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A network landscape from CNVs to Nellore cattle beef tenderness

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Abstract:

Nellore (*Bos taurus indicus*) is a breed of great importance to beef production in Brazil. The systematic study of Nellore's genome can contribute to a better understanding physiology of interest traits. One important trait to beef cattle is beef tenderness. It is already known that when compared with *Bos taurus taurus* animals, *Bos taurus indicus* have less tenderness in general. Identifying polymorphisms associated to tenderness seems to be a good way to mitigate this problem. There are several types of polymorphisms in genome, and one that has been receiving increasing attention is Copy Number Variation (CNV). CNVs are structural variations in genome, which are represented by deletions, duplications, and translocations inter or intra-chromosomal, comprising segments larger than one kb. This work aims to perform a couple of in silico network analysis from CNVs standpoint, shedding light to possible metabolic connections to tenderness. It was used 671 Nellore males to infer CNVs, through SNP-chip (Illumina Bovine HD Beadchip®, containing approximately 770 thousand SNPs) and PennCNV software methodology. CNV regions (CNVRs) were inferred by CNVRuler (recurrence 0.1). The data was crossed with quantitative trait loci (QTL, Animal QTLdb), genes (BioMart - Ensembl), metabolic pathways (Reactome), RNA-seq (previously RNA-seq analysis of some animals of our population, which established some significant transcription loci to beef tenderness (STL)) and SNP-GWAS (Prior GWAS analysis, of our population, which identified SNPs that explain the greatest proportion of additive genetic variance: highest V values), i.e, SNPs most associated to beef tenderness trait (24 hours, 7 and 14 days after slaughter). Phenotypes, in our population, were measured by Warner-Bratzler shear force (WBSF) method. The largest two hundred V values found in SNP-GWAS analysis were inspected to find which were inside CNVRs. After PennCNV-CNVRuler analysis, a total of 2,543 CNVRs were found. From these, 116 CNVR overlapped with 9 different tenderness score QTLs (trait_ID=1030) from the Animal QTLdb, most of them located on chromosome 5. The 2,543 CNVRs hold 1,985 genes, and 120 were linked with some known metabolic pathway from Reactome database. Interestingly, some genes were related to muscle contraction pathway (like Troponin T and Myosin-1). Two CNVR overlapped with STLs. For CNVR SNP-GWAS cross, in first measurement at 24 hours after slaughter, 5 CNVRs keeping 6 SNPs were found (50% in chromosome 5), for the 7 days 4 CNVRs on 8 SNPs (62,5% in chromosome 16) and for the 14 days measurements 3 CNVRs on 8 SNPs (87,5% in chromosome 6). This study indicates that CNVRs could help explain some of the variation observed in meat tenderness to Nellore cattle. However, this regions need to be validated by other methods before they can be used in breeding programs. Moreover, the integration of different analysis approaches will allow a better understanding of a given phenotype as a whole.