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Posters



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Management of non-interferon versus interferon based therapy for chronic hepatitis C virus (HCV) in a free clinic setting

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HCV is the most common cause of blood-borne infections and is the most common reason for liver transplants in the United States. Recent advances with sofosbuvir/ribavirin or ledipasvir/sofosbuvir have confirmed to be successful in eradicating HCV with minimal to no side effects versus previous treatment with telaprevir/peg interferon/ribavirin, resulting in discontinuation of therapy due to severe side effects. This study reports clinical management of 40 patients with HCV using sofosbuvir/ribavirin or ledipasvir/sofosbuvir for a reporting period 2013-2015 versus clinical management of 42 patients who were treated with telaprevir/ peg interferon/ribavirin based therapy for a reporting period 2011-2013. All 40 patients completed therapy with 37 attaining sustained viral response (SVR) at 12 or 24 weeks. 3 patients did not attain SVR with initial treatment and were placed on ledipasvir/ sofosbuvir for 12 weeks and attained SVR at completion. Previous studies indicated 42 completed therapy, with 36 attaining SVR at 24 weeks with telaprevir/peg interferon/ribavirin. Minimal side effects were noted with sofosbuvir/ribavirin. No side effects were noted with ledipasvir/sofosbuvir. Side effects included 1 patient with anemia, 1 patient with hyperammonemia and 3 patients with headaches. In comparison to telaprevir/peg interferon/ribavirin based therapy where 7 patients discontinued therapy due to severe side effects consisting of, depression, peptic ulcer disease, hyperammoniemia and extreme thrombocytopenia. The data demonstrated a statistically significant improvement with minimal to no side effects. Previous studies indicate a success rate of 85% with telaprevir/ peg interferon/ribavirin and 100% ledipasvir/sofosbuvir.

Biography

Mark Asperilla has completed his Fellowship at Chicago Medical School in Infectious Diseases in 1987. He has recently received the Ellis Island Award among many other awards, in addition to his many board certifications, institutional and administrative responsibilities. He is the Director of Infectious Disease and Infection Control at Bayfront Health Port Charlotte. He has published many articles in journals, editorials and book chapters. He volunteers his time with the Virginia B Andes Clinic to consult and treat patients who are uninsured and 200% poverty and also volunteers his time managing a free Hepatitis C Clinic.

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Food borne Salmonella in Algeria

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Salmonella infections represent one of the primary causes of food borne diseases with a relevant impact on developing countries. The increase of antimicrobial resistance is also a major health concern, seriously limiting the control of invasive *salmonellosis*. Despite a paucity of available data *Salmonella* infections are clear an emerging problem in several North-African countries and food borne *Salmonella* outbreaks are also commonly observed in Algeria. In this work we provide genotypic and antimicrobial susceptibility baseline data of 46 *Salmonella* from human (n=17) and avian (n=29) origin isolated in Algeria during 2015-2016. The isolates were mostly resistant to nalidixic acid (93%) followed by streptomycin (63%), tetracycline (47%), ampicillin (43%), ciprofloxacin (26%) chloramphenicol (22%), trimethoprim-sulfamethoxazole (17%) and ceftriaxone (8%). Sixty percent of the isolates were multidrug resistant and 98% carried one or two plasmids ranging in size from 5 to 150 kb belonging to IncFIIA, N, I1, FIB and P groups. Among human isolates, an intact *Salmonella* Genomic Island 1 (SGI1) was detected in 8 S. Typhimurium DT104 carrying two integrons of 1 and 1.2 kb and in three serogroup C2-C3strains carrying one integron of 1.6 kb with the cassettes *aac(3)-Id/aadA7 plus sul1*.TEM-1and CTX-M1 beta-lactamases genes were detected in six and two isolates respectively. These findings improve the information on food borne *Salmonella* in Algeria, evidencing the presence of MDR strains potentially dangerous to humans and provide useful data to health control authorities for the prevention of these infections.

Biography

Bilal Djeghout is currently pursuing his PhD at the University of Sassari at The International PhD School of Life Sciences and Biotechnologies. He has completed his Master's degree in Molecular Biology of Prokaryotes from the University of Guelma, Algeria.

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Pure red cell aplasia in a patient with human immunodeficiency virus infection

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A 52 year old patient with a known case of human immunodeficiency virus infection on zidovudine, lamivudine and nevirapine Since 2 years, presented with severe fatigue. He had severe anemia with hemoglobin of 3.5 gm% with normal leucocyte and platelet counts. He had no lymphadenopathy or hepatosplenomegaly. His CD4 count was 584 and HIV viral load was undetectable. Zidovudine was thought to be the cause of anemia and cART was changed to tenofovir, lamivudine and efavirenz. He was given 3 units of packed red cell transfusion and was discharged from the hospital. Patient returned 3 weeks later with severe anemia. A bone marrow study was done which showed selective suppression of erythrocyte precursors suggestive of pure red cell aplasia. Parvovirus serology was negative. Lamivudine was substituted with emtricitabine with no response. Antiretroviral therapy was temporarily discontinued for 4 weeks with no response. Corticosteroid therapy was given but anemia persisted. Finally antiretroviral treatment was continued with weekly erythropoietin therapy. He has responded with increase in hemoglobin in 4 weeks.

Biography

Rama Bhat has completed his MBBS and MD in Internal Medicine from Mysore University and Goa University in 1988 and 1993 respectively. He is currently working as a Professor of Medicine at Manipal University, India. He has published 12 articles in national and international journals.

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Revised anti-staphylococcal activity of conventional antibiotics in the presence of *Lactobacillus* paraplantarum cell free supernatant

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In view of the capability of *S. aureus* causing a wide array of infections ranging from localized skin infections to life threatening systemic infections and due to emerging drug resistant *S. aureus* strains (MRSA/ORSA/VISA), there is a need to explore other alternative options to manage such deadly strains. Use of probiotics is one such option as several probiotic strains have been reported to have anti-staphylococcal activity. In the present study, efficacy of antibiotics in the presence of probiotic cell free supernatant (CFS) against *S. aureus* strains was evaluated by radial/agar well diffusion assay as well as by minimum inhibitory concentration (MIC) determination. Out of the four probiotics used, CFS of *L. paraplantarum* revealed the maximum anti-staphylococcal activity. To use the probiotic/CFS in conjunction with conventional antibiotics against *S. aureus*, antibiogram of S. aureus as well as L. paraplantarum was determined. On the basis of resistance pattern of both, the two combinations (CFS/ampicillin and CFS/oxacillin) were selected. These two combinations were found to have synergistic/additive effect as per the fractional inhibitory concentration (FIC) index. It was inferred from the study, MICs of both the antibiotics in presence of CFS were reduced significantly. It is worth mentioning that the strains which were earlier resistant to oxacillin were rendered sensitive to it in the presence of CFS as per CLSI guidelines. It can be concluded from the study that CFS and ampicillin/oxacillin combination might help in rejuvenating the use of conventional anti-staphylococcal antibiotics for the treatment of multi-drug resistant strains.

Biography

Lavanya Rishi is currently pursuing her graduation in Medical Sciences (MBBS second year student) in Himalayan Institute of Medical Sciences, India. She has been a meritorious student at the Secondary and Senior Secondary level. Recently, she has been awarded short term studentship (STS-2015) by Indian Council of Medical Research, India to work on the project "Possible augmentation in the anti-staphylococcal activity of conventional antibiotics with probiotic cell free supernatant".

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Epidemiological pattern of influenza in Tunisia: Season 2015-2016

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Introduction: The Influenza is an acute viral infection transmitted by air. It is a highly contagious disease that can cause serious complications, especially among vulnerable people; it presents a major public health issue with a considerable socio-economic impact.

