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Prevalence of hepatitis D virus in Sindh Camp; Punjab epidemiological survey

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Introduction
Hepatitis D virus or delta virus (HDV) is a small, defective RNA virus that can infect only individuals who have hepatitis B virus which acts as the carrier host. The prevalence of HDV antibodies in Pakistani hepatitis B surface antigen (HBsAg) positive individuals is approximately 16.6%. So there is a pool of at least 800,000 anti-HDV positive HBsAg positive individuals in the country. Although the prevalence of hepatitis virus infections in Pakistan is still unknown, limited data indicate that the exposure rate to HBV is 35-38% with 4% being carriers and 32% having anti-HBV surface antibodies through natural conversion. Studies in Pakistan have shown that the prevalence rate of HDV is 4.8-14% for, and that it is continuously increasing. Hence there is an urgent need to create awareness about the prevalence of both hepatitis B and D, and to develop preventive measures aimed at minimizing the prevalence of these diseases in the country.

Objectives:
The main objective of this study was to determine the epidemiological burden of HDV in Pakistani population. There is paucity of data on this aspect and we aimed to bridge the knowledge gap with this study.

Methods & Materials: A descriptive study was conducted from 1st January-31st November 2014 at RAHILA Research & Reference laboratory, Karachi, Pakistan. A total number of 500 serum samples were collected from patients coming to multiple clinics for diagnostic HDV testing at various public sector hospitals in Southern Punjab & Sindh, Pakistan.

Results: The results showed that 105/500 (21%) tested positive for HDV, 5/500 (1%) tested border line while 390/500 patients (78%) were negative for HDV by ELISA method.

Conclusion: This study aimed to provide epidemiological burden of HDV in Pakistani population. The results show that a moderate percentage of study cohorts was tested positive indicating the significance of HDV testing along with HBV. HDV testing can serve as management tools for clinicians for therapeutic purpose.
Epidemic of hepatitis C in a remote village of Kashmir, India

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**Background:** Introduction: In the developing world, unsafe therapeutic injections and transfusions are likely to be the major modes of transmission. In India, the prevalence appears to be highly variable, according to the geographical site or the population group analysed (0.09–7.89%). There was a cluster of seven cases of hepatitis C in the village Takiya Magam in January 2013. In response, the Rapid Response Team surveyed the entire population for prevalence of antibody against hepatitis C.

**Methods & Materials:** An investigation of the outbreak was conducted by surveying the household contacts of the 7 hepatitis C cases in the first phase of investigation followed by screening of the entire 2600 population of the village in the second phase. Of the 2600 persons living in the village 2051 (78.88%) agreed to get tested for anti-HCV. The entire village was screened using the Rapid Card Diagnostic Test (SD Bioline rapid immunochromatographic test for antibody Ig G). Blood samples were collected and serum separated within hours of collection and transported to the laboratory for use. All anti-HCV positive cases were further evaluated clinically by a team of gastroenterologists.

**Results:** Out of the population of 2600, 2051 consented to getting tested. This included 1199 males (49.04%) and 1269 females. Of the 2051 subjects, 787 (38.37%) were anti-HCV positive by both rapid and third generation ELISA. The age group ranged from 30 months years to 75 years, with 113 subjects being below the age of 15 years (14.35%).

**Conclusion:** In our study, we have witnessed the widespread use of injections in all the four villages and the same situation may exist in the rest of the state. Stopping the re-use of unsterilized disposable needles and syringes is important to interrupt the transmission not only of HCV but other viruses that may be transmitted via therapeutic injections. Unregulated use of injections by quacks has to be stopped in conjunction with health education of the population regarding safe injections.
Studies on co-infections of malaria, bacteraemia and intestinal parasites among primary school pupils in Owerri Metropolis and Environs, Imo State, Nigeria

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Background: Studies on co-infections of malaria, bacteraemia and intestinal parasites in primary school pupils in Owerri metropolis and environs were carried out from January 2010 to January 2012. Species and prevalence of these co-infections were determined.

Methods & Materials: Stool and urine specimen were collected with sterile containers, blood specimen collected with syringe and EDTA bottles from 650 hospitalized and 500 non-hospitalized pupils (who served as control). Parasitological investigations on the stool specimen included Macroscopic Analysis, Direct Wet Method and Formol Ether Concentration Technique; on urine specimen by Centrifuging and Microscopy, on blood specimen by Thick and Thin Blood Smear Method. Bacterial Inoculation, Isolation and Identification were done by subjecting the respective specimen to culture using Nutrient Agar, Manitol, Salt Agar, Blood Agar, Cled Agar, Mac-Conkey, Deoxycholate Citrate (DCA), Selenite F. broth, Alkaline Peptone water, Brain Heart Infusion Broth and SS Agar.

Results: Among the hospitalized pupils, 208 (32%) were infected with both Plasmodium falciparum and bacterial organisms, including Staphylococcus aureus 40 (6.2%), Escherichia coli 69 (10.6%), Salmonella typhi 87 (13.4%), Klebsiella pneumonie 10 (1.5%) and Pseudomonas aeruginosa 2 (0.3%). A total of 187 (28.8%) were infected with Plasmodium falciparum and intestinal parasites, including, Trichuris trichiura 33 (5.1%). Ascaris lumbricoides 53 (8.1%), Entamoeba histolytica 43 (6.7%), Hookworm 34 (5.2%) and Strongyloides stercoralis 24 (3.6%). A total of 125 (19.3%) were infected with Plasmodium falciparum, as well as with both intestinal parasites and bacterial organisms, including, Ascaris lumbricoides and Staphylococcus aureus 26 (4.0%), Ascaris lumbricoides and Escherichia coli 16 (2.5%), Entamoeba histolytica and Staphylococcus aureus 22 (3.4%), Entamoeba histolytica and Escherichia coli 24 (3.7%), and, Hookworm and Escherichia coli 20 (3.1%). Among the non-hospitalized pupils, 54 (10.8%) pupils were infected with Plasmodium falciparum and bacterial organisms, including Staphylococcus aureus 17 (3.4%), Escherichia coli 28 (5.6%) and Salmonella typhi 9 (1.8%). Another 33(6.5%) of non-hospitalized pupils were infected with Plasmodium falciparum and intestinal parasites, including Hookworm 22 (4.3%) and Entamoeba histolytica 11 (2.2%). A total of 520(80.0%) hospitalized pupils had co-infections. A total of 87(17.4%) non-hospitalized pupils had co-infections.

Conclusion: High prevalence of coinfections of malaria with bacterial organisms and intestinal parasites was underscored.
Thyroid dysfunction in patients with chronic hepatitis C

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Background: Hepatitis C virus (HCV) is a cause not only of hepatic cirrhosis and hepatocellular carcinoma but also extrahepatic symptoms that are observed in 40-74% HCV-patients. An increase in thyroid dysfunction incidence was observed in HCV-patients was observed in comparison to the healthy population. Particularly, 13% of patients were characterized by hypothyreosis, in 25% antithyroid antibodies were detected, whereas in 30% of patients thyroid dysfunction was observed during antiviral therapy. A significant negative influence of thyroid dysfunction on HCV prognosis was demonstrated. However, no direct association between HCV and thyroid pathology has been revealed yet.

Methods & Materials: To investigate the variants of thyroid status in HCV-patients (Altai region, Russia). Methods: A prospective dynamic physical, laboratory and instrumental investigation of 240 HCV-patients (47.5% men and 52.5% women aged from 18 to 50 years). Particularly, the investigation included thyrotropin, total T3 and T4, free T3 and T4, thyroperoxydase antibodies, and ultrasound examination of thyroid.

Results: In 50% of HCV-patients various changes in thyroid hormones levels and morphometric features of thyroid dysfunction were revealed: thyrotropin - 2,1 ± 1,42 mkME/ml, total T3 - 2,4 ± 1,27 nmol/l, total T4 - 108 ± 1,25 nmol/l, free T4 - 14,8 ± 5,25 nmol/l, thyroperoxydase antibodies 11 ± 4,71Ed/ml. Increase thyrotropin at 14,1%; decrease in thyrotropin – 20,8%; total T3 increase 12,5% reduction below normal in only 6,6%. Reduced free T4 at 15,8%, thyroperoxydase antibodies detected in 30%. By ultrasound: diffuse changes in structure (in 42,5% of patients), nodes (26,6%), cysts (13,3%) and the lack of structural changes (17,5%). Thyroid dysfunctions was presented by euthyreosis (60%), hypothyreosis (20%), hyperthyreosis (10%), and autoimmune thyreoiditis (10%). An interrelation between thyroid dysfunction development and the HCV anamnesis length has been estimated.

