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## SUMMARY OF THESIS\*

CAVALHEIRO, Norma de Paula - **Hepatite C: transmissão entre casais**. São Paulo, 2004. (Tese de Doutorado - Faculdade de Medicina da Universidade de São Paulo).

### HEPATITIS C: TRANSMISSION BETWEEN COUPLES

**Introduction:** The occurrence and the efficiency of HCV sexual transmission in the absence of other risk factors are still very controversial. I investigated and analyzed 24 couples, both infected with HCV, of whom 22 shared the same viral subtype. A phylogenetic analysis of NS5b region showed high sequence homology among the infected couples.

**Objective:** Analysis of the Hepatitis C transmission between heterosexual couples.

**Methods:** The study recruited 45 couples, 24 were included, with anti-HCV positive and clinical diagnosis of active chronic hepatitis. HCV infection was diagnosed by positivity of serum samples for anti HCV (third-version enzyme immunoassay) and by circulating HCV-RNA detected by Polymerase Chain Reaction (PCR). All blood samples were collected between 1999 and 2002. Sequencing of the 5'NC region was performed utilizing the research available TRUGENE HCV 5'NC Test (Bayer Health Care Diagnostics, Tarrytown, NY, USA). Sequencing of the NS5B region was performed by RT-PCR amplification with Titan One Tube RT-PCR Kits (Roche Molecular, Mannheim, Germany) and CLIP sequencing using a prototype NS5B genotyping assay (Bayer Health Care Diagnostics, Tarrytown, NY, USA). Sequence analysis was completed using the Open Gene DNA Sequencing System, Gene Objects software package (Version 3.1), and Gene Librarian module (Bayer Health Care Diagnostics, Tarrytown, NY, USA). Multiple sequence alignments of the NS5B region were performed with Clustal W (Clustal W Multiple Sequence Alignment Program, v1.7, June 1997), and phylogenetic trees were generated using the Neighbor Joining Method. A standardized questionnaire and interview was used to collect data concerning risk factors and sexual behaviors. Follow up of all subjects was conducted at the hepatitis clinic of the Clinical Hospital of the University of Sao Paulo and at the Hospital Guilherme Alvaro in the city of Santos, in the state of Sao Paulo, Brazil.

**Results:** Among the 24 couples, 22 had matching viral subtypes with homology scores (NS5b) ranging from 93.0% to 99.4%. Of the 22 couples with matching subtype, two (9.1%) were infected with subtype 1a, nine (40.9%) with subtype 1b, one (4.6%) with subtype 2b and ten (45.5%) with subtype 3a. The two couples that did not show matching viral subtypes had scores of 70.1% and 82.2%, and were infected with subtypes 2b and 1b, and 1b and 1a, respectively. The average of duration of marriage was 22.4 years (range 2-45 years) and the per capita income was an average of US\$ 2,270/year. Based on the questionnaire and interviews, cause of infection of the 24 couples could be attributed to: blood transfusions 9 (37.5%), drug use, I.V. 17 (70.8%) and inhalation 15 (62.5%), acupuncture 4 (16.7%) and tattooing 5 (20.8%). Shared hygienic utensils showed a much higher correlation of possible route of transmission, and are better explained by the sequence homology data than by the other associated risk factors. A total of 6 (25.0%) couples shared tooth brushes, 16 (66.7%) shared shaving blades, 21 (87.5%) shared nail clippers and 14 (58.3%) shared manicure cutters. The two couples that had different subtypes, both of them related transfusion blood and I.V. drug use.

**Conclusions:** The high similarity found among the genome chains of HCV supports the hypothesis of transmission between these couples. The shared use of personal hygiene utensils and the amount of time spent living together made it difficult to interpret the data. Also, the shared use of personal hygiene utensils can make it difficult to interpret the data in relation to the sexual transmission of HCV. The hypothesis in relation to the direction of the HCV transmission, from man to woman, was reinforced in this work.

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