

Analysis of BTA6 in Bruna Italiana and Pezzata Rossa cattle assayed with 2,535 SNPs

Paolo Ajmone-Marsan¹, Rosanna Marino¹, Davide Perini¹,
Francesca Sibella¹, Ezequiel Luis Nicolazzi¹, Lorraine Pariset²,
Stefania Dall'Olio³, Luca Fontanesi³, Alessandro Bagnato⁴,
Fausta Schiavini⁴, Antonia Bianca Samoré⁴, Tullio Luttmann⁵,
Enrico Santus⁶, Michele Blasi⁷, Nicolò Pietro Paolo Macciotta⁸,
Alessandro Nardone²

¹Istituto di Zootechnica, Università Cattolica del Sacro Cuore, Piacenza, Italy

²Dipartimento di Produzioni Animali, Università della Tuscia, Viterbo, Italy

³DIPROVAL, Sezione di Allevamenti Zootechnici, Università di Bologna, Italy

⁴Dipartimento di Scienze e Tecnologie Veterinarie per la Sicurezza Alimentare, Università di Milano, Italy

⁵Associazione Nazionale Allevatori Pezzata Rossa Italiana (ANAPRI), Udine, Italy

⁶ Associazione Nazionale degli Allevatori di Razza Bruna (ANARB), Verona, Italy

⁷Laboratorio Genetica e Servizi (LGS), Cremona, Italy

⁸Dipartimento di Scienze Zootechniche, Università di Sassari, Italy

Corresponding author: Paolo Ajmone-Marsan. Istituto di Zootechnica, Università Cattolica del Sacro Cuore. Via Emilia Parmense 84, 29100 Piacenza, Italy - Tel. +39 0523 599205 – Fax: +39 0523 599276 – Email: paolo.ajmone@unicatt.it

ABSTRACT

A high density SNP marker panel (54,000 SNPs) was used to investigate the genome of 775 Bruna Italiana and 493 Pezzata Rossa bulls. Observed and expected heterozygosities were calculated overall and per chromosome. In both breeds, values were not significantly different. *Bos taurus* Chromosome 6 (BTA6), carrying the casein loci, was analysed in higher detail. Overall, 2,535 markers were assayed on this chromosome. After discarding monomorphic markers, those having more than 10 missing values, and those having minor allele frequency below 2%, 1,814 and 2,061 SNPs were retained in Bruna Italiana and Pezzata Rossa, respectively. To detect signatures of ancient and recent selection, we calculated F_{IS} inbreeding coefficient values of all BTA6 polymorphic markers, within sliding windows of groups of 5 adjacent SNPs and within 122 adjacent regions spanning 1 Mb intervals. These preliminary analyses indicated that genotyping of several thousand SNPs potentially allows the detection of the footprint of selection dodging the confounding effects of the population demographic history (i.e., effective population size, genetic structure, and mating pattern). A wider understanding of how and where selection shaped patterns of genetic variation along the genome may provide important insights into the dynamics of evolutionary change, facilitating both the identification of functionally significant genomic regions and genotype-phenotype correlations. Outlining such regions could allow focusing the fine mapping strategy to identify candidate genes and causative mutations affecting important economic or adaptive traits.

This work has been supported by the SelMol project financed by MIPAAF.