JOURNAL INFORMATION

Definition

Thrita is an international, peer-reviewed, open access, quarterly journal funded by Prof. Parvin Pasalar. Thrita is the official journal of Kowsar Corporation in scientific collaboration with Tehran Students' Research Centers Network (TSRCN). Kowsar Corporation acts as a science, technology and medicine (STM) publisher which publishes more than 45 journals in different fields of sciences. Tehran Students' Research Centers Network is an academic student organization that includes Students' Scientific Research Centers of 8 medical universities of Tehran.

Scope

Thrita publishes the latest researches and findings those performed by medical sciences researchers all over the world.

Scientific-Research Approval

We are honored to inform our readers that Thrita has succeeded to receive Scientific-Research Approval of the Commission for Accreditation and Improvement of Iranian Medical Journals.

DEAR COLLEAGUES,

As the director of Iran Hepatitis Network and Global Hepatitis Community, I would like to mention that viral hepatitis is one of our priority in healthcare system now. The burden of hepatitis B virus (HBV) and hepatitis C virus (HCV) infections in the region mandates us to work more in this issue. We made a link between epidemiologists, clinicians, pathologists, virologists, specialists in transfusion medicine as well as research and laboratory centers from Iran and the world. We would like to facilitate scientific communication between researchers who are working in the field of viral hepatitis and other liver diseases. One of our activity is Tehran Hepatitis Conference which has been held for 5 times yet in Tehran, Iran.

I would like to take great pleasure in inviting you to participate in the 6th International Tehran Hepatitis Conference (THC6) hosted by Iran Hepatitis Network which will take place in Iran, May 2015. In THC5, around 1500 scientists participated and we had distinguished speakers from Canada, South Korea, Germany and the region. I invite all universities, research centers and other scientific professions in hepatology and liver diseases to join us.

In a close collaboration between Iran Hepatitis Network (IHN) and European Association for the Study of the Liver (EASL) the first day of the THC6 will be dedicated to the lectures of scientific leaders of hepatology from Europe and Iran. The Best of EASL day at THC6 will take place 27 May, 2015 with an interesting and comprehensive scientific program concentrated on viral hepatitis and other liver diseases. The guests from EASL will present the new findings in hepatology and the Iranian distinguished speakers will present their experience on management of liver diseases in Iran. We take great pleasure to invite you to participate in the Best of EASL day at THC6 which intends to promote the knowledge of hepatology in Iran and the region.

Kind Regards,

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THC6 Chairman
Professor of Gastroenterology and Hepatology

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O099 EFFECT OF CHLOROQUINE THERAPY ON ANTHROPOMETRIC PARAMETERS, VIT D3, FERRITIN AND BIOCHEMISTRY PARAMETERS AT HCV INFECTION PATIENTS: PILOT TRIAL

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ABSTRACT

Objective: Hepatitis C virus infection frequently leads to chronic hepatitis C which may progress to cirrhosis and even to hepatocellular carcinoma. This study aimed to investigate the effective parameters in patients chronically infected with HCV with non-response criteria and chloroquine therapy.

Methods: This study is the continuation of our previous paper with method Triple-blind, Randomized Controlled Pilot Study. Patients after understood the study procedures and signed informed consent, they randomized into treatment group (Chloroquine 150 mg once daily, for 8 weeks) and control group (placebo once daily, for 8 weeks). The inclusion criteria was including male, between 18 and 60 years of age, confirmed chronic hepatitis C with non-response criteria, Genotype 1. Data were analyzed with an intention to treat perspective of at the end follow up (12 weeks), considering to variables such as anthropometric parameters, Vit D3, Thyroid function, ferritin and biochemistry parameters evaluated. All statistical analyses were performed using SPSS for Windows (Version 10 SPSS Inc, Chicago, IL, USA).

Results: Our results showed a decrease in median AST from 48 to 33, ALT from 57 to 42($p=0.03$), Cholesterol 144 to 131($p=0.04$(, TG 86 to 67 and Ferritin levels in plasma samples of chloroquine treated patients at the end of the first follow up (week 4) and second follow low up(weeks 8-end of treatment).

Conclusions: According to the results suggest that a chloroquine therapy may be very useful for HCV treatment in patients that are non-response and, it help to normalize some biochemical, ferritin and vitamin D status

O129 A COST-UTILITY ANALYSIS OF DIFFERENT ORAL ANTIVIRAL MEDICATIONS IN PATIENTS WITH CHRONIC HEPATITIS B IN IRAN: A MICRO-SIMULATION ECONOMIC DECISION MODEL

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ABSTRACT

Introduction: Although hepatitis B infection is the major cause of chronic liver disease in Iran, no study has been carried out yet in the country to make an economic evaluation of medications in patients with chronic hepatitis B (CHB). Therefore, it is unknown what the cost-effectiveness of different options of medication therapy for this disease is regarding to the local conditions of the country.

Objective: The aim of this study is to compare the cost-utility of medication strategies in patients with chronic hepatitis B infection in Iran.

Methods: An economic evaluation of cost-utility was conducted to assess five oral medication strategies including: Adefovir, Lamivudine, Adefovir + Lamivudine, Entecavir, and Tenofovir. A Markov micro-simulation model was used to estimate the clinical and economic outcomes in a life time horizon based on societal perspective. Medical and non-medical direct costs and indirect costs were included in the study and Life-Years Gained (LYG) and Quality-Adjusted

Life-Years (QALY) were determined as the measure of effectiveness. The results were presented in terms of Incremental Cost Effectiveness Ratio (ICER) per QALY or LYG. The model was consisted of nine states of the disease; the transition probabilities for the movement between the states were obtained using expert opinions and clinical evidences collected from all over the world. Probabilistic sensitivity analyses (PSA) was used to measure the effects of uncertainty in model parameters.

Results: Finding showed the Tenofovir treatment strategy was more effective and less costly than other oral medication strategies. In addition, Tenofovir had the highest QALY and LYG for the HBeAg -ve and HBeAg +ve with 13.52 and 15.21; 2133 and 21.53 (discounted) in all comparisons, respectively. Also, PSA proved the robustness of the model results. So that, The cost-effectiveness acceptability curves showed that Tenofovir was the most cost-effective treatment in 86.1% and 87.7% of the simulations for the HBeAg -ve and HBeAg +ve with willingness to pay (WTP) thresholds less than purchasing power parity (PPP) $ 45270 (maximum WTP per QALY), respectively.

Discussion and Conclusion: Regarding to The results, using Tenofovir in patients with CHB was a highly cost-effective strategy; in addition, compared with other available medication options, Tenofovir was the most cost-saving strategy which could be the best option utilized as a first-line medication and also be used as a switch for other medications.

O149 HEPATITIS D VIRUS PROMOTES INHIBITORY EFFECTS ON REPLICATION OF HEPATITIS B VIRUS ISOLATES CONTAINING PRECORE AND BASAL CORE PROMOTER MUTATIONS

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Abstract

Background: The two commonly seen hepatitis B virus (HBV) genome alterations related to HBeAg negativity, basal core promoter and precore mutations (BCP: A1762T/G1764A, and PC: G1896A/C1858T, respectively), are associated with a significant increase in HBV viremia in HBV mono- infected patients. However, presence of these mutations in the HBV genome of patients coinfected with hepatitis D virus (HDV) is accompanied with lower levels of HBV DNA in both serum and liver. The aim of this study was to investigate the frequency of PC and BCP mutations in HBV genome of HBV-HDV infected patients with active HBV replication and to assess the functional impact of HDV on mutant HBV replication *in vitro*.

Methods: Serum samples from 71 consecutive HBV-HDV infected patients were collected, PCR amplified, sequenced and analyzed to compare HBV genome alterations between replicative isolates of HBV in HBV mono- and HBV-HDV double-infected individuals, in a case-control study. Replication competent HBV 1.28 plasmid vectors (genotype A, subtype adw2) containing wild-type sequence or PC (G1896A/C1858T) and BCP (A1762T/G1764A) mutations, were applied for transient transfection of Huh7 human hepatoma cells, alone (HBV-mono transfection) or along with HDV pcDNA3.1-D2 vector (HBV-HDV double transfection). HBV progeny DNA and HBV-DNA from released virions were detected and quantified to evaluate intra- and extra-cellular HBV replication.

Results: Among 71 HBV-HDV infected patients, 24 had detectable HBV replication, allowing successful HBV sequencing in 19 cases which were matched with 38 sequences from HBV infected patients (control). PC and BCP mutations were frequent in mono-, but scarcely found in HBV-HDV infected patients with active HBV replication. Functionally, co-transfection of HBV mutants with HDV strongly reduced the replication of PC- or BCP-carrying HBV constructs.

Conclusion: In conclusion, our study confirmed the prior investigations reporting a predominance of wild type precore HBV and lower frequency of BCP mutations in HBeAg negative patients in HBVHDV coinfections. Moreover, our observations suggest that delta hepatitis can endorse selective adaptations in HBV through assortment of isolates with preferentially wild type PC/BCP domains more likely to escape inhibitory effects of HDV.

O228 NON-INVASIVE SERUM FIBROSIS MARKERS: A STUDY IN CHRONIC HEPATITIS

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ABSTRACT

Introduction: Chronic hepatitis is specified as inflammatory disease of the liver lasting for more than six months. Role of noninvasive fibrosis markers as prognostication factors of the presence or absence of significant fibrosis on liver biopsy of patients with chronic hepatitis is the aim of this study.

Methods: Two hundred twenty-one patients with chronic hepatitis involved in the study between 2011 and 2013. Routine biochemical indices and serum fibrosis markers such as aspartate aminotransferase (AST) to alanine aminotransferase (ALT) ratio (AAR), AST to platelet ratio index (APRI) and Fibrosis 4 score (FIB-4) were evaluated, and the histological grade and stage of the liver biopsy specimens were scored according to the Ishak scoring system. Diagnostic accuracies of these markers for prediction of significant fibrosis were assessed by Receiver Operating Characteristic (ROC) curve analysis.

Results: Contemporaneous laboratory indices for imputing AAR, APRI, and FIB-4 were identified with liver biopsies. From all, 135 males (61.1%) and 86 females (38.9%), with mean age of 39.6±14.4 were studied. Significant correlation between stages of fibrosis and FIB-4, APRI and AAR were detected, with a correlation coefficient higher than that of other markers in the patients with Hepatitis B (r = 0.46), C (r = 0.58) and autoimmune hepatitis (r = 0.28). FIB-4 (AUROC = 0.84) and APRI (AUROC = 0.78) were superior to AAR at distinguishing severe fibrosis from mild-to moderate fibrosis and gave the highest diagnostic accuracy.

Conclusions: Application of these markers was good at distinguishing significant fibrosis and decreased the need for staging liver biopsy specimens among patients with chronic hepatitis.

O232 CANOLA (BRASSICA NAPUS) OILSEEDS AND EXTRACTS AS NOVEL AND SUPERIOR TOOLS IN FORMULATION OF A PLANT-BASED HCV VACCINE CANDIDATE

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ABSTRACT

Hepatitis C virus (HCV) with 3% prevalence, is the leading cause of chronic liver diseases and cirrhosis worldwide. Despite introduction of recent antiviral treatments, development of a vaccine remains the most cost-effective means for global eradication of HCV, while none is available to date. The oilseeds of ¨canola (*Brassica napus)*¨ are relatively new plant-based platform for expression and formulization of recombinant immunogens via utilization of their oil-bodies as adjuvant. Herein, N-terminal hydrophilic region (413 bp) of HCV capsid (core) protein (HCVcp; sysnthetic codonoptimized gene) was inserted into the pBI1400 binary vector and transformed into canola via *Agrobacterium tumefaciens* mediated transformation. Transgenic plants confirmed by PCR at DNA level (via specific primers) and by western blotting at protein level (via specific antibodies). Quantification analyses by ELISA indicated expression yields around 10μg of HCVcp/gram of seed. Immunization studies in BALB/c mice for canola-derived HCVcp (cHCVcp) compared to NI-NTA purified *E.coli*-derived HCVcp (*e*HCVcp) indicated that cHCVcp could elicit almost similar immune responses in 10x lower concentrations than *e*HCVcp (0.35 vs 3.0 μg/injection/animal). Besides, immunization by cHCVcp elicited higher IFN-α & IL-4 cytokines (Th1/Th2 responses) at both protein and mRNA levels compared to that of *e*HCVcp (assessed by ELISA & RT-PCR respectively) while generally oil extracts of canola as an adjuvant demonstrated a better eliciting profile of IFN-α For both cHCVcp and *e*HCVcp compared to that of Freund. Results of this study indicated that canola (as a plant-based expression platform) and its oil extracts might be superior for formulation of HCV vaccine candidates.

O253 IMMUNE RESPONSES TO A CD8-CTL EPITOPE OFN HCV CORE PROTEIN (AA: 39-48) IN THE CONTEXT OF A SYNTHETIC POLYTOPE AND NATIVE PROTEIN-A COMPARATIVE STUDY

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ABSTRACT

Hepatitis C virus (HCV),a positive strand RNA virus encoding for three structural (Core, Envelope 1 and 2) and seven nonstructural (NS) proteins, is the main cause of chronic liver inflammation and cirrhosis globally while no vaccine for this viral infection is available to date. Although introduction of Direct Antiviral Agents (DAAs) against HCV in recent years provided revolutionized treatment approaches, but due to the high cost and number of therapeutic limitations, availability of a vaccine is the only possible way for global eradication of HCV. Enhancement of cellular responses, CD8+CTLs and Th1 cytokines by T-cell based vaccines is a recognized approach in HCV vaccine design and accordingly more recently, for the first time a clinical trial (NCT01436357) by a T-cell viral vector-based prophylactic HCV vaccine was started. In this context, HCV polytopic peptides (HCVpp) based on isolated-T cell epitopes arranged in tandems has also gained importance but the immune potency of a single epitope in the context of polytope compared to the natural protein is not known. To this end, an HCVpp containing dominant H-2d and HLA-A2-restricted CD8+CTL epitopes of HCV proteins including: C (Core, aa 132-142), E2 (Envelope2; aa 614-622), N (NS3; aa 1405-1414), E1 (Envelope1; aa 405-414) and C1(core; aa 39- 48) in tandem of CE2NE1C1 was synthesized. In design of the HCVpp, different algorithms were employed to optimize the proteasome mediated epitope processing and minimize the creation of junctional epitopes. To obtain HCV core protein containing C1 epitope, N-terminal hydrophilic region (413 bp) of HCV core protein (HCVcp) in backbone of pIVEX2.4a vector was expressed in *E.coli* BL21-A1 and purified by NI-NTA agarose beads as previously described (roohvand et al, JBC, 2009). Plouronic acid F127 as a human compatible adjuvant was used in formulation of the immunogens (HCVcp & HCVpp) and groups of BALB/c mice were immunized by the immunogens and controls (antigen free adjuvant and PBS). Evaluation of immune responses by proliferation assay (the non-radioactive colorimetric method of Cell Proliferation ELISA BrdU), Interferon gamma-Elispot and in vivo CTL assay (Carboxy Fluorescein diacetate, succinimidyl Ester (CFSE) dye method) for the H-2d-C1 epitope indicated that percentage of specific lysis (CTLs) and IL-4 values for both immunogen (HCVcp and HCVpp) were statistically identical while proliferation rate and IFN-α Levels were slightly in favor of HCVcp. Results of this study indicated the proper induction of cellular responses towards isolated CD8-CTL epitopes in context of a polytope compared to that of the native protein.

O257 TRANSFECTION OF INSECT CELLS (SF9) BY RECOMBINANT BACULOVIRUS CONTAINING HCV CORE+1 OF GENOTYPE JFH1

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ABSTRACT

Background: Recently, a new protein, named Core+1, has been described to be produced through a +1 ribosomal frame shift in the Core protein coding region in Hepatitis C virus. The purpose of this study was to design and build a recombinant baculovirus vector containing HCV (JFH1) Core+1 sequence and confirm the expression of recombinant protein Core+1 in insect cells.

Material and Methods: Core+1 gene of HCV (JFH1) was synthesized commercially into pUC57 plasmid. Then the synthesized target gene was subcloned into the plasmid pFastBac-HTA. The recombinant vector was used to transform the competent E.coli DH10Bac containing the donor clone. The recombinant baculovirus bacmid was produced following transposition. Recombinant bacmid was verified by PCR and then transfected into Sf9 insect cells to package a new recombinant baculovirus.

Results: Sequence analysis and white-blue colony selection confirmed that the Core+1 sequence from HCV (JFH1) was successfully cloned into the pFastBac-HTA vector which was used to transform the E.coli DH10Bac. Sf9 cells were transfected using the recombinant bacmid.

Conclusions: Design and construct the recombinant baculovirus vector containing the HCV (JFH1) Core+1 sequence was performed for the first time. Baculovirus expression system provides a high yield post-translational modification tool for HCV Core+1 protein expression which is similar to Core+1 protein that produced during natural infection with HCV.

O274 MOLECULAR CHARACTERIZATION AND FUNCTIONAL ANALYSIS OF HEPATITIS B SURFACE GENE IN HIV POSITIVE PATIENTS WITH OCCULT HEPATITIS B INFECTION

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ABSTRACT

Background: Occult hepatitis B virus infection (OBI) is described by the presence of HBV DNA with negative HBV surface protein (HBsAg) in the serum outside the seroconversion window period of HBV infection. Occult HBV infection in HIV co-infected patients has been well recognized as a clinical entity.

Objectives: The aim of this study was to determine the hepatitis B virus small surface gene mutations in OBI positive, HIV co-infected patients which might be related to the emergence of occult HBV infection and evaluation of the impact of those mutations on the expression of small surface gene and its excretion in HUH7 cells using commercial diagnostics.

Materials and Methods: Viral DNA was extracted from the serum of 166 Iranian HIV infected patients with negative HBsAg status whom referred to Iranian research center for HIV/AIDS who had previously tested for HBV DNA by real time PCR. 25 of sera from OBI cases were selected for nested PCR .Nested PCR was performed to amplify small surface gene .Following direct sequencing and mutational analysis , we observed a high frequency of P127T, P127L and S136Y mutations in our study population . We further constructed the expression vectors encoding wild type as well as mutants genotype D HBsAg to analyze the effects of these mutations through transient transfection of HUH7 cells. For extra and intracellular expression assay, the supernatant and cell lysate were harvested and subsequently tested quantitatively for HBsAg in the third day post-experiment.

Results: Quantification of expressed HBsAg in supernatants and cell lysates revealed that there was a significant reduction in mutants compared to wild type. This expression reduction in cell lysates were consistent with corresponding supernatants.

Conclusions: Among the plenty etiologic factors supposed for occult Hepatitis B virus infection, we found HBsAg mutations which are associated with reduced HBsAg detection. Further analyses of these mutations may lead us to understand the mechanisms related to occult HBV and to design strategies for a better control of the infection.

O281 INTRODUCING A MATHEMATICAL ALGORITHM FOR PREDICTING VIRAL LOAD IN HBV INFECTED SUBJECTS USING SURROGATE MARKERS

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ABSTRACT

Background: Suitable methods for personalized clinical monitoring of HBV-infected patients are very crucial in resource-poor setting areas. Therefore, finding surrogate markers as predictive indicators for monitoring of these patients is an important need.

Materials and Methods: Demographic data and laboratory findings including age, gender and SGOT, SGPT and viral load (Arthus, Qigen, Germany) for 100 HBV infected subjects were collected at the first admission from 2011 to 2013. Data mining (Rapid Miner, V5.3 and mathematical tools were carried out for investigation. Decision tree was developed to forecast viral loads according to age, gender, SGOT and SGPT and the pathways for these levels. Naive bayes algorithms then were used to calculate probability of these pathways.

Results: In this study probability of having viral load more than 10_5 copies/ml was 0.59 and for less than 10^5 is 0.41. It could be possible to predict the viral load for every patient. The sensitivity and specificity of this algorithm for prediction of viral load were 100% and 71% respectively. However, the method needs a comprehensive cohort study for a reliable mathematical algorithm. Decision tree was presented in a separated file.

Conclusions: Mathematical analysis and data mining findings according to these algorithms could be considered as valuable markers for introducing a surrogate algorithm for personalized monitoring of HBV-infected subjects and starting anti-viral therapy in the absence of sophisticated detection assays.

O282 DIAGNOSIS OF HEPATITIS DISEASE USING FUZZY K NEAREST NEIGHBOR APPROACH

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ABSTRACT

In this paper, we present an effective and efficient diagnosis system using fuzzy k-nearest neighbor (FKNN) for Hepatitis diagnosis. The proposed FKNN-based system is compared with the support vector machines (SVM) based approaches. In order to further improve the diagnosis accuracy for detection of Hepatitis, the principle component analysis was employed to construct the most discriminative new feature sets on which the optimal FKNN model was constructed. The effectiveness of the proposed system has been rigorously estimated on a Hepatitis data set in terms of classification accuracy, sensitivity, specificity and the area under the receiver operating characteristic (ROC) curve (AUC). Experimental results have demonstrated that the FKNN-based system greatly outperforms SVM-based approaches and other methods in the literature. The best classification accuracy obtained by the FKNN based system using a 10-fold cross validation method can ensure a reliable diagnostic model for detection of Hepatitis. Promisingly, the proposed system might serve as a new candidate of powerful tools for diagnosing Hepatitis with excellent performance.

