

CONSTRUINDO SABERES, FORMANDO PESSOAS E TRANSFORMANDO A PRODUÇÃO ANIMAL

GENOME WIDE ASSOCIATION STUDY FOR MEAT COLOR TRAITS IN NELORE CATTLE

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Color is the main factor determining consumers purchase decision, since it is an indicator of quality, freshness and food safety. Environmental conditions affect muscle metabolic properties i.e. *Myoglobin* concentration, redox state, mitochondrial activity, muscle fibers structure and others, which largely determine meat color. However, there are evidences of an additive genetic component affecting meat color traits. Advances in genotyping technologies have allowed the inclusion of molecular markers in Genome-wide association studies (GWAS), which enable to identify genetic variants associated with complex traits providing a better understanding of genetic mechanisms controlling them. We performed GWAS with the aim of identifying genomic regions of large effect on meat color traits in Nelore cattle, as well as to find potential candidate genes within those regions and to describe their biological roles. Phenotypic records of meat color traits (L^* , lightness; a^* , redness; b^* , yellowness) from around 4,450 Nelore males were used, of which a total of 3,794 were genotyped considering 414,577 SNPs. The single step GBLUP approach was used, which allows the inclusion of all animals with known phenotypes and/or genotypes records. The analyzes were carried out using the BLUPF90 family programs in a single trait model, including the fixed effect of contemporary group, defined by farm, yearling management group, season and year of birth, as well as the linear covariate of age at slaughtering, and the random effects of direct additive genetics and residual. GWAS results were reported as the proportion of variance explained by windows of 150 adjacent SNPs. The top 10 ranking windows explained 13.64%, 15.12% and 13% of genetic variance of L^* , a^* and b^* , respectively. These regions are located on chromosomes 2, 5, 6, 9, 13 and 18 for L^* ; chromosomes 3, 4, 6, 7, 11, 24 and 28 for a^* and chromosomes 1, 2, 6, 11, 13, 14 and 18 for b^* . In addition, 129, 70 and 83 positional candidate genes were identified within these regions, respectively. Functional analysis showed that genes associated with meat color traits are mainly involved in mitochondrial activity, energy metabolism and muscle's structure integrity. These biological processes seem to indirectly affect meat color stability by generating changes in *Myoglobin's* biochemical structure.

Keywords: GWAS, genomic regions, muscle coloring, variation.

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