RESUMO - PROTOZOOLOGIA E PATÓGENOS TRANSMITIDOS POR VETORES

MOLECULAR INVESTIGATION OF BACTERIAL AGENTS IN CHIGGER MITES FROM MULTIPLE HOSTS ACROSS DIFFERENT REGIONS OF BRAZIL

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Chigger mites are a group of mites comprising three families (Trombiculidae, Leeuwenhoekiidae, and Walchiidae) whose larval stage is parasitic. They are of

medical and veterinary importance because they parasitize animals and accidentally humans, potentially causing dermatitis and acting as vectors of Orientia spp., zoonotic bacteria responsible for scrub typhus. In addition, DNA from Rickettsia spp., Anaplasma phagocytophilum, Ehrlichia sp., Bartonella spp., Borrelia spp., Coxiella burnetii, and Hepatozoon spp. has been detected in these mites; however, experimental studies confirming their vector competence are still lacking. The present study aimed to detect Bartonella spp., Erlichiaceae agents, Borrelia spp., and Orientia spp. in chigger mites deposited in the Acarological Collection of the Butantan Institute (IBSP) and collected from different vertebrate hosts (orders Rodentia, Carnivora, Chiroptera, Didelphimorphia, Galliformes, and Passeriformes) across fifteen Brazilian states. For this purpose, DNA from 248 mites (genera Apolonia, Blankaartia, Eutrombicula, Herpetacarus, Microtrombicula, Pseudoschoengastia and Quadraseta) was individually extracted. The presence of amplifiable DNA in all samples was confirmed by PCR targeting the endogenous 18S rRNA gene. Samples were screened for Bartonella spp. (cPCR targeting the nuoG gene), Ehrlichiaceae (cPCR targeting the 16S rRNA gene), Borrelia spp. (qPCR targeting the 16S rRNA gene), and Orientia spp. (qPCR targeting the 16S rRNA gene), and all samples tested negative for the investigated agents. The lack of microorganisms detection may be associated with low parasitic loads, the limited sensitivity of the detection methods used for this type of sample, or the absence of infection in the analyzed mites. Further studies with larger sample sizes and more sensitive techniques, such as third-generation molecular approaches (e.g., digital PCR) and next-generation sequencing, are needed to better understand the circulation of these agents in these ectoparasites.

Palavras-chave: trombiculidae; bartonella spp; ehrlichiaceae; borrelia spp; orientia spp.