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SUMMARY OF THESIS*

BASSIT, Leda Cattini – TTV: prevalência e caracterização do novo vírus de DNA transmissível pelo sangue em diferentes populações de São Paulo. São Paulo, 2001. (Tese de Doutorado – Faculdade de Ciências Farmacêuticas da Universidade de São Paulo).

TTV: PREVALENCE AND PHYLOGENETIC CHARACTERIZATION OF A NOVEL BLOOD-BORNE DNA VIRUS IN DIFFERENT GROUPS FROM SÃO PAULO, BRAZIL

Recently, an infection caused by a novel TT-virus (TTV), which was initially associated with post-transfusion non-A-G hepatitis, led us to investigate the TTV infection (clinic-epidemiological aspects, phylogenetic characterization and distribution of TTV genotypes) in different groups from São Paulo. The study included (i.) 138 children without history of blood transfusion or of liver disease, (ii.) 401 blood donors and (iii.) 130 Patients with Bleeding Disorders (PBD). TTV infection was investigated by PCR-based amplification of the untranslated region (UTR) and its prevalence was as high in low-risk groups (81-85%) as in PBD (98%). The distribution of this infection according to the age groups only showed significant difference in the children group. Almost all the children aging 2 to 4 years (95%) were infected by TTV. However, this prevalence decreased continuously thereafter and reached a lower prevalence of 47% in adolescents of male gender aging 15 to 17 years. TTV DNA was also detected by a hemi-nested PCR amplification directed to the N22 region in blood donor and PBD samples; sequencing

of these amplified products was also performed. Concerning PBD, a high frequency of N22 was found in 42% in comparison to 5.5% in blood donors. There was no association of N22 findings with ALT level and epidemiological aspects in the prior group. Therefore, there was an association of N22 with patients co-infected with HCV, hemophilia A and patients who had been treated with fresh blood products. The distribution of TTV genotypes was similar in both studied groups and genotypes 1 and 2 of the Group I prevailed on the others. A less frequent Group of TTV (Group II) was also observed in two patients. The TTV genotype varied in the same patient when samples were collected in the course of time. The high prevalence of the UTR-specific isolates found for the low-risk groups indicates that the parenteral route of transmission does not seem to play a major role for this infection. These findings widely contributed for the epidemiological studies of TTV infection and for its phylogenetic characterization in Brazil.

*This thesis is available at the Library of the Instituto de Medicina Tropical de São Paulo