EP001 - TOXOPLASMOSIS AND NEOSPOROSIS SEROPREVALENCE IN FREE-RANGE CHICKENS FROM UBERLÂNDIA – MG.

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Free-range chickens have been used as indicators of soil contamination with Toxoplasma gondii and Neospora caninum because they feed from ground, which can be contamined with oocysts. The aim of this work was to investigate the seroprevalence of T. gondii and N. caninum infection in free-range chickens (Gallus gallus) from Uberlândia-MG. Brazil, because it is unclear until now the importance of the infection mediate by oocyst ingestion present in food or water. After serum sample collection, ELISA immunoassays were carried out using soluble antigen of N. caninum (NLA) and T. gondii (STAg), in the concentrations of 20 or 10 µg/ml, respectively. It was analyzed 208 chicken serum samples from 16 neighborhood areas in Uberlândia, which where used at the dilution 1/50. Anti-chicken IgY conjugate labelled with peroxidase in the ratio 1/30.000. Regarding the results obtained, it was found 91% of soropositivity for T. gondii, in contrast with 73% of soropositivity for N caninum. Afterwards, it was performed Western blot assay (WB) under the same conditions, as confirmatory assay. A representative number of five samples found positive for both parasites was chosen, confirming their positivity for T. gondii, in all of them, whereas only three were co-infected by N. caninum. Based on the results obtained in this study, it can be concluded that the occurrence of infection by T. gondii and N. caninum in the urban perimeter of this city was high, indicating that the parasites are widely distributed in the environment, and the free-range chickens are true epidemiological sentinel for toxoplasmosis and neosporosis. Supported by: CNPq, CAPES, FAPEMIG

EP002 - EVALUATION OF CANINE SEROPREVALENCE AT THE DIAGNOSIS OF VISCERAL LEISHMANIASIS IN THE CITY OF GOVERNADOR VALADARES-MG FROM 2008 TO 2012. PINHEIRO, A.C.^{*1}; DE OLIVEIRA, E.A.²; TOSETTO, W.G.²; CANDIDO, E.J.¹; PEDRA, M.S.¹;

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Visceral leishmaniasis is a zoonotic disease caused by the protozoa of the genus Leishmania infantum, and transmitted by the bite of the sandfly Lutzomyia longipalpis infected with the parasite. It is considered one of the parasitic diseases of major impact on public health, it is among the six endemic prioritized in the world, and it can affect the human when he is in contact with the transmission cycle of the parasite. The domestic dog is the main urban reservoir of L. infantum as it is close to human, it is attractive to the insect vector, and it presents high rates of infection. In Governador Valadares, of Minas Gerais state, Brazil, from 2008 to 2012, 115 human cases were diagnosed, with 16 deaths recorded. The city is considered by Brazilian Ministry of Health as an area of intense transmission. The aim of this study was to evaluate the canine serodiagnosis between 2008 and 2012. Blood samples were collected in 29.724 dogs, for serum production, by the Center of Zoonosis Control of the city. The samples were analyzed and the tests were performed: enzyme linked immunosorbent assay (ELISA), as a screening, and indirect immunofluorescence assay (IFAT) to confirm the positive cases. From the samples examined, it was obtained the diagnosis of 8.643 seropositive dogs, with annual seroprevalence average rate of 29%, coming to 46%, in some neighborhoods. Analyzing both human and canine cases, it was remarked the ocorrence of a larger number of human cases in neighborhoods with a larger number of canine cases. The data indicate a high rate of seroprevalence and that the role of the dog in the transmission of visceral leishmaniasis can be correlated in the distribution of human cases in the city of Governador Valadares. Further analyzes are in progress.

EP003 - TAXONOMIC IDENTIFICATION AND DIAGNOSTIC EVALUATION OF NATURAL INFECTION BY LEISHMANIA SPP. IN THE SANDFLY FAUNA (DIPTERA: PSYCHODIDAE) OF RIO BRANCO MUNICIPALITY (ACRE, BRAZIL) USING MOLECULAR ASSAYS. <u>PEREIRA, T.A.</u>⁻¹; PEREIRA, D.P.¹; BOITÉ, M.¹; DA MOTA, F.F.²; MELO, M.¹; DA COSTA REGO, T.A.N.¹; RODRIGUES, A.F.¹; BRAZIL, R.P.¹; BRITTO, C.¹ 1.FIOCRUZ, RIO DE JANEIRO, RJ, BRASIL; 2.IOC, RIO DE JANEIRO, RJ, BRASIL. **e-mail:**:pereirathata@gmail.com

Notifications concerning cutaneous leishmaniasis have increased in the recent years in the State of Acre, and without records of visceral leishmaniasis in the state. However, studies on the sandfly fauna in Acre are still limited. The main objective of the present investigation was to bring more knowledge about the sandfly fauna in the municipality of Rio Branco (Acre) and to evaluate natural infection index by Leishmania spp. in the captured sand flies. Insects were collected with the support of the Municipal Surveillance and Health board, from April 2011 until April 2012, using HP light traps distributed in six areas. Sand flies were identified according to the methodology proposed by Galati (1995). Phlebotomine Q were individually analyzed for the detection of natural infection by Leishmania spp. through the use of multiplex PCR assays coupled to non-radioactive hybridization with specific probes. For the multiplex PCR two primer pairs were used, one specific for the conserved region of kDNA minicircles from Leishmania genus and a second pair that amplifies a specific constitutive gene of sand flies. In order to identify the Leishmania spp. infecting sand flies, cloning and sequencing of the 234 bp fragment corresponding to amplified products containing the hsp 70 gene were performed. A total of 455 phlebotomine specimens was collected; 173 \Im were individually submitted to molecular diagnosis. The taxonomic identification revealed 20 phlebotomine species. The specimens Trichophoromyia spp. genus, Trichophoromyia auraensis, and Nyssomyia whitmani were the most abundant. The diagnostic analyzes detected 12 Q phlebotomines positive for Leishmania spp. infection, corresponding to 6.9%. From these, 5.2% were related to Trichophoromyia spp., 1.1% to Evandromyia saulensis and 0.6% to Pressatia spp. Following sequencing the Leishmania spp. amplified products derived from the 12 positive samples, it was possible to identify 5 samples corresponding to L.(V.) braziliensis. Supported by: Faperi / Cnpg