ZOOTECNIA BRASIL
Centro de Convenções da PUC-GO | Goiânia-GO
27 a 30 de agosto de 2018

55ª REUNIÃO ANUAL DA SOCIEDADE BRASILEIRA DE ZOOTECNIA

ZOOTEC 28º CONGRESSO BRASILEIRO DE ZOOTECNIA

CONSTRUINDO SABERES, FORMANDO PESSOAS E TRANSFORMANDO A PRODUÇÃO ANIMAL

CROSS-VALIDATION STUDY OF QTLs ASSOCIATED WITH SEXUAL PRECOCITY IN TROPICAL BEEF CATTLE

Thaise Pinto de MELO*[1], Marina Rufino Salinas FORTES[2], Lucia Galvão de Albuquerque[1,3], Roberto Carvalheiro[1,3]

*corresponding author: thaise_p.melo@hotmail.com

[1] School of Agricultural and Veterinarian Sciences, Sao Paulo State University (UNESP), Via de Acesso Prof. Paulo Donato Castelane, 14884-900, Jaboticabal, SP, Brazil

[2]School of Chemistry and Molecular Biosciences, The University of Queensland, Saint Lucia Campus, Qld 4072, Australia

[3]National Council for Science and Technological Development, 71605-001, Brasilia, DF, Brazil

The aim of this study was to validate in a Nellore population, genomic regions associated with sexual precocity in Brahman cattle. The discovery dataset was constructed by selecting SNPs in genic regions previously associated with sexual precocity in Brahman. Traits studied were heifer early pregnancy (EP), defined as success (1) if heifers calved before 31 months of age or failure (0) if not; and scrotal circumference (SC) measured around 18 months of age. Statistical methods used were Bayes Cpi, whose model followed: $y = 1\mu + \sum_{i=1}^{n} g_i b_i \delta_i + e$, where y is the vector of EP and SC pre-corrected phenotypes for contemporary group (formed by concatenating information of herd, year and season of birth, weaning and yearling management groups), 1 is a vector of ones, μ is the overall mean, g_i is the vector with the genotypes of the animals for the i^{th} SNP effect in b_i, and δ_i is an indicator variable, which takes value 0 or 1; and a regression model, described as: $y = 1\mu + X\beta + Zu + e$, where y, 1, μ and e were described before, β is a vector containing marker effects, u is a vector of random polygenic additive effects, X and Z are incidence matrices relating marker effects in β and random effects in u. Significant SNPs presented P-values $< 1x10^{-4}$ for regression and Bayes factor ≥ 3 for Bayes Cpi analyses. These SNPs or their ± 250 kb surrounding region were considered validated. For EP, 13 SNPs were validated on chromosomes 6, 14, 16, 17, 21, 22 and 23. These regions harboured 12 genes. For SC, 7 SNPs were validated on chromosomes 2, 4, 13, 20 and 28, and these regions harboured 7 genes. In summary, genes in validated regions were associated with reproductive events: semen production (*MARCH1*), male sterility (*PTN*), uterine receptivity (*LMOD1*), fetal growth (*ST3GAL1*), female fertility (*PLCB1*), embryonic death (*ENC1*) and were expressed in reproductive tissues of mammalian species: ovary, cumulus cells, cervical tissue (*ST3GAL1*), placental extracellular matrix, granulosa cells, embryonic fibroblasts (*COL5A2*), uterus, endometrium (*PLCB1* and *ENC1*) and male reproductive tract (*PGAM2*). We could validate in Nellore 20 SNPs located in regions previously associated with sexual precocity in Brahman cattle. These SNPs and their ± 250 kb surrounding region are strong candidates to be affecting sexual precocity in Nellore and Brahman.

Keywords: Bos indicus, Brahman, GWAS, Nellore, reproductive traits, SNPs

Acknowledgments: The authors would like to thank Sao Paulo Research Foundation (FAPESP #2009/16118-5), National Council for Scientific and Technological Development (CNPq #559631/2009-0) for financial supporting; the Coordination for the Improvement of Higher Education Personnel (CAPES) for the scholarship for the first author and Alliance Nellore for providing the data used in this study.