RESUMO SIMPLES - PROTOZOÁRIOS E AGENTES TRANSMITIDOS POR VETORES DE IMPORTÂNCIA EM SAÚDE

GENETIC VARIABILITY OF ANAPLASMA MARGINALE IN NATURALLY INFECTED CATTLE FROM THE STATE OF RIO DE JANEIRO

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Anaplasmosis in cattle, caused by the gram-negative and obligatory intracellular bacterium Anaplasma marginale, is a disease that causes serious economic and health impacts in livestock farming. This infection is mainly transmitted by the tick Rhipicephalus microplus and is characterized by anemia, fever, weight loss, reduced productivity, abortions, and even death in more severe cases. One of the factors that makes this disease so challenging is its great genetic diversity. Genetic variations in the genes encoding the surface proteins MSP1a

and MSP4 promote the antigenic diversity of Anaplasma marginale, favoring adaptation mechanisms and evasion of the host's immune system. This study aimed to assess the genetic diversity of Anaplasma marginale found on conventional and organic system farms located in the State of Rio de Janeiro. The samples collected and used in this study were approved by the Animal Use Ethics Committee (CEUA) of the Federal Rural University of Rio de Janeiro (UFRRJ), under protocol number 1051220524. Blood samples were collected from 388 cattle across eight different properties between 2022 and 2025. The collection was performed via the coccygeal artery, and the samples were individually stored in tubes containing ethylenediaminetetraacetic acid (EDTA). DNA extraction was carried out using the phenol-chloroform method on all blood samples, following the manufacturer's recommendations. After the extraction process, polymerase chain reaction (PCR) was performed for the GAPDH gene to validate the procedure’s effectiveness. All samples showed viable DNA and were subjected to a second PCR to detect agents of the species Anaplasma spp. by targeting the MSP4 gene through amplification of an 831 base pair fragment. At least one sample positive for the MSP4 PCR from each property was randomly selected for genetic variability analysis using the MSP1α gene. Phylogenetic analysis was conducted using MSP1a gene sequences of A. marginale obtained in this study, along with additional sequences retrieved from the NCBI GenBank database (09/25/2025). For the MSP4 gene targeting Anaplasma spp., 259 out of 388 samples tested positive, representing 66.8%. Eight strains were found on five properties, six of which were different from each other, and two were repeated. After sequencing the MSP1a gene and analyzing data with the BLASTn program, it was possible to locate globally strains with a high similarity percentage to those found in this study. The phylogenetic analysis of the MSP1a gene of A. marginale revealed that the isolates obtained grouped into two main lineages, named clade H1 and clade H2. Collectively, the findings indicate that Anaplasma marginale has a high prevalence and wide genetic variability in cattle herds in the state of Rio de Janeiro.

Palavras-chave: anaplasma marginale; genetic diversity; cattle; strains.