



DETECTION OF *BRUCELLA SPP.* IN DOGS AND CATS

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Brucella spp. is a coccobacillus, Gram-negative, nonmotile and nonencapsulated genus of bacteria, found in different animal species. It causes a zoonotic disease known as brucellosis. Currently, 12 species of the *Brucella* genus are known to exist, but only five of them are capable to infect humans (*B. melitensis*, *B. abortus*, *B. suis*, *B. canis*, *B. inopinata*). The transmission to humans is caused by consuming unpasteurized or undercooked products, inhalation, skin penetration, conjunctival contact to contaminated fluids and, rarely, from person to person by transplacental route or blood transfusion. In humans, brucellosis might cause symptoms such as: fever, body pain, weight loss, night sweats, cough, vomiting and diarrhea. In severe clinical conditions the infection may also cause splenomegaly, arthritis, sacroiliitis, scrotal edema, cervical stigma and lymphadenopathy. There is no effective vaccine to prevent brucellosis in humans and the extensive use of some antibiotics (as tetracyclines and aminoglycosides) is the only treatment available. In dogs, brucellosis mainly causes reproductive alterations such as infertility, abortions and stillbirths. It occasionally affects other tissues, causing uveitis, discospondylitis, osteomyelitis and dermatitis. Cats are still considered refractory hosts for the disease. The objective of the following research was to detect the presence of *Brucella* in pets in the northeast mesoregion of Rio Grande do Sul Federal State, Brazil. The research was performed using dogs and cats testicle samples (n=102) collected from the castration project of the Veterinary Medicine undergraduate course of the University of Caxias do Sul. The testicles were macerated, submitted to DNA extraction and then a Polymerase Reaction Chain (PCR) was performed. The primers used in this procedure amplify a 317 base pairs (bp) target sequence that includes the gene-code IS711 region of the *Brucella* genome. To the present moment, from 102 samples collected, 46 have been analyzed by PCR. Five of them were considered putative positive samples. The rest of the samples will later be tested, and the positive samples of the previous PCR analysis will be submitted to a *B. canis* species-specific PCR and DNA sequencing.

Palavras-chave: PCR, Zoonosis, Pets

Apoio: UCS, CNPq