Purpose: Review the epidemiological situation of influenza in Tunisia in the 2015-2016 Season. Determine if the A(H1N1) virus has a particular virulence in Tunisia during the 2015-2016 Season and to make recommendations to overcome challenges.

Methods: This retrospective study is based on data issued by the National influenza surveillance unit; it relies on a descriptive analysis of influenza surveillance data provided by the network of sentinel sites and national influenza center (NIC).

Results & Discussion: Influenza surveillance in Tunisia has been in established in 1999 with the creation of network sentinel sites but it significantly developed on March 2014, by the enhancement of the national influenza surveillance system. In Tunisia, clinical, epidemiological and virological surveillance of influenza began in week 40/2015 (1st of October 2015) and ended in week 18/2016 (30th of April 2016). During the period of study: 96240 cases ILI (Influenza-like illness) were collected from a total of 1394782 patients seen at sentinel ILI sites, representing 6.9% of total patients versus 7.7% during the 2014-2015 season. The epidemiological surveillance of influenza on the Tunisian territory showed that the influenza epidemic was spreading in the winter season 2015/2016 during 14 weeks from the 25th of January 2016 (2016/W4) to the 29th of April 2016 (2016/W18) with an incidence rate of 10.3%. It started a little later than it did during the previous season and lasted relatively longer (14 weeks versus 8 weeks). During the 2014-2015 Season; influenza reached its peak during the coldest weeks (S6 to S9) and there was an inverse trend of the monthly average temperature. This correlation has not been observed during this season having regard to the shift of the cold season. In fact, this flu season peaked during the week of 14 to 20 March 2016 (2016/S12), later than usual. These findings were also observed in Europe and in USA. All of the 24 governorates of Tunisia have been affected by the influenza and the incidence is higher in the most populated regions. Children 5 to 16 years are the most affected. Among the visits for influenza-like illness (ILI), 190 severe cases were hospitalized representing a comparable proportion to the previous season (0.19% vs. 0.2%) and were mainly infected with A (H1N1) pmd09 virus (57% of cases). The average age for these severe cases was 46.5 years with extreme ages varying between 6 months and 73 years. Their lethality was significantly higher than that observed during the previous season (20% vs. 3%) and was H1N1 associated in 73.7% of cases. During week 12, there was an increased circulation of influenza viruses in Tunisia and subsequently there were the highest number of deaths (10 deaths representing 26.3% of all influenza deaths). 37.1% of influenza deaths had no risk factors. The cocirculation of the three influenza viruses began in late January (W4) with a gradual increase in the circulation of the type A (H1N1) pmd09 virus. During the week W12, the type A(H1N1)pmd09 virus was more common than the type B. The seasonal distribution of three types of influenza viruses was Virus A(H1N1)pmd09 (57.4%), Virus A(H3N2) (38.5%) and Virus B (3.5%). The positivity rate for influenza was 24.4% vs. 28.4% during the previous season.

Biography

Sakly Mouna has completed her Medicine studies from El Manar University, Faculty of Medicine of Tunisia. She has submitted her Doctoral thesis in Medicine in 2002, completed Master of Advanced Studies in Economy Health and Hospital Management from the Faculty of Medicine of Tunisia in 2009, Master of Advanced Studies in Tobacco from the Faculty of Medicine of Tunisia in 2010 and Certification Green Belt Lean Manufacturing and Management L2M in 2016. She is the Coordinator of child health programs and primary health care quality program in Tunisia and she is also the Tunisian focal point on disability and deafness and a National Trainer in the counseling and HIV screening among pregnant women. She has published some papers in reputed journals. She is a Reviewer of Public Health Review, France since 2016 and a Teacher of the national maternal and newborn health program in the University Mohamed El Matri at Tunisia.

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Colistin's dark face: The revival of polymyxin antibiotics

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Background & Objectives: Colistin (polymyxin E), an old antibiotic replaced by other less toxic antibiotics in the 1970s has been increasingly used over the last decade due to multidrug resistance in Gram-negative bacteria and lack of new antibiotics. However there is a dearth of information on the pharmacodynamics and toxicodynamics of colistin and its non-active prodrug colistimethate sodium (CMS). Optimized dose regimens have not been establishment for different types of patients, especially in the critically ill population.

Material & Methods: Recent reports have not described neurotoxicity associated with intravenous CMS with the exception of cases in the cystic fibrosis population, among whom neurotoxicity has manifested as paraesthesias and ataxia in 29% of patients treated (dosages in excess of 5 mg/kg per day). Our patient received intravenous CMS dosages 6 mg/kg per day. Only one case according most recent literature has described a profound encephalopathy with lack of brainstem reflexes in postsurgical patient. We report a 56 year old man who developed renal, hematological and neurotoxicity on the 5 day after administration endovenous colistin and cefepima (CMS dosages of 160 mg/8 hours, equivalent to approximately 6 mg/Kg per day). The patient has made perforated diverticulitis with descending colon resection and end colostomy left flank. On day 6 post-surgery nosocomial pneumonia by *Pseudomona aeruginosa* MR sensible to colistin was diagnosed.

Results: Electroencephalogram was compatible with severe encephalopathy. Peripheral eosinophil count had increased to 12%. He recovered promptly after stopping the drug.

Conclusions: The awareness of colistin's potentially fatal effects must be kept in mind when using. Vigilance of the encephalopathic picture can also facilitate the diagnosis of colistin mediated neurotoxicity in a patient with altered mental status of otherwise unknown aetiology. In our opinion, the establishment of any relationships between the daily dosage of CMS, colistin levels and neurological events is needed, especially in the critically post-surgical ill patient population.

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The influence of IL-10 gene polymorphisms on the susceptibility to hepatitis B virus infection: A metaanalysis

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Interleukin 10 (IL-10) is a cytokine with anti-inflammatory functions. The results of different studies vary in the roles of the IL-10 SNPs in the susceptibility to the hepatitis B virus infection. In particular, the -1082 A/G, -819 C/T and -592 A/C polymorphisms have most often been implicated. We have performed a meta-analysis including 31 case-control studies to summarize the data on the association between IL-10 SNPs and susceptibility to HBV infection. All the relevant studies in NCBI PubMed, EMBASE, Medline and Web of Science were searched and poor qualified studies were excluded. 31 studies were included. Data are presented as the odds ratio (OR) with a 95% confidence interval (CI). Investigation of heterogeneity among individual studies and the publication bias were also evaluated. This study revealed a significant association between the IL-10 -819 C/T polymorphism and HBV infection susceptibility in the Asian population. Our results indicated that the presence of the IL-10 -819 C allele significantly increased the risk for persistent HBV infection. In our meta-analysis, sensitivity analysis showed that the combined result was not associated with the worldwide population. In contrast, the IL-10 -1082 A/G and -592 A/C polymorphisms were not associated with an increased susceptibility to HBV infection. Our meta-analysis supports the growing body of evidence that the presence of the IL-10-819 C/T SNP is associated with persistent HBV infection in Asians. In addition, IL-10-819 C/T polymorphism might be a risk factor for HBV in Asians but not in Europeans.

