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(1,6%) in Africa. Risk factors for acquisition of HCV were intravenous drug use (88,3% - average starting age at 15,4 years), transfusion (6,6%), sexual intercourse (3,2%), unknown (1,6%). Simultaneous infection with c and d subtypes were found in 36 patients (60%), and in 17 (28,3%) it was not done. Mean value of HCV-RNA was 3217816 IU/ml (55 pt); the remaining laboratory results on average were AST - 78 U/L, ALT- 110 U/L and GGT- 143 U/L. Hepatic biopsy was performed in 18 patients (52,9%) who underwent treatment.

Twenty patients (33,3%) were coinfecting with HIV (mean viral load - 76877 cp/mm³, CD4 - 470 cel/mm³) and 14 (70%) under HAART.

Twenty eight (46,6%) patients had already had previous contact with HBV and 3 (5%) were also AgHBs +.

Thirty four of the sixty patients (56,6%) were treated.

Conclusions: Genotype 4 represents 13 % of the total of the HCV patients attending this Unit. Subtypes c/d are the majority. They were mainly IDU and relationship with Africa was not found as a risk factor. In coinfecting patients HCV-RNA levels were higher. The remaining laboratory findings were similar in HCV vs HCV/HIV.

59.027

HCV Genotype Prevalence Among HCV Infected I.V. Drug Users in the Republic of Macedonia in 2004 and 2005

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Background: Hepatitis C virus infection is a global world problem with defined transmission modes. I.V. drug users are among the significant carriers and transmitters of this infection. Based on genetic heterogeneity, HCV strains are divided into 6 major groups, genotypes, each with different distribution worldwide and with possible effect on pathogenesis and therapy.

Material and Methods: The prospective study performed in 2004 and 2005 at our Clinic included drug users according to epidemiological data. Antibodies for HCV were verified using ELISA kits: ORTHO HCV 3.0 ELISA, ABBOTT HCV EIA 2-nd GENERATION, Murex anti HCV/Version III. HCV RNA and genotypes were detected with RT/PCR using Amplicor (Hoffman La Roche). Patients were grouped according to age, sex, nationality and genotype presence. HBV and HIV were also tested using Behring ELISA kits on Behring Processor.

Results: Out of 137 anti HCV positive drug users that visited the Clinic to learn their HCV status or begin with antiviral therapy, 83 were tested by PCR HCV. Genotype 1 was detected in 34 (41,0%), genotype 3 in 45 (54,2%), concurrent genotype 1 and 3 in 1 (1,2%), genotype 4 in 1 (1,2%), and 2 (2,4%) cases with positive PCR HCV without genotyping. 2 persons with genotype 1 and 1 with genotype 3 had concurrent HBV infection. The results were compared with a 1995-1998 study, which included 27 persons, from whom 17 were infected with genotype 1, 7 with genotype 3 and 3 with positive PCR HCV, without possibility for genotyping.

Conclusion: The most frequent genotype of the tested drug users is genotype 3 (54,2%) and the number of those with genotype 1 has decreased compared with the past study when genotype 1 dominated. In the present study, for the first time we have genotype 4, and mixed infection with concurrent genotype 1 and 3. Considering the increasing number of drug users in our country, their international communication, and the natural history of HCV infection, we expect a new picture of genotypes maybe in the next 5 years. To decrease their number in our low-resource country, if we could afford treating them with drugs such as Interferon and Ribavirin, we would motivate them to stop using drugs and eliminate all psychosocial problems arising thereof.

59.028

Seroprevalence and Risk Factors of Hepatitis B Virus Infection in Health Care Workers at Prasat Neurological Institute, Thailand

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Background: The prevalence of hepatitis B carriers in Thailand is about 6-10%. Hepatitis B vaccination was included in the Extended Program of Immunization (EPI) and has been introduced to all Thai newborns since 1992, but did not include retroactive vaccination of health care workers (HCWs). The purpose of this study was to define the seroepidemiology of Hepatitis B virus (HBV) infection among HCWs in Prasat Neurological Institute (PNI), and to evaluate the risk factors of HBV markers.

Methods: Blood samples were taken from HCWs in PNI for HBV profiling (HBsAg, antiHBs and antiHBc) by Microparticle Enzyme Immunoassay (MEIA) methods. Questionnaires include demographics, type and duration of work, history of blood exposure, HBV vaccination and non occupational risks of hepatitis were interviewed.

Results: Among 548 enrolled HCWs, 79 (14,4%) were male and 469 (85,6%) were female, aged ranges between 20 to 61 years old, working year between 1 to 41 years. Among 548 HCWs 29 (5,29%) were HBsAg positive, 135 (24,6 %) had immunity from past HBV infection, 40 (7,3 %) were Isolated antiHBc, 105 (19,2%) had protective level antiHBs, 7 (1,3 %) had low antiHBs level and 232 (42,3 %) had full negative profiles. Comparing between HBsAg positive and negative groups, no statistically significant differences were found among different risk groups including those with different levels of occupational exposure, frequency of blood contact and working years. However, there were statistically differences in sex (male:11,39% vs. female:4,26%, p=0,009), history of HBV vaccine (vaccinated:0,83% vs. non-vaccinated:7,42%, p=0,014), family history of hepatoma (12,77% vs. 4,04%, p=0,002), history of jaundice (17,39% vs. 4,4%, p=0,008) and history of viral hepatitis (29,63 vs. 3,66%, p=0,000).

Conclusions: Not different from Thai populations, prevalence of HBV carriers among HCWs at PNI was 5,29%. Based on the significant risk factors of HBsAg positive, current HBV vaccination program should also include HCWs who were born before Thailand EPI program

59.029

Molecular Epidemiology of Hepatitis A Virus in a Group of Portuguese Citizens Living in Lisbon Area

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Hepatitis A virus is the most important cause of acute infectious hepatitis worldwide. The nucleotide sequence analysis of HAV has classified the virus in seven different genotypes, which include humans groups I-III and VII. In Portugal due to improvements in sanitation, epidemic outbreaks of Hepatitis A (HAV) infection have become less frequent. Thus, in view of changing epidemiology it has become even more important to have a reliable and widely applicable technique for detection, quantification and characterization of HAV infection and transmission.

Objective: Detection and genetic characterization of HAV cases by molecular methods.

Materials and Methods: In this study, 29 sera samples were tested; 10 symptomatic children from an acute hepatitis A outbreak occurred between December 2004 and June 2005 in a Roma community; and 18 sporadic cases studied in Lisbon area in 2005. A sample of LCR involved in a case of meningitis was also included. Anti-HAV IgM was detected by (MEIA). Nested reverse transcription (RT-PCR), with primer located at the VP1 region, was performed to detect HAV genome. In positive samples, molecular characterization of VP1-P2A region was followed by phylogenetic analysis.

Results: All samples were positive for anti-HVA, 29 (100%). For HAV RNA, 21 (72,4%) were positive. Phylogenetic analysis revealed that all the samples belong to III A genotype.

Comments: This study is the first, to our knowledge, that characterized hepatitis A virus in Portugal and show that subtype III A may have an important epidemiological role. Furthermore, we report a special case in which HAV may be involved in meningitis. The results of this study show that HAV phylogenetic studies can provide important information for the design of appropriate public health measures.

59.030

A Survey of Epidemiological Status of Hepatitis C Infection Among Shirazian Blood Donors in 2005

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