Conclusion: 1) The incidence of thyroid dysfunction in HCV-patients is significantly increased; 2) Euthyreoid and hypothyreoid were the most common among all observed thyroid dysfunction cases; 3) The violation of thyroid function of HCV-patients can be considered as extrahepatic manifestations. The presence of thyroid dysfunction in patients with early stages of fibrosis will select candidates for the antiviral therapy.
Hepatitis C virus NS3 protease resistance testing: analysis computational to detect resistance mutations

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Background: Chronic hepatitis C infection is caused by the hepatitis C virus (HCV) and affects an estimated 200 million people worldwide. HCV infection is a major cause of chronic hepatitis, liver cirrhosis and hepatocellular carcinoma globally. The treatment for HCV chronic infection with pegylated interferon alpha plus ribavirin inhibitors is unspecific and is effective in only 50% of patients. This has prompted the development of drugs that target virus proteins, such as NS3 protease. These direct acting antivirals have demonstrated a potent effect in vitro and in vivo; however, virus mutations associated with the development of resistance have been described. The objective of this work is detecting mutations in NS3 protease of HCV, which confers resistance to direct acting antivirals.

Methods & Materials: We have designed and developed an online information system named Biomedical Mutation Analysis (BMA), which allows users to calculate changes in nucleotide and amino acid sequences for each selected sequence. It is used as reference NS3 protease sequence of HCV based on the main positions associated to resistance mutations of direct acting antivirals in vitro and in vivo described in the literature. The algorithm of BMA allows the computational analysis of codons at the positions associated to mutations with resistance to direct acting antivirals aimed at HCV NS3 protease. The analysis allows determining for each position of interest, the number of nucleotide substitutions necessary, for changing the amino acid that generates resistance.

Results: BMA provides the results of the computational analysis by three visualization techniques. The first technique is an online textual visualization which includes results regarding mutations that contain detailed information of nucleotide and amino acid changes, for each position of interest. The second technique is a report generated automatically and sent to the user via email, which contains the summary and details of each analyzed patient with the correspondent sequences. The third technique is a “Force-Directed Graph”, which identifies mutations of each sequence of patients through nodes grouping, where nodes correspond to each analyzed sequence.

Conclusion: BMA allows the computational analysis quickly, easily and effectively. Furthermore, the development of different visualization techniques allows a proper interpretation and understanding of the results.
Dengue situation and epidemiological features in the South of Vietnam from 1975 to 2014

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**Background:** Dengue is a hyper-endemic disease in the South of Vietnam. Before 1999, Dengue report was intergrated into notifiable disease. Since 1999, specific surveillance system for Dengue has been established to collect Dengue information, included: cases, virus and vector. Clinical Dengue cases hospitalized in public hospitals of all administrative levels have been recorded. Virus isolation has been applied to monitor the circulation of Dengue serotypes on 2% to 5% clinical cases. These cases have been selected through out the year and randomly from all hospitals in the South. Monthly vector survey has also been conducted in at least 2 sites/province including 1 representative rural and 1 representative urban/suburban area.

**Methods & Materials:** Analysis of surveillance data from 1975 to 2014.

**Results:** Dengue cases have been increased by every 10 years: average cases in 10 years from 1975-1984 to 2014 in turns was 16,313 cases; 38,039 cases; 50,734 cases and 59,306 cases. Dengue cases/100,000 person has increased from 6 cases in 1976 to 444 cases in 1998. There is a co-circulation of all 4 Dengue serotypes. Morover, there has been a change of predominant serotypes from years to years: predominant serotype from 1990 to 1997 was DENV-1; in 1998 was DENV-3; from 1999 to 2000 was DENV-2; in 2001 was DENV-4; from 2002 to 2006 was DENV-2 and from 2007 to 2014 was DENV-1. Change of predominant serotype accounted for the increase of cases such as: DENV-3 in 1998, DENV-4 in 2001, DENV-2 in 2003 and DENV-1 in 2007. Results of vector survey from 2000 show that Breteaux and mosquito density index in the South have decreased since 2000: from 71 in year 2000 to 38 in year 2014 and from 0.9 mosquito/house in year 2000 to 0.3 mosquito/house in year 2014.