Poster Presentations

P067 NATURAL HISTORY OF CHRONIC HBV INFECTION: A COHORT STUDY WITH UP TO 11 YEARS FOLLOW-UP IN BIRJAND HEPATITIS CLINIC, IN EAST OF IRAN

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ABSTRACT

Background: Infection with hepatitis B virus (HBV) is a major medical problem in the world. Hepatitis B Virus (HBV) has infected approximately 2 billion people worldwide, of whom more than 350 Million are chronically infected. Considering that every year millions of hepatocellular carcinoma and cirrhosis following viral infection of the liver, lose their lives, follow up course of the disease and to determine prognosis and Influence of treatment on progression disease is very important.

Objective: The present study aims to Follow up of patients with chronic hepatitis B(CHB) infection in Birjand Hepatitis Clinic, in east of Iran.

Materials and Methods: A cohort study was conducted on 235 chronic hepatitis B patients which followed at least three years in the years 2002-2013. All patients that the conditions in the study were retrospectively retrieved from the archive clinics were prepared and the checklist. Data analysis and descriptive analysis using SPSS 20 software using mean and standard deviation of proportions and the t-test and chi-square analysis was performed.

Results: The study was conducted on 235 patients. The mean age of the subjects were 33.36±11. 132 (56.2%) were male and 103(43.8) were females and 193(82.1%) of patients were married. The average of follow-up period was 5.26±1.9 years (3-11). 10 patients (4.3 %) HBsAg-negative patients during the study. Based on the this study results 45 patients (19.1%) HBeAg were positive that, 17 patients (38%) of them were HBeAg negative. relationship between HBeAg and outcome was statistically significant. (p=0.026) There were 3 patients (1.6%), with Anti HDV positive. In this study of 235 patients who were followed up, 35 (14.9%) in the active stage of the disease were of these 9 patients (3.8%) progress to cirrhosis and in 2 patients (0.3%) of those who had cirrhosis and carcinoma was reported. During this study, 3 patients (1.3%) of chronic carriers died, of these 2 patients (66%) had cirrhosis and 1 patient (33%) of them, in addition to cirrhosis and hepatocellular carcinoma, respectively.

Conclusions: The result this study showed that 14.9% of carriers to chronic active hepatitis and finally 4.7% of carriers Progress to complications associated with the disease and only 4.3% are HBsAg-negative patients. Thus, this study showed that the follow-up of these patients to determine their disease status change and the decision to begin necessary treatment and prevention of the importance extension.

P085 HEALTH LITERACY DISPARITIES ABOUT HEPATITIS B: A NATIONAL ASSESSMENT IN IRAN

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ABSTRACT

Background: Worldwide, about 350 million people are infected with Hepatitis B virus (HBV), most of them in Asia. Up to 1 million of them die due to these sequels annually. Few studies concerned about the HBV awareness of Iranian young people. As health education programs should be based on the awareness of target group about the disease, we conducted a national survey to evaluate the health literacy and the vaccination status of Iranian young people regarding HBV.

Objectives: The purpose of our study was to find Iranian adolescents' health literacy deficit about hepatitis B (HBV) and associated factors.

Patients and Methods: We conducted a questionnaire-based national survey of 18-year-old adolescents according to stratified cluster random sampling in Iran during 2007.

Results: Assuming 75% as the appropriate awareness, only 21.3% of adolescents had good literacy about hepatitis B. Lower levels of education, living in urban areas, celibacy and male gender were associated with lower health literacy. The health literacy of HBV infected people about major routes of HBV transmission was low (P < 0.001). According to the participant's answers, radio and TV as the most important tools for their awareness about HBV; there-

fore, implementing educational campaigns through these media is necessary for Iranian community.

Conclusions: There are important deficits in adolescents' health literacy about HBV. We should focus on implementing educational campaigns about HBV through media tools for Iranian community.

P093 DETECTION RESIDUAL HOST CELL DNA BY POLYMERASE CHAIN REACTION TECHNIQUE IN RECOMBINANT HEPATITIS B VACCINE

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ABSTRACT

Background: Biopharmaceutical products such as recombinant HBV vaccines are produced by fermentation using either microbial or eukaryotic cells grown in complex media. Crude preparations of vaccine substances from fermentation contain a number of DNA contaminations from host cells, which are present as impurities. Therefore, removal of the host cell materials is desirable to prevent potential adverse effects. The aim of this study was to develop a sensitive polymerase chain reaction (PCR) method for quantification the level of host-cell DNA (HCD) in recombinant HBV vaccines.

Materials and Methods: we designed specific primers for all strains of Pichia pastoris as a host cell. To determine the specificity of primers, 20 samples from human genome and 10 samples from diverse genomes (Bacteria and viruses) were analyzed. Furthermore, pair-wise alignment using NCBI BLAST program was also performed. To determine the sensitivity of assay, a serial dilution of each standard plasmid from 10^3 to 10^6 copies/μl was prepared.

Results: Only Pichia pastoris and no other irrelevant genomes were detected in PCR reaction for determination of specificity of primers. In addition, NCBI BLAST approved that the primers do not attach to any other sequences except all strains of Pichia pastoris. The sensitivity or limit of detection of the assay was determined 6 copies/μl.

Conclusions: WHO reported that the acceptable lev-

el of HCDs in biopharmaceutical products is 10 picogram. Therefore this fact confirmed the sensitivity of the assay. The assay introduced here is demonstrated to be suitable for detection the residual DNA from Pichia pastoris in recombinant HBV vaccines.

P094 HEPATITIS A SEROPOSITIVITY AMONG NEWLY ADMITTED MEDICAL STUDENTS OF ISFAHAN, KERMANSHAH, AND HAMEDAN: A SEROPREVALENCE STUDY

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ABSTRACT

Background: Health science students are at an increased risk of hepatitis A virus (HAV) infection even under accidental infection. The aims of this study were to assess the seroprevalence of HAV in 1st year medical students and to determine the risk factors of HAV vaccination program among this population.

Materials and Methods: A cross-sectional study was conducted in autumn 2010. A total of 1028 newly admitted medical students in Isfahan, Kermanshah and Hamedan were included in the study. Participant data were obtained through predesigned data collection sheets. A serum sample was obtained for serologic testing for the presence of IgG anti-HAV using a commercially available enzyme-linked immunosorbent assay kit. Descriptive statistics, Chi-square and logistic regression tests were performed for statistical analysis and $P < 0.05$ was considered as significant.

Results: The prevalence of HAV was detected in Isfahan, Hamedan, and Kermanshah newly admitted students 67.5%, 79.2%, and 50.6% respectively. There were significant relations between anti-HAV (IgG) positivity in drinking water and medical students provinces ($P < 0.001$, RR = 0.58 and 0.65 respectively). The household size did not significantly influence the anti-HAV (IgG) positivity in studied subjects ($P = 0.09$, RR = 1.26).

Conclusions: Our results indicate that more than

one-third of the medical students in all three faculties were seronegative for IgG anti-HAV and hence at an increased risk of developing HAV infection as a result of occupational exposure. Therefore, we suggest students in a health care set up should undergo vaccination against HAV after prevaccination immunity screening.

P101 CURCUMIN: A PROMISING NATURAL CHEMOTHERAPEUTIC AGENT IN TREATING HEPATOCELLULAR CARCINOMA

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ABSTRACT

Hepatocellular carcinoma (HCC) is the third leading cause of death from cancer worldwide. Unfortunately, it is a relatively chemotherapy-resistant cancer and the outcome of liver resection as well as liver transplantation is unsatisfactory. Thus, there is a critical medical need to investigate and evaluate possible alternative approaches. Curcumin, a naturally occurring yellow pigment isolated from turmeric (Curcuma longa), exhibits chemopreventive and chemotherapeutic properties against tumors in animal models and clinical trials. Experimental evidences suggest that the anticancer effect of curcumin is via induction of apoptosis through stimulating pro-apoptotic enzymes such as caspases or via inhibiting cell survival pathways including TGF-beta, Akt, NFkappaB, AP-1 and JNK. In addition, curcumin has been shown to inhibit vascular endothelial growth factor (VEGF) and hypoxia inducible factor (HIF)-1a, the key factors relevant to development of new blood vessels that feed the tumor and cause it to grow. Curcumin's therapeutic potential against HCC has been investigated in several recent studies. Curcumin has showed a unique chemotherapeutic effect in reversing diethylnitrosamine (DENA)-induced HCC in rat models, possibly mediated through its pro-apoptotic, anti-oxidant, anti-angiogenic, as well as antiproliferative effects. Furthermore, curcumin was shown to induce mitotic arrest and apoptosis in various hepatoma cell lines. Interestingly curcumin was indicated to prevent metastasis and progression of HCC via inhibiting a member of matrix metalloproteinases, MMP-9. Thus, available findings show promising therapeutic properties of curcumin as a natural chemotherapeutic agent in treating HCC.

P112 BIOINFORMATICS ANALYSIS IN POLYMERASE GENE OF HEPATITIS B VIRUS ISOLATED FROM IRANIAN PATIENTS

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ABSTRACT

Background and Aims: The HBV genome consist of a partially double-stranded circular DNA molecule whose length corresponds to approximately 3,200 nucleotides. The genome is a compact gene layout composed of 4 overlapping ORFs (polymerase, envelope, core and X) so that in comparison with the length of the genome, the total coding capacity is approximately 1.5 times greater. High rate of mutations in HBV genomes comes from the lack of proof-reading mechanisms due to the virus replication via reverse transcription of an RNA intermediate. The *S* open reading frame (ORF), which codes for the hepatitis B surface protein (HBsAg), is overlapped by the polymerase (*P*) gene. Therefore, drug-resistance associated mutations in polymerase gene can result in changes in the HBV surface protein which can influence virion secretion as much as mutation introduced in the S ORF by other mechanisms. It is also probable to reduce binding of HBsAg to anti-HbS antibodies. The aim of this study is to assess the frequency of mutations in *polymerase* gene associated with chronic type B hepatitis.

Methods: The overlapping surface and polymerase reading frames of chronic type B hepatitis patients were analyzed using the internet tools such as HBVRegDB, HepSEQ, HBVseq and Geno2pheno. Then, data from different databases were compared.

Results: The results showed that some mutations in polymerase gene of HBV isolated from Iranian patient strongly associated with chronic type B hepatitis.

Conclusion: According to previous studies, due to the overlapping nature of the open reading frames coding for the polymerase and the surface protein, drug-resistance associated mutations in polymerase gene usually reduces binding of HBsAg to anti-HbS antibodies. So, better understanding of functional

consequences of distinct mutational patterns may help us to guide antiviral strategies and management of chronic HBV infection.

P122 EVALUATION OF ADDING VITAMIN D TO STANDARD HCV REGIMEN (PEG-INTERFERON PLUS RIBAVIRIN) ON EARLY VIROLOGIC RESPONSE (EVR)

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ABSTRACT

Introduction: Chronic HCV-infected patients tend to have vitamin D deficiency, recent studies found that vitamin D has immunomedulator effect. We therefore assessed the effects of vitamin d supplementation on viral response to PEG-INF/RBV.

Methods: In a randomized control trail 60 patients with HCV (30 with genotype 1 and 30 with genotype 2, 3) were randomly divided into two groups, 30 to oral vitamin D supplementation (1600 IU/day maintain serum level > 32 ng/mL) together with 180 μg PEG INF-2a plus oral ribavirin during the treatment and 30 to nonsupplementation (control), The primary end point was undetectable HCVRNA at week 12 of treatment as complete EVR. Vitamin D serum level was measured during treatment at base line, week 4, 12 of treatment.

Results: Demographic characteristics were similar in both groups. Vitamin D deficiency (<30 ng/dl) was seen in 58% of patients. Complete RVR rate at week 12was significantly higher in the vitamin D group with genotype 1 than in the control group with same genotype (93% vs 66% P = 0.02).but complete RVR rate in vitamin D group with genotype 2,3 was not more than the control group same genotype (100% vs 86% P = 0.63). Baseline serum vitamin D levels were lower at baseline (22 ± 15 ng/mL) and increased after 12 wk vitamin D treatment, to a mean level of (52 ± 38 ng/mL [P value=0/02]). Complete EVR was more common in intervention group in patients with genotype 1 (P=0/002).

Conclusion: Vitamin D deficiency was common in HCV patients so adding vitamin D to conventional Peg/RBV therapy for patients with HCV genotype 1 significantly improves viral response.

P135 SNAPSHOT ON DRUG-RESISTANCE RATE IN NUCLEOS (T)IDE ANALOGUE- NAÏVE AND– TREATED PATIENTS WITH CHRONIC HEPATITIS B IN CLINICAL PRACTICE

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ABSTRACT

Background & Aims: Drug resistance resulting from reverse transcriptase (RT) mutations is a major concern with nucleos(t)ide analogues (NAs) treatment in chronic hepatitis B (CHB). The aim of the present study was to determine the prevalence of drug-resistance mutation in NAs- naïve and treated patients with CHB in clinical practice.

Methods: The full-length of HBV RT region from 62 NAs- naïve and 125 NAs-treated patients were amplified and directly sequenced. Among the 125 NAs-treated patients, 60 were in the group of receiving a mono-therapy with tenofovir, 17 with lamivudine and 7 with adefovir. The remaining 41 patients were in the group of receiving lamivudine-adefovir combination therapy.

Results: The mutational analysis on RT region revealed that 3.2% (2/62) of NAs- naïve and 36% (45/125) of NAs-treated patients carried a virus with at least one drug-resistance mutation. The highest rate of patients with at least one drug resistance mutation was observed in the group of patients receiving lamivudine (94.1% [16/17]) and lamivudine-adefovir (53.6% [22/41]), followed by adefovir (42.8% [3/7]), and tenofovir (6.7% [4/60]).

Conclusion: This study showed that more than one-third of NAs-treated Iranian patients carried NAs-resistant HBV strains, and that the HBV mutants associated with resistance to NAs might also present in untreated patients. This suggests the use of anti-HBV drugs with higher genetic barrier and potency in first line therapy.

P138 FATTY ACIDS IN CEREBROSPINAL FLUID IS CORRELATED WITH LIVER ENZYMES TESTS

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ABSTRACT

Background: Alterations in fatty acid homeostasis have been associated with nonalcoholic fatty liver disease by inducing fat storage. Yet, fatty acids may also indirectly affect hepatic function by acting on the central nervous system. The aim of the present study was to determine whether fatty acids in cerebrospinal fluid (CSF) are independently associated with liver enzymes tests.

Methods: CSF and serum samples were collected from 49 patients (age 18-65) at the university hospitals as part of routine diagnostic testing. Along with serum liver enzymes aspartate aminotransferase, alanine aminotransferase and alkaline phosphatase, the fatty acid composition of CSF was measured by gas-liquid chromatography.

Results: The saturated fatty acids including palmitic acid (16:0) and stearic acid (18:0) were positively, and the unsaturated fatty acids including oleic acid (18:1n-9) and linoleic acid (18:2n-6) were negatively correlated with liver enzymes tests. In regression analysis with adjustment for body mass index, the elevated liver enzymes tests were positively associated with total saturated fatty acids ($p=0.52$, $p<0.001$) and negatively with total monounsaturated fatty acids ($p=-0.47$, $p<0.001$) contents of CSF.

Conclusion: CSF fatty acids may be linked to peripheral markers of liver function, suggesting an indirect impact of central fatty acids on hepatocytes function and metabolism. Further clinical attention and research is warranted to elucidate associations of central fatty acids to liver disease in human.

P141 DISASTER IN HIV PATIENTS: SEVEN CASES WITH QUADRUPLE DEADLY CO-INFECTION, SHIRAZ, IRAN

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ABSTRACT

Background: Some co-infections commonly seen in people infected with human immunodeficiency virus (HIV) e.g. Hepatitis B virus (HBV), Hepatitis C virus (HCV), Tuberculosis (TB), *Toxoplasma gondii* and *Neisseria gonorrehoeae*. We aimed to determinate deadly co-infections among HIV patients.

Methods: This retrospective study was performed on 824 HIV patients within a ten year period since 2004. ELISA and confirmation Western Blot test was used for detection of HIV infection. HBsAg, anti-HCV Ab and anti-IgG Ab were using for diagnosis of HBV, HCV and *T.gondii*, respectively. TB and gonorrhea was routinely diagnosed by clinical manifestations and conventional microbiologic tests.

Results: Case No. 1, co-infected with HIV-HBV-HCV-TB, 45 years old, CD4+ lymphocyte counts 250 ul Cells/mm. No. 2, co-infected same as No. 1, age 37, CD4+ lymphocyte 1185. No. 3, coinfected with HIV-HCV-TB-gonorrhea, age 44, CD4+ lymphocyte 361. No. 4, co-infected with HIVHCV- TB-Toxoplasma, age 36, CD4+ lymphocyte 54. No. 5 and 6 co-infected with HIV-HBV-HV- Toxoplasma, age 36 and 51, CD4+ lymphocyte counts 90 and 777, respectively. No. 7, co- infected with HIV-HBV-HCV-gonorrhea, age 36, CD4+ lymphocyte 413. All cases were male and infected with HIV via drug injection route. Moreover, all of them had history of drug addict, prison and HAART therapy. Only exception was case No. 6 which had no history of addiction and HAART therapy, also had unknown transmission rout for HIV acquisition.

Conclusion: As seen in our findings, co-infections are a serious treat for HIV infected patients which may have deadly consequence. Moreover, history of prison and drug addiction seems have significant risk for this condition.

P151 PDCD1 GENETIC DIVERSITY AT POSITION +7785 HAS NOT SHOWN CORRELATION WITH HCV INFECTION

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ABSTRACT

Background: The genetic variations of co-stimulatory molecules such as (PDCD1) programmed cell death 1 gene may affect Pd-1 mRNA expression level which influence the extent of T-cell activity during T-cell mediated immunity. Therefore, it has an important role in chronic infections like HCV infection. We aimed to investigate the association of SNP in PD-1 gene at position +7785 C to T (PD-1.5 or 872) in chronic individual and healthy controls.

Materials and Methods: 162 individuals with chronic HCV infection and 111 healthy controls were enrolled in this study. DNA was extracted from whole blood using salting out method. SNP in PD1 gene was determined by PCR-RFLP method in patients and control groups.

Results: The percentage of CC, CT and TT genotypes at position +7785 C/T in PD-1.5 gene were 42.5%, 43.2% and 14.1%in patients and 44.1%, 39.6% and 16.2% in controls respectively. Distribution of the genotypes and alleles at this locus were not significantly different between patients and controls ($P > 0.05$).

Conclusion: Regarding the data, polymorphisms at PD-1.5 position might not affect the chronicity of HCV infection. Investigating of other SNPs in PD1 gene is suggested.

P153 NON-ALCOHOLIC FATTY LIVER DISEASE AND OBESITY IN CHILDREN: REVIEW ARTICLE

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Abstract

Context: Non-alcoholic fatty liver disease (NAFLD) is the term for a wide range of conditions caused by a build-up of fat within the liver cells. NAFLD is probably the most common cause of liver disease among children in industrialized countries. In this article we aimed to review the current knowledge and ideas concerning pediatric non-alcoholic fatty liver disease, with a focus on its relationship with the obesity.

Evidence Acquisitions: The relevant English published papers were searched using online databases of PubMed, Science Direct, and ISI Web of Science. We summarized the findings of 20 relevant studies in this review.

Results: Most of the studies have reported that the pediatric non-alcoholic fatty liver disease is caused by central obesity with insulin resistance and additional factors influencing inflammatory activity (steatohepatitis). Ongoing inflammation leads to fibrosis and end-stage liver disease.

Conclusion: The increased risk of NAFLD in children with higher BMI can be concluded. As obesity is characterized by BMI, there seems to be a meaningful relationship between pediatric NAFLD and obesity.

P159 INTERLEUKIN-10 PROMOTER POLYMORPHISM -1082 A/G (RS1800896) IN PATIENTS WITH HEPATITIS B VIRUS INFECTION

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ABSTRACT

Background: The natural history of hepatitis B virus infection is variable; thus the clearance or persistence of the infection depends on cytokines and their genetic control. Experimental data have demonstrated the role of Interleukin-10 (IL-10) as an anti-inflammatory cytokine. Variations at specific sites on IL-10 gene may affect the overall expression of its molecules thus the immune response. In the present study we examined genotype and allele frequencies of IL-10 single nucleotide polymorphism (SNP) - 1082 (rs1800896) and compared them with healthy controls, and determined whether there is an association with susceptibility to hepatitis B virus infection.

Methods: A case-control association study was performed with one SNP from the IL-10 gene cluster, on a sample population of 150 hepatitis B virus infected patients and 150 healthy volunteers. DNA was isolated from collected blood samples via salting out method. IL-10 SNP -1082 (rs1800896) was identified using Polymerase Chain Reaction (PCR), Restriction

Fragment Length Polymorphism (RFLP) assay was used for polymorphism genotyping.

Results: Among hepatitis B patients, 56.7% were males and 43.3% were females with a mean age of 40.97±13.86 years, comparing to our control group with 42% men and 58% women (mean age: 46.08±14.98). Age and gender associations generated *P-values* less than 0.05 (*P=0.03* and *P= 0.011* respectively); therefore, logistic regression was applied to remove the possible confounding effects. -1082 (rs1800896) genotypes were assessed for all patients, of which 64 (42.7%) were homozygous for AA genotype, 65 (43.3%) were heterozygous and 21 (14%) were homozygous for GG genotype. The frequencies of AA, AG and GG genotypes among controls were 40.7%, 42.7% and 16.7% respectively. No significant difference was observed in the frequency of IL-10 gene polymorphism -1082 (rs1800896) between hepatitis B patients and healthy subjects, even after adjustment for age and gender (*P=0.682*). Individuals carrying the G allele were more frequent among the control group (38% versus 35.7%), while the incidence of A allele was slightly increased in the patients, however the difference was not statistically significant (*P=0.554*).

Conclusions: No association was observed between -1082 (rs1800896) single nucleotide polymorphism within IL- 10 gene and chronic hepatitis B infection; therefore this polymorphism appears to have no influence on susceptibility to chronic hepatitis B.

P161 EFFECT OF DONOR AGE ON THE RESULT OF LIVER TRANSPLANTATION: REVIEW ARTICLE

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Abstract

Objective: Numerous researches have been carried out about the effect of donor age on the result of liver transplantation. In this study, we aimed to review the previous papers.

Methods: Online databases of PubMed, Science Direct, and Google Scholar were searched using the keywords of "liver transplantation", "liver graft", and "donor age". We studied the papers in which the relationship between donor age and outcome of the transplantation was assessed. 20 English papers were summarized.

Results: In most of the studies it was reported that donor age has no effect on the outcome of liver transplantation. However, other factors like gender may alter the effect. Additionally, some of the studies show that the regeneration capacity of the young liver is more than an old one which is not an important factor in health and doesn't challenge the transplantation.

Conclusions: It can be concluded from almost all of the studies that there is no specific relationship between donor age and the result of liver transplantation

P163 EVALUATION OF HIGH OXYGEN SATURATION IN CIRRHOTIC PATIENTS

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ABSTRACT

Background: Hypoxemia is common among cirrhotic patients. It is resulted from the cirrhosis complications like hepatopulmonary syndrome. However, there isn't any report of cirrhotic patients with hemoglobin oversaturation.

Aims: The aim of this study was to investigate the relation of O_2 oversaturation in cirrhotic patients who are candidate for liver transplantation.

Methods: In this case/control study 384 cirrhotic patients, referred to Shiraz Organ Transplantation Center, were selected. Hemoglobin saturation was measured by ABG (Arterial blood gas). They were divided to two groups; the oversaturated patients (Hb sat $O_2 \geq 98\%$) as case and the patients with (Hb sat $O_2 < 98\%$) as control group. Causes of cirrhosis were categorized into seven groups: Autoimmune hepatitis (AIH), Primary sclorosing cholangitis (PSC), cryptogenic, Hepatitis B virus, Hepatitis C virus, Wilson disease, and other causes. Causes of cirrhosis, age, sex, and smoking state, CXR, pulmonary function test (PFT), MELD score, and place of residence's altitude were compared between case and control groups.

Results: 18.5% of patients were oversaturated. 64.7% of control group were male versus 59.2% of case group. Mean age was (39.95±14.786) for control group and was (37.25±16.293) for case group. He-

moglobin oversaturation in patients with AIH was significantly higher than other causes of cirrhosis (p-value=0.009).Control patients with PSC were significantly higher in proportion to other causes of cirrhosis (p-value=0.04). Place of residence's altitude was (1144.25±565.468) in control group and (1318.52±395.716) in case group which was significantly higher in case group (pvalue=. 039). There was no significant difference between the age, sex, smoking state, CXR, PFT, and MELD score of case and control groups.

Conclusion: Hemoglobin saturation was higher in patients with AIH than other causes of cirrhosis. Also, oversaturation in cirrhotic patients has correlation with altitude of living site.

P164 RISK FACTORS OF HCV TRANSMISSION AMONG PATIENTS IN MOTAHARI HEPATITIS CLINIC OF SHIRAZ ON 2014-2015; A CROSS SECTIONAL STUDY

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ABSTRACT

Introduction: Hepatitis C virus (HCV) is the most common cause of chronic liver disease in Iran that may lead to cirrhosis and hepatocellular carcinoma. There is no vaccine till now for HCV, so identification of risk factors is very important to prevent the transmission of HCV. In this study we aimed to determine the route of transmission of HCV infection.

Methods: In this cross sectional study, all the HCV infected patients with positive HCV antibody that referred to Motahari hepatitis clinic in Shiraz on 2014-2015 were asked for possible transmission route of HCV. Age, sex, marital status, history of high risk activities and how realized that they were infected with HCV obtained and analyzed by SPSS version 21.

Results: Of 111 patients, 95 were male (85.58%). The mean age was 42 years. Twenty two patient were single, 77 married and 12 of them divorced or were widow. 61 patients noted past history of IV drug injection. Dental procedure declared by 104 of cases. 46 patients had unsafe sexual contact with their partner. Tattooing reported by 32 persons. 25 infected

people had blood transmission in past. 11 patients reported previous imprisonment. Bloodletting reported by 25 patients. The major reason which patients understood their HCV infection were screening tests for liver diseases and blood donation which respectively reported by 95 and 16 patients.

Conclusion: In this study, dental procedure, IV drug injection, unsafe sexual contact, tattooing, blood transmission and bloodletting considered as major possible risk factors of HCV transmission respectively.

P165 RISK FACTORS AND DEMOGRAPHIC FEATURES OF HBV INFECTION IN PATIENTS REFERRED TO MOTAHARI HEPATITIS CLINIC OF SHIRAZ 2014-2015

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ABSTRACT

Introduction: hepatitis B is one of the major global health issues. According to some reports, the incidence of HBV infection is decreasing in Iran. Diagnosis of new cases despite effective vaccination shows the importance of evaluating the risk factors of HBV. The aim of this study was to determine these risk factors for HBV infection.

Methods: In this cross sectional study, the risk factors of all HbsAg positive patients referred to Motahari hepatitis clinic of Shiraz in 2014-2015 were determined. Demographic features (age, sex and marital status) and other risk factors were analyzed with SPSS version 21.

Results: 88 patients referred to hepatitis clinic in 2014-2015. The mean age was 40, which 58 patients were male (65%). 70 patients were married, 11 patients single, 7 widow or divorced. 74 patients reported dental procedures in past. 23 patients had history of HBV vaccination. 38 patients had history of hepatic disease in their family (65%). 6 patients had history of imprisonment. 4 patients had history of blood transfusion. 17.04% had history of unsafe sexual contact. The major reason which patients referred to the clinic was screening tests.

Conclusion: One important thing to be noticed in our study, is that most of the patients which had HBV infection hadn't received vaccine. Overall, in pres-

ent study it was concluded that several risk factors of hepatitis - which were determined - supports the result of other studies about HBV.

P168 OUTCOME OF ACCIDENTAL EXPOSURE PRONE TO BLOOD BORNE VIRAL INFECTIONS IN AN EDUCATIONAL HOSPITAL, 6 YEARS FOLLOW UP

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ABSTRACT

Background: The risk for transmission of blood-borne viruses (BBVs) such as Human immunodeficiency virus (HIV), hepatitis B virus (HBV) and hepatitis C virus (HCV) due to occupational exposure is a major concern in the health care setting.

Methods: We reviewed case notes of 337 healthcare workers (HCWs) accidentally exposed to BBVs over six years, from January 2009 to March 2015. The data were reviewed in labbafinejhad hospital; which is specialized 231 bed public tertiary care referral hospital with a total number of 930 HCWs are potentially at accidental risk of acquiring BBVs.

Results: The reviewed HCWs cases (337) were classified in to 131 nurses, 80 medical doctors, 59 medical technicians (37 surgical operation , 17 laboratory and 5 radiology technicians),53 cleaning personnel, 13 nursing students and 1 medical student .Injuries were categorized as 258 needle sticks , 40 sharp cuts , 39 blood splashes on eyes. 244 HCWs were exposed to known serologically tested HIV, HBV and HCV negative patients , 44 cases had exposure to HBS Ag positive , 6 cases to HCV Ab positive and 3 cases to HIV seropositive patients. One HIV positive patient was co infected with HCV infection. A total of 40 HCWs had occupational exposure to unknown sero-status patients. HBS Antibody titer of the 44 HCWs, who had HBV exposure, was higher than 10 mlu/ml. HIV exposed HCWs received post exposure prophylaxis (PEP). Follow up of HCWs who had HBV, HCV and HIV exposures showed no acquired infection.

Conclusion: Key components in reducing risk for accidental exposure to BBVs are education of HCWs for use of universal precautions, HBV vaccination for achieving appropriate HBS Ab level, implementing proper PEP and medical evaluation follow up.

P169 EVALUATION OF INTERLEUKIN-27 GENE POLYMORPHISM (2905 T/G) IN PATIENTS WITH CHRONIC HEPATITIS C VIRUS INFECTION

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ABSTRACT

Background: Hepatitis C Virus (HCV) infection is one of the major health problems worldwide and has affected more than 185 million people. HCV infection may lead to chronic Liver complications, Liver Cirrhosis and Hepatocellular Carcinoma (HCC) and it is a notable cause of liver-related death and liver transplantation. Variation of disease whether become chronic or complete clearance from the host body is dependent on two factors; viral factors and host immunity. Cytokines have principal roles in the immunity modulation in progression of HCV infection. Interleukin 27 (IL-27) is a member of IL-12 family. IL-27 is pro-inflammatory cytokine and can promote TH1 responses from CD4+ naïve T cells. Single nucleotide polymorphisms (SNPs) in interleukin-27 gene are linked to treatment responses. SNPs are important genomic markers which can influence on the activity of IL-27 and may change the outcome of HCV infection. Aim of this study was to determine the association between IL-27 gene polymorphism rs17855750 (2905 T/G) with chronic hepatitis C virus infection.

Materials and Methods: Samples were collected from 125 HCV infected patients and 125 samples of healthy controls in Taleghani Hospital and studied. ELISA used as a serological test to examine and confirm chronic HCV infection. The polymerase chain reaction-restriction fragment length polymorphism was performed to determine IL-27 gene polymorphism. DNA-sequencing was applied on 10 percent of samples to validate genotyping results.

Results: The genotype frequencies of 2905 T/G polymorphism in the chronic HCV patients were significantly different from the healthy control group (P- value 0.017) with the genotype distribution of TT=80%, TG=20% and GG=0% in patients and TT=89.6%, TG=8.8%, GG=1.6% in healthy group; however there were no significant differences between allele frequencies (P-value 0.156).

Discussion: The rate of progression of hepatitis C virus (HCV) infection is variable, likely due to a combination of host genetic and environmental factors. IL-27 importance suggested that it could be a useful candidate for HCV development. The results showed an association between genetic variants of IL-27 SNP 2905 T/G and the evaluation of chronic HCV infection and it may have proinflammatory intent on chronic Hepatitis C Virus infection.

P176 SEVEN YEARS TRENDS IN PREVALENCE OF MAJOR TRANSFUSION-TRANSMISSIBLE VIRAL INFECTIONS IN SHIRAZ BLOOD TRANSFUSION ORGANIZATION

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ABSTRACT

Background: Increasing blood supply safety is one of the most important goals of blood transfusion services. Evaluation of the prevalence of infectious diseases in blood donors is essential for blood donor screening effectiveness.

Materials & Methods: Cross-sectional analyzed the prevalence rate and trend of blood borne infections among Shiraz blood donors during 2007-2014.

Results: The prevalence of HIV between 2007 and 2014 were, 0.0096%, 0.0088%, 0.010%, 0.008%, 0.003%, 0.002%, 0.004% and the prevalence of HBS were 0.36%, 0.28%,0.29%, 0.12%, 0.09%,0.06%and0.06% and the prevalence of HCV were, 0.19%, 0.16%,0.15%, 0.07%,0.06% , 0.05%and 0.03%The Cochran Armitage trend test was used for determination trend change. The prevalence of hepatitis B and HIV was decreased from 2007to 2012 (P<0.001). The prevalence of HCV did not change over 2007 to 2009. The prevalence rate of HIV and HCV decreased significantly from 2010 (P<0.05). The prevalence of HBS, HCV and HIV was more in first-time and male blood donors (P<0.05).

Conclusion: The results showed that the strategies used for improving blood safety were efficient. The prevalence rate of TTVI in Shiraz blood donors is less than normal population and decreased over the time that may be due to effective donor selection, the lower prevalence rate of TTVI in donor population and more safety measures implanted in recent years in Iran.

P178 THE PRE-S2 SEQUENCE MUTATIONS ASSOCIATED WITH HBV DISEASE CONSEQUENCE AMONG DIFFERENT PATIENTS GROUPS

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ABSTRACT

Background: Sequence variation in Pre-s2 gene of Hepatitis B Virus (HBV) is enumerated as important viral factors contributed to infection outcome. While some studies indicated the role of Pre-S2 mutations in diseases progression when evaluated in B and C genotypes, the data supporting this idea on genotype D is limited.

Objectives: The aim of this study was to investigate if deletion mutation in Pre-S2 region attributed to disease progression. Here, the mutations in this region compared among patients with Hepatocellular carcinoma (HCC), Liver cirrhosis (LC) and asymptomatic carriers (ASCs). Material methods and Patients: A total of 60 sera samples were collected from patients infected with HBV. They included 30 asymptomatic carrier (ASCs) individuals samples (22 male and 8 female, mid age: 51) and 30 HCC and Cirrhosis (20 HCC and 10 LC), (26 male and 4 female, mid age: 53). The viral DNA was extracted using DNA extraction kit, and then HBV Pre-s2 gene region were amplified by Nested-Polymerase Chain Reaction (Nested-PCR). Finally, DNA sequences of samples were qualified by Alignment tools (BLAST) then each group was compared with each other by Several Multiple Sequencing Alignment softwares.

Results: The results indicated higher rate of mutations among ASCs group than HCC/LC samples. In 26 ASCs samples (from total 30 samples) 13 critical point mutations in Pre-s2 was detected. Furthermore, in 7 ASCs, 7 deletion mutations were also revealed after analysis. In opposite, 5 point mutations and no sign of deletion mutation in LC/HCC group were confirmed after comparing their sequence with references.

Conclusion: The rate of deletion/point mutations in asymptomatic carriers was so higher than HCC and

cirrhotic patients so it indicated that in HBV genotype D, Pre-s2 deletions are dispensable factors for HBV disease progression.

P180 THE SURVEY OF PRE-S1 SEQUENCE MUTATIONS AMONG DIFFERENT HBV INFECTED GROUPS, POSSIBLE ASSOCIATION WITH DISEASE CONSEQUENCE

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ABSTRACT

Background: Mutations in Pre-S1 gene of Hepatitis B Virus (HBV) is accounted as one of the most important viral factors associated with HBV infection outcomes. On behalf of researchers some deletion/substitution mutations of Pre-S1 region might be responsible for disease progressive toward Liver Cirrhosis (LC) and hepatocellular carcinoma (HCC).

Objectives: The aim of this study was to compare the mutations of Pre-s1 region of HBV genotype D in HCC, Liver cirrhosis and asymptomatic carriers (ASCs).

Material and Methods: A total of 60 sera samples were collected from patients infected with HBV. They included 30 asymptomatic carrier (ASCs) individuals samples (22 male and 8 female, mid age: 51) and 30 HCC and Cirrhosis (20 HCC and 10 LC), (26 male and 4 female, mid age: 53). The viral DNA was extracted using DNA extraction kit, and then HBV Pre-s1 gene region was amplified by Nested-Polymerase Chain Reaction (Nested-PCR). Finally, DNA sequences of samples were evaluated first by online Alignment tools (BLAST) then groups were compared together by Several Multiple Sequencing Alignment softwares.

Results: Out of 60 subjects, 33 samples had 14 deletion and 21 point mutations in Pre-s1 region. In 18 ASCs samples, 11 critical substitution mutations, 14 deletions and in 15 HCC/LC, 10 substitution mutations but not any deletions, were confirmed through comparing with other reference sequences. There were less critical mutations detected in Pre-s1 and interestingly no deletion mutations among LC/HCC groups.

Conclusion: In spite of our imagination, higher

rate of mutations among asymptomatic carriers was clearly delineated here which indicated that in genotype D, Pre-s1 deletions are dispensable factors for progression of disease toward cirrhosis and HCC.

P184 THE DOMINANT PREVALENCE OF GENOTYPE D AMONG DIFFERENT HBV INFECTED PATIENT GROUPS, A STUDY FROM REFERRAL CENTER IN SOUTH OF IRAN

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ABSTRACT

Background: There are more than 7 well described Hepatitis B Virus (HBV) genotypes worldwide. This genetic diversity has been associated with differences in clinical outcomes. In Iran, genotype D was determined as the most common type of virus. In compare to others, Genotype D virus harbors a natural omission in Pre-s1, from aa 2 to 13.

Objectives: The aim of this study was to determine HBV genotype through survey in Pre-s1 region and phylogenetic analysis coincidently.

Materials and Methods: A total of 60 sera samples were collected from patients infected with HBV. They included 30 asymptomatic carriers (22 male and 8 female, mid age: 51), 20 HCC and 10 Cirrhotic patients (26 male and 4 female, mid age: 53). The viral DNA was extracted using DNA extraction kit, and then HBV Pre-s1 gene region was amplified by Nested-Polymerase Chain Reaction (Nested-PCR). The sequences of samples were qualified by Alignment tool (BLAST) then they were compared with other genotypes sequences from Genbank by Multiple Sequencing Alignment.

Results: The sequencing results showed that all of 60 samples were containing genotype D related deletions in Pre-s1 region, from aa2 to 13, which was indicative for the presence of this genotype in all of them. Blast analysis and phylogenetic survey was also supportive of this finding.

Conclusion: In our region, HBV genotype D is dominant among different patient groups in Shiraz- Iran.

P190 WILLINGNESS TO RECEIVE TREATMENT FOR HEPATITIS C VIRUS AMONG DRUG INJECTORS ON METHADONE PROGRAM: IMPLICATIONS FOR HCV KNOWLEDGE AND EDUCATION

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ABSTRACT

Objectives: Although, Persian people who inject drugs (PWID) have high prevalence of Hepatitis C Virus (HCV), a few receive HCV treatment mostly because of poor knowledge about the infection and its treatment. We assessed the factors which were associated with willingness for HCV treatment in a group of PWID who were maintained on methadone treatment.

Methods: 187 PWID were surveyed in seven community methadone programs in Tehran. Participants reported socio-demographic characteristics, the details of drug use and injection and HCV knowledge and treatment history. They were also serologically tested for HCV.

Results: The study found that 28.3% were HCV seropositive. 85% were unaware of their HCV status. Awareness of current HCV status (OR = 3.43; 95% CI, 1.33-7.26; P = 0.012), knowledge of available HCV treatment centers in the community (OR = 7.9; 95% CI, 1.24-5.38; P = 0.004), lifetime attendance at a HCV educational program (OR = 2.9; 95% CI, 2.33-8.56; P < 0.001) and recent attendance at Self-Help Groups (OR = 4.6; 95% CI, 3-43-9.36; P < 0.001) were significantly predictors of willingness for HCV treatment among PWID on methadone program

Conclusion: PWID on methadone program should be provided with HCV education. More attention should be paid to increasing willingness for HCV treatment. The roles of educational programs and Self-Help Groups in encouraging PWID for HCV treatment require further studies.

P192 SHARED METHAMPHETAMINE INJECTION AMONG TREATMENT SEEKERS AND POSITIVE HEPATITIS C STATUS: THE FIRST REPORT FROM PERSIAN IRAN

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ABSTRACT

Shared methamphetamine injection is an emerging route of drug use among Persian methamphetamine injectors. It is a primary vector for hepatitis C virus. The aim of the current study is to determine the prevalence and correlates of shared methamphetamine injection in a sample of Iranian methamphetamine injecting treatment seekers in the south of Tehran. We surveyed male and female methamphetamine injectors at three drop-in centers and 18 drug-use community treatment programs. Participants reported socio-demographic characteristics, drug use, high risk behaviours, current status of viral infections and service use for drug treatment. Bivariate and multivariate logistic regression models were used to test associations between participants' characteristics and shared methamphetamine injection. Overall, 209 clients were recruited; 90.9% were male; 52.6% reported current methamphetamine injection without any shared injection behaviour and 47.4% reported current shared methamphetamine injection. Shared methamphetamine injection was found to be primarily associated with living with sex partners (AOR 1.25, 95% CI 1.13-1.98), reporting three years of dependence on methamphetamine injection (AOR 1.61, 95% CI 1.27-2.12), injection with pre-filled syringes in the past 12 months (AOR 1.96, 95% CI 1.47-2.42), homosexual sex without condom use in the past 12 months (AOR 1.85, 95% CI 1.21-2.25), the paucity of NA group participation in the past 12 months (AOR 0.67, 95% CI 0.41-0.99), the paucity of attending psychotherapeutic sessions in the past 12 months (AOR 0.44, 95% CI 0.28-0.96) and positive hepatitis C status (AOR 1.98, 95% CI 1.67-2.83). Deeper exploration of the relation-

ship between shared methamphetamine injection and sexual risk among Iranian methamphetamine injectors would benefit HIV/sexually transmitted infection prevention efforts. In addition, existing psychosocial interventions for methamphetamine-injecting population may need to be adapted to better meet the risks of shared methamphetamine injectors.

P211 INTERLEUKIN-28B (RS12979860) GENE VARIATION AND TREATMENT OUTCOME AFTER PEGINTERFERON PLUS RIBAVIRIN THERAPY IN PATIENTS WITH GENOTYPE 1 OF HEPATITIS C VIRUS

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ABSTRACT

Background: The success of treatment of chronic hepatitis C (CHC) with pegylated interferon-α (PEG-IFN-α) and ribavirin (RBV) is affected by several host, viral, and treatment factors. This study was designed to describe the association of interleukin (IL) 28B genotypes for rs12979860 with sustained virologic response (SVR) in patients with genotype 1 CHC infection treated with PEGIFN α-2 and RBV.

Materials and Methods: Interleukin-28B genotype in 100 studied patients was detected by tagman real-time polymerase chain reaction. Before treatment blood samples were obtained, then patients were treated for 48-week with a combination therapy using of the PEG-IFN α-2 and RBV. SVR evaluated 6 months after stopping therapy, and was defined as undetectable plasma hepatitis C virus-RNA.

Results: Among studied patients, 65% were IL-28B CT, 27% CC, and 8% TT. In all studied patients, SVR was 58.3%, relapse 15.6%, and null virological response 26.1%. SVR rates were 76.9% in IL-28B-CC, 56.4% in IL-28B-CT, and 12.5% in IL-28B-TT patients. Relapse rates were 7.7% in IL-28B-CC, 12.9% in IL-28B-CT, and 62.5% in IL-28B-TT patients. There was a significant difference between response to treatment in patients IL-28B-CC, CT, and TT (P = 0.003). IL-28B genotype CC, (odds ratio = 0.053, 95% confidence interval; 0.005-0.54, P = 0.03), was the independent predicting factor.

Conclusion: Interleukin-28B was an important predictor of CHC treatment outcome with Peg-IFN-α and RBV. IL-28B-CC seems to be more important than IL-28B-CT/TT in predicting positive treatment response.

P215 THE EFFECTS OF SINGLE NUCLEOTIDE POLYMORPHISM OF IL28B GENE (RS12980275) ON TREATMENT RESPONSE TO PEGYLATED INTERFERON/RIBAVIRIN IN IRANIAN PATIENTS WITH HEPATITIS C

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ABSTRACT

Background and Purpose: The standard of care treatment for infected patients with HCV is based on a combination of pegylated interferon alpha and ribavirin. Recently, the rs12980275 SNP polymorphism, located upstream of the interleukin 28B gene, was shown to be strongly associated with response to anti-HCV therapy. This study investigated the distribution of the (G/A) polymorphism with sustained virologic response (SVR) to chronic Hepatitis C virus infection among Iranian population.

Material and Methods: This cross-sectional study was performed in 75 blood samples including 50 SVR positive and 25 negative samples from individuals suffering from chronic hepatitis C, and 50 healthy controls. DNA was extracted from the samples and the frequency of the polymorphism was analyzed using PCR-ARMS method. Finally, the products were detected on agarose gel.

Results: In the analysis of the data for G/A polymorphism, the GG genotype was identified in 29 patients of whom 28 (39.4%) achieved SVR, while the GA heterozygous was found in 75 patients and SVR was achieved in 42 (59.2%). Finally, the AA was detected in 14 patients and only one (1.4%) responded to treatment.

Conclusion: Patients with G allele had significantly higher SVR rate than those with A allele. These data suggest that genotype detection of rs12980275 SNP may be useful as an important predictive biomarker for SVR in patients infected with HCV. However, further studies with more samples lead to more validated results.

P217 ASSOCIATION OF IL28B GENE (RS8099917) POLYMORPHISM WITH TREATMENT RESPONSE IN CHRONIC HEPATITIS C PATIENTS TREATED WITH PEGYLATED INTERFERON/RIBAVIRIN IN IRAN

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ABSTRACT

Background and Purpose: The standard of care treatment for infected patients with HCV is based on a combination of pegylated interferon alpha and ribavirin. Recently, the rs8099917 SNP polymorphism, located upstream of the interleukin 28B gene, was shown to be strongly associated with response to anti-HCV therapy. This study investigated the distribution of the (G/T) polymorphism with sustained virologic response (SVR) to chronic Hepatitis C virus infection among Iranian population.

Materials and Methods: This cross-sectional study was performed in 75 blood samples including 50 SVR positive and 25 negative samples from individuals suffering from chronic hepatitis C, and 50 healthy controls. DNA was extracted from the samples and the frequency of the polymorphism was analyzed using PCR-ARMS method. Finally, the products were detected on agarose gel.

Results: In the analysis of the data for G/T polymorphism, the TT genotype was identified in 45 patients of whom 42 (59.4%) achieved SVR, while the GT heterozygous was found in15 patients and SVR was achieved in 12 (39.2%). Finally, the GG was detected in 4 patients and only one (1.4%) responded to treatment.

Conclusion: Patients with T allele had significantly higher SVR rate than those with G allele. These data suggest that genotype detection of rs8099917 SNP may be useful as an important predictive biomarker for SVR in patients infected with HCV. However, further studies with more samples lead to more validated results.

P220 SEROPREVALENCE STUDY OF HEPATITIS B VIRUS AMONG HOSPITALIZED INTRAVENOUS DRUG USERS IN TEHRAN, IRAN (2012-2013)

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ABSTRACT

Background: Injecting drug use is a major cause of both morbidity and mortality worldwide. Injection drug use has been the most growing rout of drug abuse in Iran in the past decade and it has been responsible for the transmission of blood born infections such as Hepatitis B Virus (HBV) infection.

Methods: This was a cross-sectional investigation which conducted on 100 male Intravenous Drug Users (IDU). The records of 100 IDUs hospitalized from 2012-2013 at Loghman Hospital were reviewed. Their serum samples were tested for the presence of HBsAg (Hepatitis B Surface Antigen) by Enzyme-linked Immunosorbent Assay (ELISA).

Results: The Prevalence of HBsAg was 1%. The majority Prevalence of HBsAg was among adults age 25-45 years.

Conclusion: Many studies highlighted that blood borne viral infections are prevalent among intravenous drug users. Fewer infected cases in this study promises that in case of performing on time detriment prevention and decreasing measures, will cause future satisfying results in this case.

P221 VERTICAL HEPATITIS IN A FIVE YEAR PERIOD IN ZABOL HOSPITAL

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ABSTRACT

Introduction: Hepatitis B and C are the most common causes of hepatitis among newborns in developing countries. Vertical hepatitis refers to hepatitis transmitted from the mother to the infant during pregnancy, at the time of delivery, or during the first 28 days after birth. In this study we tried to evaluate

vertical hepatitis situation in the only educational hospital of Zabol city from 2009 till 2013.

Materials and Methods: In this descriptive study, patient's documents of labor ward were studied from 2009 till 2013. Information related to hepatitis infected newborns collected using checklist tool. Data analyzed using SPSS-21 software.

Results: Our study showed out of total 47,987 deliveries, 853 (1.78%) stillbirths, 325 (0.68%) abortions and 46809 (97.40%) successful births were recorded in which 266 (0.56%) cases were related to hepatitis in Zabol hospital in 2009-13. Out of all hepatitis infected newborns 50, 79, 67, 30 and 40 were recorded in 2009, 2010, 2011, 2012 and 2013 respectively. Average recorded number of hepatitis in each month was 4.43 in this duration. Our analysis showed no significant change in hepatitis incidence in Zabol in this period. (p>0.05)

Conclusion: According to the results, vertical hepatitis is a major health problem in Zabol. This subject could be related to women's hygiene and mother's health. We are suggesting new managements of health policies and paying more attention to vertical hepatitis problem in this area.

P229 LONG TERM THERAPEUTIC CONSEQUENCES IN PATIENTS WITH AUTOIMMUNE HEPATITIS

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ABSTRACT

Introduction: Autoimmune hepatitis (AIH) is a chronic inflammation of the liver, the cause of which is unknown. The long-term outcome of patients with AIH has not been well-defined. The aim of this study was to clarify the long-term outcomes and determinants of outcome in patients with AIH.

Methods and Material: In this cohort, a total of 150 AIH patients were enrolled in the study. Patients were followed up for an average of 60 months. Clinical, biochemical, pathological and imaging data were gathered from all the patients at both the beginning and the end of the follow-up with 3 checkpoints between these time periods. Results are expressed as mean ± SD. P< 0.05 was statistically significant.

Results: One hundred and fifty patients, 113 female, 37 male, mean age 42.39 ± 14.58 years, participated in the study. The most common symptoms were icter (88.7%), fatigue (84.7%), pruritus (80%) and loss of appetite (36.6%) at diagnosis. Seventy-three patients (48.7%) reached remission; thirty-four patients (22.7%) relapsed, thirty-two patients (21.3%) had incomplete response and eleven patients (7.3%) had treatment failure. Predictors for disease progression were age at presentation of 20-40 years and number of relapses (P< 0.05). The prognosis of patients experiencing two or more relapses was significantly poorer than that of patients with remission or a single relapse both in univariate (P < 0.001) and multivariate (P < 0.001) analyses.

Conclusions: Repeated relapses of disease are significantly associated with a poorer long term consequences in patients with autoimmune hepatitis.

P230 EVALUATION OF SURVEILLANCE SYSTEMS FOR HEPATITIS B IN IRAN

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ABSTRACT

Hepatitis B is one of the major health problems in the world, especially in developing countries So that in 70 to 80 percent of chronic hepatitis caused by hepatitis B virus and the main cause of mortality in hepatitis, hepatitis B is. The surveillance system for hepatitis B in the following target groups for screening are recommended: Donors who early in the incubation period of the disease can HBV transfer and detection techniques are known to remain so in achieving blood stored absent any risk of contamination but by PCR cannot be enabled (the now do not operate anywhere in the world) * Pregnant women in the third trimester and so screening is recommended for all women in America. Screening of different target groups in America than Iran is so that in America, in addition to the target groups which are screened in Iran, People in areas with moderate and high rates of hepatitis B (incidence greater than or equal to 2%) and those not vaccinat-

ed as children whose parents are in areas with high rates of hepatitis B (HBsAg prevalence of greater than or equal to 8%) were born. and homosexual men are not part of the target group screening in Iran. Including opportunities for surveillance of hepatitis B can be found at different levels of health and family physicians cited that Family physicians have a plan to increase the percentage of people who care and early detection of the disease and prevent progression to cirrhosis and liver cancer caused by hepatitis decrease. Another strength of the system of care for hepatitis B hepatitis B vaccine produced by the Pasteur Institute in 86 years that the work of the hepatitis B vaccine was sufficient. Planning to identify carriers of hepatitis, health care necessary to prevent the infection of others, testing of hepatitis B in pregnant women contamination and timely action to prevent the contamination of infected mothers, the contact with infected needles (needle stick) and health education, disease transmission, …. Of the things that can increase knowledge and changing attitudes and behaviors lead to control of this disease.

P242 LACK OF ASSOCIATION BETWEEN IL12A SINGLE NUCLEOTIDE POLYMORPHISM (RS6887695G/C) AND CHRONIC HEPATITIS B VIRUS INFECTION

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ABSTRACT

Background: The hepatitis B virus (HBV) infection is considered to be one of the most important etiological factors of liver complication around the world. Interactions of host immune responses with HBV have a crucial role in the outcome of the infection. IL12 is an important pro-inflammatory cytokine that stimulates natural killer cells and T-lymphocytes to produce IFN-α, promotes T-helper 1 responses and enhances CD8+ cytotoxic T-cell activity. These unique properties of IL12 indicate that it might play an important role in control and clearance of HBV. On the other hand, single nucleotide polymorphisms (SNPs) are presumed to be associated with the differential production of cytokines. In this study, association of IL12A rs6887695 G/C polymorphism with chronic HBV infection has been investigated.

Materials and Methods: Genotypes distributionofIL12A rs6887695 were determined in 120 HBV chronic patients and 120 healthy controls using polymerase chain restriction fragment length polymorphism (PCR-RFLP) method.

