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

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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 genetic 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: \[ y = 1\mu + \sum_{i=1}^{r} g_i b_i + \delta_i + e \], 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), \( I \) is a vector of ones, \( \mu \) is the overall mean, \( g_i \) is the vector with the genotypes of the animals for the \( i \) SNP effect in \( b_i \), and \( \delta_i \) is an indicator variable, which takes value 0 or 1; and a regression model, described as: \[ y = 1\mu + x\beta + Zu + e \], where \( y \), \( 1 \), \( \mu \) and \( e \) were described before, \( \beta \) 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 \( \beta \) 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 (ST3GALT1), female fertility (PLCB1), embryonic death (ENC1) and were expressed in reproductive tissues of mammalian species: ovary, cumulus cells, cervical tissue (ST3GALT1), 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

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