in the cattle genome, and close to *GABBR1* gene (Fig. 5). Animal olfaction, olfactory receptor genes, and receptor-coding genes for GABAergic synapses are primarily related to animal behaviour and responses to stimuli. Further studies with higher amount of data will be necessary to validate this locus and estimate other QTLs associated to docility. Nevertheless, the results suggest the potential for genomic and marker-assisted selection on temperament traits, which could improve animal welfare, social sustainability, and animal productions.

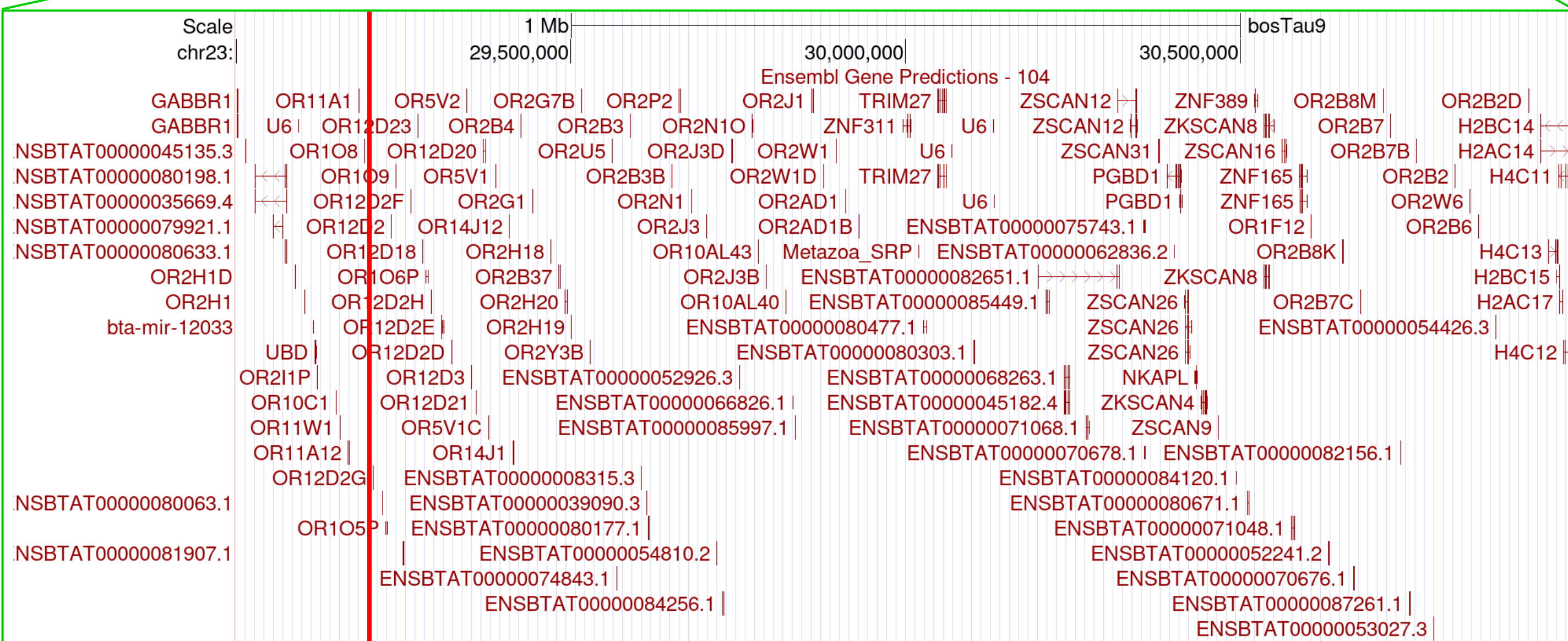


Fig. 5: A highlight on BTA23:29000000-31000000, the largest olfactory receptor gene cluster in bovine genome (Lee et al. BMC Genomics (2013) <https://doi.org/10.1186/1471-2164-14-596>). The red line represent the significative SNP.

