



66th
Brazilian
Congress of
Genetics

2021

GENÉTICA

13 a 16 | setembro | 2021 ON-LINE

Homenageados: pesquisadores e profissionais da saúde



XIX SIMPÓSIO DE CITOGENÉTICA E GENÉTICA DE PEIXES



REGEM 32

32ª - REGEM

Reunião de Genética de Microrganismos



II Congreso
Latinoamericano
de Genética para la
Conservación

CLaGeneC

II CLaGeneC

II Congresso Latino-Americano
de Genética para Conservação

SOBRE

POLYMORPHISMS ASSOCIATED WITH WHITE STRIPING BREAST MYOPATHY IN CHICKENS

Débora Ester Petry Marcelino ¹; Adriana Mércia Guaratini Ibelli ^{2,3}; Jane de Oliveira Peixoto ^{2,3}; Letícia Alves Salmória ³; Maurício Egídio Cantão ²; Mônica Corrêa Ledur ^{2,4}

¹ Facc - Faculdade Concórdia; ² Embrapa Suínos e Aves, Concórdia, SC; ³ Programa de Pós-Graduação em Ciências Veterinárias, Universidade Estadual do Centro-Oeste (Unicentro), Guarapuava, PR.; ⁴ Programa de Pós-Graduação em Zootecnia, UDESC-Oeste, Chapecó, SC

ABSTRACT

White Striping (WS) is one of the most prevalent pectoral myopathies that negatively affects meat quality, jeopardizing also in its appearance, texture and nutritional aspects. This condition is characterized by the appearance of white streaks parallel to muscle fibers in the chicken breast and have been associated to the intense genetic selection for rapid growth and carcass and breast yields. Due to the substantial production losses caused by this myopathy, this study aimed to identify variants related to WS through the pectoralis major muscle transcriptome of 3 normal and 3 WS-affected broilers. Reads were submitted to quality control using the Trimmomatic and mapped against the chicken genome (GRCg6a) with the STAR. The Genome Analysis Tool kit 3.6 (GATK) was used for polymorphism identification and the Ensembl Variant Effect Predictor (VEP) to annotate and predict the variant effect. A total of 757 variants were found between groups and about 10% of all polymorphisms were firstly described in the current study. Most of the variants were classified as downstream, synonymous, upstream, 3' UTR, intronic, 5' UTR and missense variants. Out of coding variants, 284 were classified as synonymous, 1 inframe deletion and 57 as missense, located in 44 annotated genes. Considering the missense variants 6 were predicted with deleterious consequence in the *SYNPO*, *PDGFRB* e *TMEM59* genes (SIFT < 0.02). These genes act as actin binding, migration and recruitment of smooth muscle cells, and apoptosis, respectively, important processes that have already been related to chicken myopathies. Associations of these variants in large populations should be performed to clarify these genes as candidates for WS myopathy in broilers.

KEYWORDS: RNA sequencing; broilers; variant analysis

ACKNOWLEDGMENTS: This study was supported by EMBRAPA (01.11.07.002.04.03). LAS received a CAPES Scholarship and DEPM received a CNPq/PIBIC Scholarship at Embrapa.