

Descriptive analysis of haplotypes in a population of Canchim beef cattle¹

Mokry, FB²; Lima, AO³; Mudadu, MA⁴; Higa, RH⁵; Meirelles, SLC⁶; Silva, MVB⁷; Cardoso, FF⁸; Niciura, SCM⁴; Alencar, MM⁴; Regitano, LCA⁴

¹Projeto financiado pela CAPES; ²Pós-doutoranda do PPGGEv - UFSCar, São Carlos, SP. Bolsista da CAPES; ³Mestranda do PPGGEv - UFSCar, São Carlos, SP; ⁴Pesquisador da Embrapa Pecuária Sudeste, São Carlos, SP; ⁵Pesquisador da Embrapa Informática Agropecuária, Campinas, SP; ⁶Professora da UFLA, Lavras, MG; ⁷Pesquisador da Embrapa Gado de Leite, Juiz de Fora, MG; ⁸Pesquisador da Embrapa Pecuária Sul, Bagé, RS.
abiana_barichello@yahoo.com.br

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Genome-wide association studies are being favored by the fast progress in high-throughput single nucleotide polymorphism (SNP) detection and genotyping technologies that is making available thousands of SNPs for studying. The development of linkage disequilibrium (LD) maps and the characterization of haplotype blocks structure at the population level is very important for understanding the nature of non-linear association between phenotypes and genes. The aim in this study was to descriptively analyze haplotypes from a Canchim beef cattle population. A sample of 400 Canchim animals was genotyped by the Illumina BovineHD Beadchip that uniformly spans the entire bovine genome with over 777,000 SNPs. After quality control processing, 708,641 SNPs were left in the analysis. The haplotypes were reconstructed for each chromosome (chr) using the software called fastPhase, and then the reconstructed haplotypes were inserted into the software Haploview (using default parameters) to visualize and calculate the haplotype blocks and to estimate LD statistics based on the squared correlation coefficient between SNP pairs (r^2). Chr 1 showed the maximum number of haplotypes with 6,871 haplotype blocks, while chr 25 showed the minimum number of haplotypes with 2,154 haplotype blocks. The average size of haplotypes ranged from 11.40kb on chr 23 to 17.01kb on chr 5, and the maximum haplotype size (499.96kb) was found on chr 23. The average number of SNPs forming a haplotype was around 5 SNPs, with the minimum number of SNPs in a haplotype being 2 SNPs and the maximum number of SNPs in a haplotype being 126 SNPs located on chr 2. The haplotype blocks coverage length ranged from 26383.79kb on chr 25 to 108903.3kb on chr 1, and the percentage of chromosome coverage ranged from 58.46% on chr 23 to 69.52% on chr 9, with an average of 65.76% of the genome covered by haplotype blocks. The chromosome with the least number of SNPs in blocks was chr 27 with 10,112 SNPs, while the chromosome with the greatest number of SNPs in blocks was chr 1 with 37,483 SNPs. Further studies on Canchim haplotype block structure will allow the comparison of conserved haplotype areas shared with other breeds, and also will provide means for identification of signatures of recent selection.