Association of polymorphisms in growth hormone and leptin candidate genes with live weight traits of Brahman cattle

N. Hernández[1], J.C. Martínez-González[1], G.M. Parra-Bracamonte[2], A.M. Sifuentes-Rincón[2], N. López-Villalobos[3,4], S.T. Morris[3], F. Briones-Encinia[1], E. Ortega-Rivas[5], V.I. Pacheco-Contreras[2] and L.A. Meza-García[2]

[1]Facultad de Ingeniería y Ciencias, Universidad Autónoma de Tamaulipas, Centro Universitario Adolfo López Mateos, Ciudad Victoria, Tamaulipas, México
[2]Instituto Politécnico Nacional, Centro de Biotecnología Genómica, Laboratorio de Biotecnología Animal, Reynosa, Tamaulipas, México
[3]Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Palmerston North, New Zealand
[4]Centro Universitario UAEM Temascaltepec, Universidad Autónoma del Estado de México, Temascaltepec, Estado de México, México
[5]Asociación Mexicana de Criadores de Cebú, Tamaulipas, México

Corresponding author: G.M. Parra-Bracamonte
E-mail: gparra@ipn.mx.

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ABSTRACT. Polymorphisms in candidate genes can produce significant and favorable changes in the phenotype, and therefore are useful for the identification of the best combination of favorable variants

for marker-assisted selection. In the present study, an assessment to evaluate the effect of 11 single nucleotide polymorphisms (SNPs) in candidate genes on live weight traits of registered Brahman cattle was performed. Data from purebred bulls were used in this assessment. The dataset included birth (BW), weaning (WW), and yearling (YW) weights. A panel of 11 SNP markers, selected by their formerly reported or apparent direct and indirect association with live weight traits, was included in an assessment previously confirming their minimum allele frequency (<0.05). Live weights were adjusted BW (aBW), WW (aWW), and YW (aYW) using a generalized linear model, which included the fixed effects of herd and season of birth and the random effect of the sire and year of birth. An SNP in a growth hormone gene (GH4.1) was significantly related to aWW (P = 0.035) with an estimate substitution effect of 3.97 kg (P = 0.0210). In addition, a leptin SNP (LEPg.978) was significantly associated with aYW (P = 0.003) with an estimate substitution effect of 9.57 kg (P = 0.0007). The results suggest that markers GH4.1 and LEPg.978 can be considered as candidate loci for assisted genetic improvement programs in Mexican Brahman cattle.

Key words: *Bos indicus*; GH4.1; Growth traits; LEPg.978; SNP