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CHALLENGES AND PERSPECTIVES

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Maryon Strack Dalle Carbonare
Patrick Schmidt

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www.sbz.org.br

and

The Department of Animal Science
(*Departamento de Zootecnia*)
Universidade Federal do Paraná - UFPR
Curitiba – PR
depzoot@ufpr.br

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Association of candidate genes with sexual precocity in Brahman heifers

Suqueli García, M.F.*[1], López Valiente, S.[2], Robson, C.[3], Menchón, P.[1], Quintana, S.[4], Corva, P.M.[1]

[1]Facultad de Ciencias Agrarias, Universidad Nacional de Mar del Plata, Argentina; [2]INTA – E.E.A. Cuenca del Salado, Argentina; [3]Actividad Privada; [4]Laboratorio de Biología Molecular, Fares Taie Instituto de Análisis, Mar del Plata, Argentina.

*Doctoral student – florsuqueli@gmail.com

Age at puberty is a very relevant trait associated with the lifetime reproductive performance of beef cattle. An overarching factor that influences age at puberty in heifers is nutritional management from weaning. This study aimed to analyse the association of three SNPs in selected candidate genes with sexual precocity in Brahman heifers from a subtropical area of Argentina and to evaluate the gene-environment (GxE) interaction between those genes and nutritional management. Three SNPs on genes from different metabolic ways previously associated with puberty onset (rs42404949 on TOX; rs43711078 on SLC1A2; and rs29004488 on LEP) were selected. 421 Brahman heifers from five farms were genotyped using a PCR-High Resolution Melting assay. The heifers had been previously evaluated for sexual precocity under three different nutritional managements after weaning (M1, M2, and M3, defined by management practices and grazing strategies in each farm with an average age at puberty of 1055, 825 and 519 days, respectively). Allele and genotype frequencies were estimated for each marker and compared with chi-square tests. Age at puberty was analysed with a logistic regression model with a logit transformation using the R package „lmer". The model relating the probability of detecting a sexually developed heifer at a given age included the fixed effects of marker genotype, nutritional management and their interaction, and the random effect of sire. The association studies showed no statistically significant results on sexual development for any of the markers. However, marked differences were detected in the allelic frequencies of the SNP in TOX and the genotypic frequencies of the three SNPs among nutritional levels. For LEP, a gene associated with feed intake and body composition, genotype CT had the highest frequency (95.0%) in the best nutritional treatment (M3) and was also associated with higher live weight in M1 (freq=0.24) and M2 (freq=0.80). For TOX, the allele considered favourable for sexual precocity (T) had a higher frequency in M1 ($freq_T$=0.72) and M2 ($freq_T$=0.81) than in M3 ($freq_T$=0.43). Furthermore, in M3 the heterozygous genotypes of the TOX and SLC1A2 markers also had the higher frequencies (TOX_{CT}=0.68; $SLC1A2_{AG}$=0.79). These results point to a differential response of these genes to selection under different management strategies, and suggest the existence of GxE interactions in the evaluation of reproductive traits in Brahman heifers. These trends should be confirmed with a more detailed genomic evaluation (e.g. search for signatures of selection) with GWAS strategies.

Keywords: puberty, Brahman heifers, candidate genes, GxE interactions

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