**Conclusion:** Dengue in the South of Vietnam is similar to other countries all over the world. However, Dengue cases in the South has not increased by 2 folds in every 10 years as estimation of World Health Organization. This may due to the effective intervention that reducing vector index and the predominant serotype has not changed since 2007.
Profile of some communicable diseases among inmates of Jos central prison, Nigeria

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Background: This study was carried out in Jos Central Prison, Nigeria aimed at determining the health status of the inmates through screening for virus, bacteria and parasitic pathogenic agents.

Methods & Materials: Samples of stool, venous blood and sputum were collected from each informed and consenting prison inmate assured of the confidentiality of the result and analyzed following standard laboratory methods.

Results: One hundred and thirty one (131) inmates that presented themselves for medical treatment at the prison clinic were used for the study. The prison facility had more males (n=122) than females (n=09). Intestinal parasites were isolated from stool samples, malaria parasites and HIV-virus from the blood and mycobacterium from the sputum respectively. Among the inmates, 85 (64.9%) had various pathogenic agents comprising HIV-virus 11.5% (15/131), intestinal parasites 15.3% (20/131), malaria parasites 35.1% (46/131) and mycobacterium tuberculosis 3.82% (05/131). Of the malaria parasites, Plasmodium falciparum predominates with 71.7% (33/46), followed by P. malariae 17.4% (08/46) with P. vivax being the least and uncommon with 4.3% (2/46). Two malaria infections could not be identified to species level. All the 5 inmates with mycobacterial infection were HIV positive. The female inmates only suffered from malaria infection with a prevalence of 3.8% (5/131). The pathogens were higher among prison inmates who had been incarcerated for a longer duration than among those with shorter duration of incarceration. All the 12 inmates serving life sentence were infected with at least one pathogenic agent.

Conclusion: This study recommends for improved nutrition of the inmates and upgrade/maintenance of prison facilities to address poor hygienic condition of most prisons in the country.
Hepatitis C infection treated for 10 years period

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**Background:** Chronic HCV infection is an infection that persists for a long time. This work is a preview of HCV treated patients last 10 years in our department. The patients came to us during routine screening of drug addicts, patients with transaminase activity, or accidental findings of the anti HCV rapid tests taken for other reasons.

**Methods & Materials:** All patients were confirmed with PCR HCV RNA with viral load determination and genotyping. Common blood tests were done as well as analyses of liver function and liver biopsy. Also we made tests for exclusion autoimmune and other diseases. Patients were treated with peg. Interferon alpha2a and Ribavirin, during 24 or 48 weeks, depending of genotype. During the treatment every week we made common blood tests and liver analyses following transaminases (ALT, AST) activity.

**Results:** We treated 122 patients during this 10 years period, 27 female, 95 male. Dominant genotype was 3 (118) and 1 (4). One patient was with hemophilia as comorbidity. One treatment was interrupted due to an allergic reaction. At 82% of patients appears leucopenia, 76% trombocytopenia. The most common side effects of therapy were fatigue, lost of weight, depression. Repeated treatment due to lack of viral response we had at 3 patients. 80% of patients were with rapid and sustained viral response, but for part of them we have no information.

**Conclusion:** Good results of these available to us therapies, give hope for further finding and treatment of these patients, and therefore the prevention of late consequences of HCV infection, such as cirrhosis and hepatocellular carcinoma.
Application of a bi-clustering algorithm to macrophage gene expression analysis

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Background: Data clustering analysis has been extensively applied to extract information from gene expression profiles obtained with DNA microarrays. Genes that show similar expression patterns over a wide range of experimental conditions can be clustered together. This relies on the hypothesis that genes that belong to the same cluster are co-regulated and involved in related functions. To this aim, existing clustering approaches, mainly developed in computer science, have been adapted to microarray data analysis. Nevertheless, clustering algorithms still show limits, particularly to overcome the analysis of gene expression data by grouping genes and experimental conditions simultaneously. Another concept, called bi-clustering, allows to identify sets of genes sharing compatible expression patterns across subsets of experimental conditions.

Methods & Materials: We have recently developed a bi-clustering algorithm, called PDNS. It was used to analyze Yeast microarray data sets and showed that the obtained bi-clusters are coherent and biologically significant. In this work, we used PDNS for the analysis of macrophage gene expression data generated in vitro from the same individual blood infected with 5 different pathogens.

Results: This analysis led to the identification of sets of tightly coregulated genes across different pathogens. Gene Ontology tools were then used to assess the biological validity of obtained bi-clusters.

Conclusion: Evaluations have shown very encouraging results. The adopted approach could be applied to a wide variety of microarray data sets with applications in the study of communicable as well as non communicable diseases.
The Hajj and tuberculosis: Potential for transmission and impact on health systems

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Background: The Hajj pilgrimage is the largest annual mass gathering of culturally diverse people worldwide. Every year, it attracts up to three million Muslims from 183 nations who perform the religious ritual in unison. The crowded nature of the Hajj coupled with international diversity affords the opportune setting for the spread of infectious diseases. The risk of disease dissemination during the Hajj has long been recognised, however, the data available on the dynamics and disease epidemiology is worryingly limited. Previous outbreaks of diseases during the Hajj, including meningitis, raise concern for the possible threat of TB disease dissemination. Intimate confinement in a limited number of spaces results in overcrowding and ensues in an environment whereby potential and timely spread of disease is possible and highly probable.

Methods & Materials: Using the data on TB prevalence from the WHO, we estimated the number people with either latent or active TB, who attend the Hajj annually. An extensive review and compilation of data relating to the dynamics of the Hajj and the likelihood of TB disease transmission was carried out to assess the risk of possible TB spread.

Results: The calculated approximate number of annual Hajj pilgrims with TB disease from the WHO’s 22 high burden states totals 2949 persons. An estimated 937,929 (37.5%) of the total average of 2.5 million pilgrims attend the Hajj from these 22 high burden nations, of which 2,949 (0.31%) are suspected to have TB disease.

Conclusion: Quantification of disease transmission in the Hajj and other mass gathering situations is a challenging task. Extensive knowledge of disease aetiology and the dynamics specific to a mass gathering situation is essential. Owing to large numbers and the uniqueness of the Hajj, the relationship between its occurrence and TB has not been extensively studied. Although only calculated from the 22 high endemic nations, the Hajj draws visitors from 183 countries, consequently leaving a substantial number unaccounted for, suggesting that hundreds, possibly thousands more are visiting the Hajj and endangering many unknowing others.
Surveillance of zoonotic pathogens in Long-tailed macaques in Singapore

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**Background:** Long-tailed macaques (*Macaca fascicularis*) are one of the most prevalent mammal species in Singapore, and the population is estimated to be between 1218 to 1454. Due to increased urbanization human’s encroachment into monkey habitats has forced both species to have overlapping ecology, increasing the chances of anthroponosis and zoonosis. In the present study on macaques, we investigated the status of zoonotic pathogens. They include viruses: that are endemic in Singapore (Dengue and Chikungunya), present in rural areas of Singapore with low human transmission (Japanese encephalitis virus); that may be introduced into Singapore by migratory birds (West Nile virus); that is known to infect monkeys in Africa and Latin America (Yellow Fever virus); a zoonotic pathogen that can cause severe human neuro-invasive disease (Herpes B virus); and Lyssavirus.

**Methods & Materials:** For this study, monkey blood, brain, and trigeminal nerves samples were collected as part of on-going population management program. Saliva swabs were collected in the field by allowing monkeys to chew on a sponge soaked in sugar solution. Seroprevalence tests for antibodies against Dengue virus, Chikungunya virus, Yellow Fever virus, Japanese encephalitis virus, and West Nile virus were done using in-house immunofluorescence assay while Herpes B virus seroprevalence was studied using commercial ELISA assay. Monkey brain and saliva samples were also screened for the presence of Lyssavirus and Herpes B virus via PCR.

**Results:** No Dengue (n=600), Chikungunya (n=600), Yellow Fever (n=600), Japanese Encephalitis (n=120) or West Nile (n=120) virus specific antibodies were detected in all samples tested. Prevalence of Herpes B virus was 38% (87/228). No Herpes B virus or Lyssavirus was detected in the brain samples (n=35), trigeminal nerves (n=35) or saliva samples (n= 285).

**Conclusion:** This study demonstrates that macaques are not involved in the transmission of human endemic Dengue and Chikungunya viruses, and rural Japanese Encephalitis virus, West Nile virus, or Yellow Fever virus. Lyssavirus, as expected, was not detected in this study, though the risk of entry remains. Risk of Herpes B virus zoonotic transmission remains low as no virus was detected in saliva samples. This study represents the 1st comprehensive risk assessment of monkey-borne zoonotic diseases in Singapore.
Identification of Anaplasma phagocytophilum in canines from Culiacan, Sinaloa, Mexico

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Background: Anaplasma phagocytophilum is a bacterium that causes the disease named “canine granulocytic anaplasmosis”, being as the vector the ticks, transferring the bacterium to the blood of the vertebrates in which they feed. During the last decades anaplasmosis has become, for the high incidence and morbidity in an important zoonotic emerging disease. A. phagocytophilum before named Ehrlichia phagocytophilia, E. equi and Human granulocytic anaplasmosis, is a gram negative bacterium, affect granulocytic leukocytes of a wide range of hosts including humans, wild and domestic animals. This research work had as objective to identify A. phagocytophilum through nested PCR in canines from the town of Culiacán, Sinaloa, Mexico. 153 whole blood samples were collected from canines, with or without ticks, with or without illness from the jugular vein, collecting 5 ml of whole blood in tubes with anticoagulant.

Methods & Materials: The present investigation was performed in Culiacan, Sinaloa, Mexico. A total of 153 canine blood samples were taken from the jugular vein. The ELISA was done using the IDEXX SNAP® 4Dx® Test kit. PCR and PCR nested was performed in a thermocycler Labnet multigene, using the primers 16S rRNA. Forward: 5’-GGCTTTTGCCTCTGTGTTGT-3’. Reverse: 5’-CTTGACATCATC CCCACCTT-3’ and Forward 5’-CTTTATAGCTTGCTGCTATAAAGAA-3’ and Reverse: 5’-GT TAAGCCCTGGATTTTCAC-3’ respectively

Results: Serological test ELISA was performed, obtaining 13.77% positive samples to Ehrlichia canis/E. ewingii and 1.30% with cross reaction to A. phagocytophilum/A. platys, taken all this as positives (by sharing 92% homology). ADN is extracted by phenol chloroform technique. PCR was performed to Anaplasma spp., 4 samples amplified to 750 bp of a part the gen ARNr 16S, then was performed the PCR nested, of which 3 samples (1.96%) amplified to 500bp the gen A. phagocytophilum, obtaining cross reaction with Ehrlichia spp.

Conclusion: The results of this study confirm the presence of A. phagocytophilum in canines of Culiacan, Sinaloa, representing a risk to the animal and human health for the possible transmission of the disease to the owners and veterinarians. To the control of the bacterium more research is needed to be done in a molecular level and achieve a better understanding of the bacterium and create preventives vaccines for this zoonotic disease.
TB/HIV Co-infection- Barriers to Implementing Evidence based Practice

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**Background:** Tuberculosis and HIV are the two public health issues of great importance having a high prevalence worldwide. Infection with HIV is a strong risk factor predisposing for Mycobacterium tuberculosis infection, as both share a synergistic interaction, thus each facilitates the progression of the other. The problem of TB and HIV co-infection has emerged significantly in the recent years and it becomes graver when it is seen in the context of developing countries like Pakistan. With an enormous burden of TB, Pakistan is now also facing the challenge of concentrated epidemic of HIV especially among certain key populations.

**Methods & Materials:** A retrospective prevalence study was designed reviewing data for Tuberculosis and HIV/AIDS (from year 2007 to 2015). The data was collected from National TB control program, National AIDS control Program, and surveys of HIV and Mycobacterium infection in Pakistan. The purpose of this study is to assess the current situation of TB and HIV co-infection in Pakistan and to identify the gaps in services being provided to the patients with TB and HIV co-infection.

