I-INTERNATIONAL MEETING OF ANIMAL SCIENCE IN SEMI-ARID REGIONS
Universidade Federal do Agreste de Pernambuco – UFAPE
July 03rd to 05th, 2024, Garanhuns-PE

Genetics, biotechnology, animal breeding and reproduction

Deletion in the *MC1R* gene associated with depigmentation in zebu cattle

Marisa S. Bastos*[1], Silel Vinicius S. A. Maciel[2], Ingrid P. P. Oliveira[2], Beatriz B. Senes[2], Jackeline S. Alves[2], Gregório Miguel F. de Camargo[2]
[1]Universidade Federal de Alagoas, Arapiraca/Bahia, Brasil; [2] Universidade Federal da Bahia, Salvador/Bahia, Brasil.
* marisa.bastos@arapiraca.ufal.br

Depigmented zebu cattle are unwanted by breeders. Animals are less resistant to sunlight and more prone to skin and eye problems. Furthermore, animals with this phenotype are not registered with the Brazilian Association of Zebu Breeders (ABCZ) and, consequently, have a lower market value. In the Guzerá breed, a depigmented cow with red fur, daughter of gray animals, was reported, which presented a homozygous deletion for indel c. 311 G > - in the MC1R gene. The deletion causes an anticipation of the stop codon, which is responsible for causing depigmentation in the breed. It is known that depigmentation also occurs in other zebu breeds, and the genetic cause is not known. Thus, the objective of the study was to verify the influence of the described deletion and other polymorphisms in the MC1R gene that are related to depigmentation in zebu animals.Total genomic DNA was extracted using the commercial extraction kit, from hair follicles, from 60 animals registered at ABCZ, 10 animals from each of the following breeds: Brahman, Gir, Indubrasil, Nelore, Sindi and Tabapuã, of different coats accepted for registration. Animals with a depigmented (barroso) phenotype of the Sindi (N = 2), Gir (N = 1) and Nelore (N = 1) breeds were also added. Quantifications of the extracted DNA were carried out using NanoDrop™ to observe the quality of the extracted material. Sample dilutions were carried out and PCRs were carried out using the primers F - 5′-AGGCGGACTGAGAACAGAAG-3′ e o R 5′-GCTATGAAGAGGCCAACGAG-3′ of the *MC1R* gene with the amplicons showing 772bp. The PCR products were electrophoresed in a 1.5% agarose gel and the amplicons were purified with 20% PEG, quantified, and sequenced for both primers. Sequences were edited and analyzed using BioEdit v.7.0.9.0 software. It was observed that among the animals recorded, genotypes c. 311 G/G and G/del, with a genotype frequency of 12% for the G/del heterozygote in the animals studied. All breeds had an animal with the deletion, except for the Indubrasil breed. Among depigmented animals, the following genotypes were observed in c. 311: homozygous G/G (1 Nelore), heterozygous G/del (1 Gir and 1 Sindi) and homozygous del/del (1 Sindhi). Deletion at position 311 of the MC1R gene was observed in depigmented animals, except in the Nelore breed. Indicating a case of incomplete penetrance, as animals of the same genotype present different phenotypes. Furthermore, it is suggested that the depigmentation phenotype of the zebu breeds used presents genetic heterogeneity, as the genotypes at position 311 behaved differently in the breeds studied. It is necessary to genotype a greater number of depigmented and pigmented animals to verify the gene action of the deletion. Identifying mutations that cause depigmentation in zebu animals is important so that molecular marker assisted selection against depigmentation can be carried out, reducing the incidence of this characteristic in the breeds studied.

Key words: barroso, coat, genotyping, phenotype, indel

Financial support: Universidade Federal da Bahia (UFBA), Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES).