sódigo O-142

ESTUDO DA DIVERGÊNCIA GENÉTICA EM LINHAGENS BRASILEIRAS DE ANAPLASMA MARGINALE ATRAVÉS DA UTILIZAÇÃO DO GENE DA PROTEÍNA PRINCIPAL DE SUPERFÍCIE MSP1α

STUDY OF GENETIC DIVERGENCE IN BRAZILLIAN ANAPLASMA MARGINALE STRAINS USING MAJOR SURFACE PROTEIN 1 α GENE

LUCIANA GATTO BRITO (EMBRAPA RONDÔNIA); MÁRCIA CRISTINA DE SENA OLIVEIRA (EMBRAPA PECUÁRIA SUDESTE); RODRIGO BARROS ROCHA (EMBRAPA RONDÔNIA); FRANCELINO GOULART DA SILVA NETTO (EMBRAPA RONDÔNIA); FRANCISCO ALOÍSIO CAVALCANTE (EMBRAPA ACRE)

Bovine anaplasmosis, caused by rickettsia Anaplasma marginale, represent one of the most important diseases ofruminants worldwide, causing significant economic losses in Brazil. This pathogen can be transmitted byRhipicephalus (Boophilus) microplus infected tick; by biting flies or by blood-contaminated fomites. The major surface proteins (msp) are involved in host-pathogen and tick-pathogen interactions and have been used as markers in A. marginale characterization and genetics studies In this study were characterized A. marginale strains obtained from naturally infected cattle from Rondônia, Acre and São Paulo State. The msp1 gene was amplified from A. marginale DNA extracted from erythrocytes by PCR in a 50 &#956:I volume of PCR MasterMix (Promega, USA). Amplified fragments were purified and used directly for sequencing. The nucleotide and amino acid sequences of A. marginale msp1 were used for sequence alignment and genetics analysis. Multiple sequence alignment was performed using the Clustal X software. Nucleotides were coded as unordered, discrete characters with five possible character-states; A, C, G, T, or N, and gaps were coded as missing data. After a first proceeding and removal of the regions without genetic information, was carried the definitive alignment. Searches for the most parsimonious tree employed the branch and bound. The stability of the inferred topology was assessed via bootstrap analysis. Through alignment analysis of the slighter variable region of msp1a gene, five rickettsia isolated types were identified in the A. marginale populations from São Paulo, Rondônia and Acre states. These results indicates that the strains of Acre state were less similar with São Paulo sample and not have divergence within strains obtained of samples provided

Acre and Rondônia states.

Agradecimento Embrapa