**Results:** 250 out of 59,754 TB patients were found HIV positive (0.42%); while, 61 out of 1054 PLHIV were found to have active TB (5.78%). Sentinel sites in HIV prevalent areas or linked with HIV intervention projects, gave better yield. Quarterly coordination meetings played key role in improved understanding and addressing the issues. Joint review of the intervention revealed some gaps including staff capacity, drugs and diagnostics supplies, samples transportation, lack of involvement of community/civil society organizations, data management and dissemination.

**Conclusion:** In comparison with global and regional statistics, HIV in TB patients seems very low, may be due to its low prevalence. However, TB in PLHIV seems under-reported. Yield of the intervention can be enhanced by revising the guidelines and training material, staff capacity enhancement, improving coordination between service delivery points, coupled with relocation of some of the sentinel sites and establishment of new ones, based on the latest HIV surveillance data.
Design and preparation of RNA vaccine against hepatitis C

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**Background:** Hepatitis C virus is a blood borne disease estimated to infect more than 350 million people globally and is a leading cause of liver cirrhosis, transplantation and hepatocellular carcinoma. Current gold-standard therapy often fails, has significant side effects in many cases and is expensive. The fact that a significant proportion of infected people spontaneously control HCV infection in the setting of an appropriate immune response suggests that a vaccine for HCV is a realistic goal but no vaccine is currently available. The present study was designed to investigate the possibility of a new vaccine against the hepatitis C virus based on mRNA encoding of membrane antigens (Core 
\& E2) of hepatitis C virus

**Methods & Materials:** Nucleotide sequence of mRNA encoding core and E2 antigen of HCV virus by bioinformatics program was design and in pGE plasmid vector was prepared. Then in vitro transcription reactions are used to synthesize mRNA from this recombinant DNA template. Nanoparticles encapsulated this mRNA synthesized and delivered to Monocytes isolated from human buffy coat and the activation and differentiation of monocyte to dendritic cells was examined. Immune response such as secretion of cytokines to HCV antigen can also be studied since cells grown on permeable supports with co-culture dendritic cells and T-cells of the same person.

**Results:** This project will be ongoing and mRNA encoding antigens of virus have been produced. But the immunogenicity is under examination.

**Conclusion:** Final results of this study will be reported in future
Microorganisms isolated in patients with acute appendicitis in Regional clinical hospital, Karaganda

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Background: ESBL-positive E.coli
P.aeruginosa
appendicit
MALDI-TOF
β-lactam antibiotics

Methods & Materials: The sampling of material from the patients with acute appendicitis was performed by sterile swabs into sterile Eppendorf with broth. Seeding was performed on blood agar. Identification of isolates was realized using time of flight-mass-spectrometry on MALDI-TOF spectrometer Microflex and software system Biotyper of Daltoniks Bruker Company. The sensitivity to antibiotics was conducted by disk-diffusion method. The maintaining of database of antibiotic sensitivity was performed using the program WhoNet 5.6

Results: Since the beginning of 2014 it has been allocated 138 microorganisms. The predominant was E. coli (43%). The share of P.aeruginosa was 16%. In a few cases we isolated the other microorganisms of the Enterobacteriaceae type, non-fermentative bacteria, enterococci, streptococci, staphylococci. In determining the sensitivity to antibiotics the following results were obtained: the proportion of ESBL-positive E.coli was 10%, all the strains were sensitive to aztreonam and doripenem (95%CI 0,0-17,8), 87.5 % strains were sensitive to gentamicin (95%CI 5,6-24,7), 82.7% isolates were sensitive to ciprofloxacin (95%CI 7,3-28,7).

The part of ESBL positive P.aeruginosa was 18.8%, and 94.7% P.aeruginosa were susceptible to aztreonam (95%CI 0,3-28,2), 85.7% P.aeruginosa were susceptible to doripenem and meropenem(95%CI 1,7-31,8). High sensitivity to gentamicin was observed – 84.2% (95%CI 4,2-40,5), and 75% (95%CI 6,6-44,3) strains were susceptible to ciprofloxacin.