Results: The frequencies of rs6887695GG, GC and CC genotypes in the patients with chronic infection were 58.30%, 35% and 6.70%respectively and in healthy controls were 50%, 44.20%, 5.80%. No statistically significant difference was detected in IL12A rs6887695 genotypes between patient and control groups (P value =0.26).

Conclusions: Our findings suggest that IL12A rs6887695 SNP is not associated with chronic HBV infection in the studied Iranian population.

P250 SEROPREVALENCE OF HEPATITIS A AND HEPATITIS E VIRUS IN HEALTHY BLOOD DONORS FROM TEHRAN, IRAN

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ABSTRACT

Background: Hepatitis A virus (HAV) and hepatitis E virus (HEV) are both transmitted by the fecal oral route, and known as leading causes of acute viral hepatitis in the world, especially in developing countries. There is a lack of updated data on HAV and HEV seroprevalence in Iran. The aim of this study was to determine the seroprevalence of HAV and HEV among group of blood donors in Tehran, Iran.

Methods: A cross sectional study was performed in July 2014 until December 2014 on a total of 559 blood donors referred to Tehran Blood Transfusion Center. The samples were studies for antibodies to HAV and HEV. Data were statistically analyzed using SPSS, were calculated the mean, median, mode, standard deviation and P-value using Fishers Exact test or Chi-squared test. To HAV and HEV antibodies positivity, a P-value less than 0.05 was considered to be statistically significant.

Results: In the present study, 559 blood donors, 536 were men (95.9%) and 23 were women (4.1%) analyzed

for anti-HAV and anti-HEV antibodies, the mean ± SD age of donors was 38 ±10.3 (range: 18-63) years. Out of 559 blood donors, 107(19.1%) were first-time donors, 163(29.2%) were lapsed donors and 289(51.7%) were regular donors. Anti-hepatitis A IgG specific antibodies were found in 395(70.7%) and anti-hepatitis E were found in 45(8.1%) of the blood donor populations.

Conclusions: The result of current study shows that exposure to hepatitis A and hepatitis E among blood donors in Tehran was high. Anti-HEV prevalence was considerably similar than those previously reported in Iran. Therefore, these findings indicated that the area is still endemic for HAV and HEV prevalence.

P259 CLONING OF HCV CORE+1 GENE IN BACULOVIRUS EXPRESSION SYSTEM

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ABSTRACT

Background: The new detected HCV protein "Core+1" made from the ribosomal frame shift in Core region is an important candidate for diagnostic tools.

Objectives: This study was conducted to design a recombinant Bacmid plasmid expressing the HCV 1a Core+1 sequence in Baculovirus expression system for further diagnostic applications

Materials and Methods: In this study DNA sequence of Core+1 gene amplified by PCR for producing an insert sequence that containing this gene. The targeted gene has been cloned in pFastBac HTb vector and sequenced after treating by XbaI/NcoI restriction endonucleases. After confirming the cloning of target gene clone product transformed to the Bacolovirus (DH10bac) system. Blue- white screening of colonies and PCR confirmed the transformation.

Results: The Cloning of pFastBac vector with the purified PCR product of HCV Core+1 was confirmed. Finally, the recombinant Bacmid was successfully transformed in DH10Bac.

Conclusions: The recombinant Bac-Core+1 expression vector is considered as an important tool to transfect the sf9 cell line and expression the Core+1 protein.

P286 SURVEILLANCE AND EPIDEMIOLOGY OF HEPATITIS B, C, D AND G IN KHUZESTAN PROVINCE, SOUTHWEST IRAN- A REVIEW.

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ABSTRACT

Background: This article provides a brief overview of the different types of viral hepatitis, including their epidemiology, clinical features. HBV and HCV infectious are frequent causes of acute and chronic hepatitis worldwide and leading causes for hepatic cirrhosis and cancer. HDV is acquired only by coinfection with HBV or by superinfection of an HBV carrier. Hepatitis G virus belonging to the family Flaviviridae. This virus is transmitted via blood and blood products.

Materials and Methods: Information obtained from previous investigations on HBV, HCV, HDV and HGV infections have yielded a better knowledge about hepatitis. All descriptive/analytical cross-sectional studies/surveys from 2002 to 2011that have sufficiently declared objectives, proper sampling method with identical and valid measurement instruments. Reverse transcription polymerase chain reaction (RT-PCR) was used for RNA detectionfrom serum samples of hepatitis patients.

Results: Among intravenous drug users, 103 patients (30.9%) had HCV and 12 (3.6%) had HBV infection. On thalassemia patients, the prevalence rate of anti-HCV was 28.1%, 46 of anti-HCV positive patients were also HCV RNA positive. Out of 214 hemodialysis patients, 34 were positive for anti-HCV and 11 for HBsAg. Among Haemophilia Patients, prevalence rate of HBsAg and anti-HCV were 1.1% and 54%, respectively.co-infection of HGV with HCV and HBV was determined at 6% and 8%, respectively. And HDV prevalence was 11.5%.

Conclusions: The harmonisation and strengthening of HBV and HCV surveillance at the Khuzestanean level is of utmost importance to obtain more robust data on these diseases.

P295 COMPARATIVE STUDY ON THE CHEMICAL AND MEDICINAL EFFECTS OF INDIGENOUS SILYBUM MARIANUM FROM EGYPT AND

MEDICINAL SILYMARIN FROM CHINA ON THE TREATMENT OF LIVER FIBROSIS ON FEMALE ALBINO RA

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ABSTRACT

Liver fibrosis is one of the common problems affecting on the human health. Many herbal and medicinal plants and their extracts are widely studied. The medical Chinese silymarin got a bright reputation in relieve the liver fibrosis. A total of 72 female *Albino* rats were divided into six groups; G_1 (Control), G_2 (Fibrosis), G_3 (Chinese silymarin), G_4 (Fibrosis + Chinese silymarin), G_5 (Egyptian silymarin extract), G_6 (Fibrosis + Egyptian silymarin extract). Results showed that, serum liver enzymes activities (ALT, AST and GGT) and tissues MDA were significantly decreased in G_6 compared to those in G_2 and G_4. Serum total protein and tissues GST, CAT enzymes activities, total thiol and TAC were significantly increased in G_6 as compared to G_2 and G_4. The results revealed that, the Egyptian plant extract improved liver function and its oxidative stress parameters in comparison with the Chinese silymarin, in case of liver fibrosis. Also, GC-MS showed that the Egyptian silymarin has more peaks than that of Chinese silymarin. The smaller peak area in the Egyptian silymarin extract was about one third the big one in the Chinese silymarin. The Egyptian silymarin extract have extra components that needs further study for its identification.

P303 OCCULT HEPATITIS B INFECTION IN HEPATITIS C PATIENTS WITH HAEMATOLOGICAL DISORDERS

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ABSTRACT

Background: Occult hepatitis B infection (OBI) is recognized by finding HBV DNA in the liver (with detectable or undetectable HBV DNA in the serum) of patient with negative testing for HBV surface antigen (HBsAg). OBI is seen in Hepatitis C virus (HCV) infected patients and also one of the important mechanism for transmission of HBV and HCV is via blood transfusion. In this study we want to assess the prevalence of OBI among Iranian patients with haematological disorders (thalassemia, hemophilia and some other coagulation factors deficiency) infected with CHC.

Patients and Methods: In this descriptive cross sectional study, all patients with haematological disorders (thalassemia, hemophilia or other coagulation factors deficiency) who had CHC infection simultaneously, that referred to Tehran Hepatitis Center (TCH) between 2009 and 2010 enrolled to this study. OBI identification was based on the serum HBV-DNA detection. Data analysis was done with SPSS.

Results: All of patients were HBS Ag negative and HCV RNA positive. Only 145 patients had HBV DNA evaluation. (126 male and 19 female patients) The mean age was 28.12 ± 8.6 years. Thirty five patients had thalassemia, 95 patients had hemophilia, and 15 patients had coagulation factors deficiency. Serum HBV-DNA was negative for all cases.

Conclusions: Based on our results, it seems that there is no OBI case in the chronic HCV infected patients with thalassemia and bleeding disorders especially Hemophilia. But for getting a better decision about OBI screening particularly in transfusion centers and use of a comprehensive screening method, more original studies with more precise laboratory techniques and more sample size is still needed.

P304 SEROPREVALENCE OF HEPATITIS A VIRUS AMONG IRANIAN SOLDIERS

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ABSTRACT

Background: Hepatitis A virus (HAV) is highly contagious in individuals living in crowded conditions such as military centers. This study try to investigate the seroprevalence of HAV immunity among Iranian soldiers and determine whether vaccination should be used for military draftees.

Patients and Methods: In this cross-sectional study, a total of 1554 soldiers were recruited through random clustering sampling. Serum anti-HAV antibody was measured by Enzyme-linked immunosorbent assay (ELISA).Statistical analysis was performed using SPSS.

Results: A total of 1554 male soldiers with age ranged from 18 to 34 years (mean age: 21.2±1.9 y) at baseline were evaluated. Overall, 80.3% of the analyzed specimens were anti-HAV seropositive. The seroprevalence rates increased significantly with the age.

Conclusions: Our results suggest that generally vaccination for HAV is not necessary for Iranian military draftees. But the vaccination is recommended for high-risk groups including anti-HAV seronegative soldiers.

P305 ARE WOMEN WITH POLYCYSTIC OVARIAN SYNDROME AT A HIGH RISK OF NON-ALCOHOLIC FATTY LIVER DISEASE; A META-ANALYSIS

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ABSTRACT

Context: Insulin resistance is a hallmark of metabolic syndrome (MS). It has been proposed that both polycystic ovarian syndrome (PCOS) and nonalcoholic fatty liver disease (NAFLD) are correlated with Insulin resistance. Therefore, PCOS and NAFLD can be attributed with insulin resistance and therefore MS. The aim of this meta-analysis was to determine whether PCOS patients are at a high risk of NAFLD.

Evidence Acquisition: Google scholar, Scopus, ISI Web of Science, Embase, MEDLINE, and some Iranian databases such as scientific information database (SID), IranMedex, and MagIran were searched to identify relevant studies. We included all papers regardless of their language from January 1985 to June 2013. By using data on prevalence of NAFLD in patients with and without PCOS, odds ratio (OR) with 95% confidence intervals (CIs) were calculated in each study. Chisquared test was used to assess heterogeneity between studies.

Results: We finally included seven eligible studies. According to chi-squared test, there was a significant heterogeneity (73.6%) between studies (P = 0.001). NAFLD prevalence was significantly higher in patients with PCOS compared to healthy control, with an overall OR of 3.93 (95% CI: 2.17, 7.11).There was no significant publication bias based on Begg's and Egger's tests.

Conclusions: According to the results of this meta-analysis, there was a high risk of NAFLD in women with PCOS. We suggest evaluating patients with PCOS regarding NAFLD.