CAN GENETICS BE ASSOCIATED WITH THE HIGH FREQUENCY OF DARK, FIRM AND DRY MEAT IN BRAZILIAN NELLORE BEEF CATTLE?

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Abstract – The aim of this work is to investigate if there are genetic components associated with the higher frequency of Dark, firm and dry (DFD) meat in Brazilian Nellore beef cattle. The dataset used for this investigation was comprised of genomic and phenotypic (24h postmortem meat pH) records of 1,642 Nellore animals. For the specific analysis related to the DFD condition, phenotypes were transformed to a binary variable, where pH values ranging between 5.5 and 5.8 were considered "not affected" (zero) and values above 6.0 were considered "affected" (one). Estimates of single-nucleotide polymorphism (SNP) effects suggested possible candidate regions in chromosomes 1, 3, 7, 8, 11, 13 and 23. Our results indicate potential regions containing genes related to pH 24 hours post mortem in Nellore beef cattle.

Key Words – genomics, meat quality, pH

I. INTRODUCTION

Dark cuts has been a huge problem for the fresh meat industry and causes significant losses globally. Extensive research has shown potential causes of dark cutting or DFD meat, such as the nutrition level, animal age, stress prior the slaughter, transportation, among others. All these factors will contribute for a less glycogen offer after animal dead and the pH will remain high affecting the water holding capacity, color and texture of the meat [1]. Achieving in previous events reported by local industries extreme values close to 40% of all the meat produced in Brazil has DFD cuts. Therefore, the aim of this work is to investigate if there are genetic components associated with the higher frequency of DFD meat in Brazilian Nellore beef cattle.

II. MATERIALS AND METHODS

The complete dataset contained genomic and phenotypic information from 1,642 Nellore breed animals, having information about 24h postmortem meat pH. For the specific analysis of the DFD condition, phenotypes were transformed to a binary variable, where pH values ranging between 5.5 and 5.8 were considered "not affected" (zero) and values above 6.0 were considered "affected" (one).

Quality control (CQ) process was carried out using the PREGSF90 software [2] with the objective of reducing spurious associations and, therefore, increase the accuracy of genomic analysis. Information on SNPs located in chromosomes X and Y, mitochondrial region or markers not mapped were discarded for this investigation. Quality control parameters assumed for removing non-informative SNPS were: minor allele frequency (MAF) < 0.02, call rate by SNP < 0.95 and SNPs with a p-value in the Hardy-Weinberg equilibrium z-test less than or equal to 10−5. After quality control and data editing, information on 465,441 SNPs and 647 animals remained for the genomic investigation. Variance component estimation was performed by a threshold model, relating observed phenotype in a categorical scale to an underlying normal continuous scale, using the THRGIBBS1F90 [2] software. The proposed statistical model considered herd information and age at slaughter (as a covariate) as fixed effects. Marker effects were estimated using a GPLUP method, assuming a normal distribution for the vector of SNP effects.

III. RESULTS AND DISCUSSION

Mean posterior estimates (and confidence intervals - CI) for the genetic additive and residual effects were 2.05 (0.05 – 3.81) and 1.04 (0.87 – 1.24), respectively. The means posterior estimate for the heritability (and CI) was 0.38 (0.03 – 0.81). Estimates of SNP effects suggested possible candidate regions in chromosomes 1, 3, 7, 8, 11, 13 and 23 (Figure 1). The 10 SNPs with the higher effect were located in chromosome 8 (2 SNP), 11 (1 SNP) and 13 (8 SNP). In chromosome 8, SNPs with the higher estimated effects were the BovineHD0800029973 and BovineHD0800029973, located around 101.16Mb. In chromosome 11, the SNPS with higher estimated effect was the BovineHD1100024240, placed at 8.43Mb. For the chromosome 13, SNPS with the higher effects were the BovineHD130000008083, BovineHD130000008084, BovineHD130000008092, BovineHD130000008095, BovineHD130000008096, BovineHD130000008098, BovineHD130000008099 e BovineHD130000008100, all closely placed around 2.78Mb.

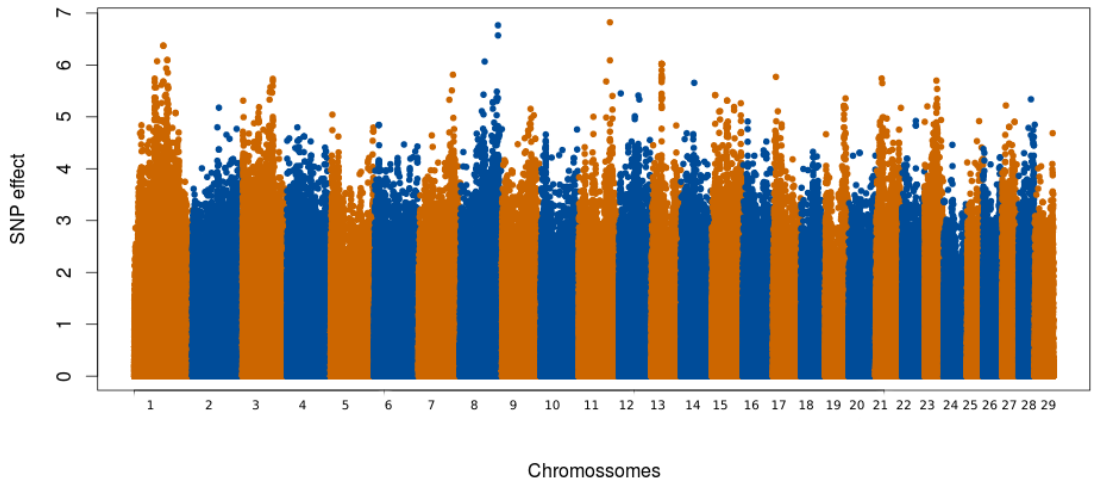

Figure 1. Manhattan plot suggesting genomic regions associated with DFD condition in Nellore beef cattle.

IV. CONCLUSION

Our results indicate potential regions containing genes related to pH 24 hours post mortem in Nellore beef cattle. Further investigation combining information of the reported genes and its biological pathways is required to better explain their possible association with high DFD frequency on Brazilian cattle.

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