Conclusion: As a result we isolated E.coli (43%) and P.aeruginosa (16%) from patients with acute appendicitis. The data of ESBL-positive strains of E.coli (10%) and P.aeruginosa (18,8%) were obtained. This fact should be taken into account when appointment of β-lactam antibiotics. The other groups of tested antimicrobials were characterized by high sensitivity.
Pulmonary Tuberculosis in Areas Affected by the Chernobyl Nuclear Disaster

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**Background:** In the result of the Chernobyl catastrophe, people in Belarus were exposed to long-term small-dosed radiation that inflicted grave consequences over the health of the population, especially children. The objective of the research was to study the incidence rates of pulmonary tuberculosis among children and teenagers living in areas affected by the Chernobyl disaster. The data for the period 2004-2014 have been analyzed.

**Methods & Materials:** All patients with pulmonary tuberculosis were divided into two groups. The first group included patients living in the affected areas of the Mogilev region of Belarus. The second group included patients living in the others areas of the Mogilev region. The average incidence rates of pulmonary tuberculosis have been counted for the age groups between 0-4 years old; 5-9 years old; 10-14 years old; 15-19 years old.

**Results:** The incidence rates of pulmonary tuberculosis for the age group between 0-4 years old were 3.6 times higher in the affected areas than in the others areas (for comparison: 3.29 cases per 100 000 people in the affected areas vs. 0.9 cases in the others areas).

The incidence rates for the age group between 5-9 years old were 4.1 times higher in the affected areas than in the others areas (for comparison: 4.75 cases per 100 000 people in the affected areas vs. 1.15 cases in the others areas).

The incidence rates for the age group between 10-14 years old were 2.1 times higher in the others areas than in the affected areas (for comparison: 2.91 cases per 100 000 people in the others areas vs. 1.36 cases in the affected areas).

The incidence rates for the age group between 15-19 years old were 3.1 times higher in the affected areas than in the others areas (for comparison: 26.1 cases per 100 000 people in the affected areas vs. 8.53 cases in the others areas).

**Conclusion:** The study has shown that the incidence rates of pulmonary tuberculosis for the age group between 0-4, 5-9, 15-19 years old has been higher in the affected areas by the Chernobyl Nuclear Disaster than in the others areas of the Mogilev region of Belarus.
Tuberculin Skin Testing in Children with Tuberculosis

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**Background:** The tuberculin skin test is the standard method of screening for infection with Mycobacterium tuberculosis. In the absence of symptoms, usually the only sign of tuberculosis infection is a positive reaction to the tuberculin skin test. A positive test indicates tuberculosis infection, but cannot distinguish between latent tuberculosis and active tuberculosis.

The objective of this study was to research the differences in sensitivity to tuberculin in children with latent tuberculosis and active tuberculosis.

**Methods & Materials:** The focus group included 110 children with latent tuberculosis and 58 children with active tuberculosis from the age group between 2-10 years old. All the children were examined by Mantoux tuberculin skin test with 2 tuberculin units of tuberculin PPD-L prior to preventive treatment or chemotherapy. Clinical, bacteriological, X-ray methods and statistical analysis have been applied.

**Results:** Both groups did not differ by quantity of boys and girls, average age. The group of children with latent tuberculosis included 55 girls (50%) and 55 boys (50%). The group of children with active tuberculosis included 29 girls (50%) and 29 boys (50%). Differences between groups is not valid ($\chi^2 = 0.027; p = 0.869$).

The average age of the children with latent tuberculosis was $6.9 \pm 2.0$ years, in children with active tuberculosis - $6.6 \pm 2.2$ years. Differences between groups is not valid ($t = -0.773; p = 0.441$).

We measured the size of the papules in children. The average size of the papules in children with latent tuberculosis was $15.7 \pm 4.3$ mm, in children with active tuberculosis - $13.3 \pm 4.7$ mm ($t = 3.447; p = 0.000$).

Children with latent tuberculosis have papules with a larger size compared to children with active tuberculosis.

**Conclusion:** We have identified the differences in sensitivity to tuberculin in children with latent tuberculosis and active tuberculosis. Children with latent TB were more expressed sensitivity to tuberculin compared to children with active tuberculosis. Our results can be applied in practice for the diagnosis of latent tuberculosis.