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Predictive pathogen biology: Genome based prediction of pathogenic potential and counter measures targets

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Horizontal gene transfer (HG1) and recombination leads to the energence of each of transposon into a regulatory gene. HGT events can Genetic changes range from acquisition of a large plasmid to insertion of transposon into a regulatory gene. HGT events can define the phylogenetic range of Torizontal gene transfer (HGT) and recombination leads to the emergence of bacterial antibiotic resistance and pathogenic traits. be identified by comparing a large number of fully sequenced genomes across a species or genus, define the phylogenetic range of HGT and find potential sources of new resistance genes. In-depth comparative phylogenomics can also identify subtle genome or plasmid structural changes or mutations associated with phenotypic changes. Comparative phylogenomics requires that accurately sequenced, complete and properly annotated genomes of the organism. Due to dramatic advances in "short read" sequencing technology, the raw sequence coverage needed for sequencing a bacterial genome now can be obtained in a couple of days for a few dollars sequencing costs, starting with only a few nanograms of genomic DNA. Assembling closed genomes requires additional mate-pair reads or "long read" sequencing data to accompany short read paired end data. To bring down the cost and time required of producing assembled genomes and annotating genome features that inform drug resistance and pathogenicity, we are analyzing the performance for genome assembly of data from the Illumina NextSeq, which has faster throughput than the Illumina HiSeq (~1-2 days versus ~1 week) and shorter reads (150 bp paired end versus 300 bp paired end) but higher capacity (150-400 M reads per run versus ~5-15 M) compared to the Illumina MiSeq. Bioinformatics improvements are also needed to make rapid, routine production of complete genomes a reality. Modern assemblers such as SPAdes 3.6.0 running on a standard Linux blade are capable in a few hours of converting mixes of reads from different library preps into high quality assemblies with only a few gaps. Remaining breaks in scaffolds are generally due to repeats (e.g., rRNA genes) are addressed by our software for gap closure techniques that avoid custom PCR or targeted sequencing. Our goal is to improve the understanding of emergence of pathogenesis using sequencing, comparative genomics and machine learning analysis of ~1000 pathogen genomes. Machine learning algorithms will be used to digest the diverse features (change in virulence genes, recombination, horizontal gene transfer & patient diagnostics). Temporal data and evolutionary models can thus determine whether the origin of a particular isolate is likely to have been from the environment (could it have evolved from previous isolates). It can be useful for comparing differences in virulence along or across the tree. More intriguing, it can test whether there is a direction to virulence strength. This would open new avenues in the prediction of uncharacterized clinical bugs and multidrug resistance evolution and pathogen emergence.

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A clinical and mycological study of onychomycosis

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Onychomycosis is a major public health problem with a high incidence. The aim of this study was to determine the prevalence of various causative agents of onychomycosis and to study the clinical and mycological patterns of onychomycosis. A prospective study was conducted from September 2015 to March 2016 in university hospital center of Tlemcen in Algeria. The nails were evaluated clinically and the nail samples were subjected to direct microscopy and culture. 73% samples were found to be positive by direct microscopy and culture. Toe nails were affected more frequently than finger nails and distolateral subungal onychomycosis was the most common clinical type of infection which was seen in 74.73% patients. The etiological agents were yeasts (63.33%) and dermatophytes (36.67%). Among dermatophytes, *T. rubrum* was the commonest etiological agent. In our study, the mycological examination is the key for the positive diagnostic of onychomycosis, although yeasts were the main causative agents.

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Detection and molecular characterization of enteropathogenic bacteria isolated from children with acute diarrhea, slaughtered animals and raw meat samples in Tehran, Iran

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Infectious diarrhea is a leading cause of morbidity and mortality globally. Worldwide, enteropathogenic bacteria are responsible for one of the most important infectious diseases linked to the food industry and they affect animal welfare with the potential to give rise to public health problems. As in many countries, in Iran Shiga toxin producing Escherichia coli (STEC) strains have been frequently isolated from cattle, raw meat and young humans. In this study, we have explored the epidemiology of diarrheagenic Escherichia coli (DEC), Shigella spp., Salmonella spp. and Campylobacter spp. from differing sources in Tehran Province of Iran. Total 445 samples, which include 235 domestic cow feces, collected from three semi-urban community farms, 134 ground beef samples from slaughtered bovine/sheep sources (specifically a Tehran abattoir) and 76 stool samples acquired from human children (1 to 60 months of age) with acute diarrhea were sequentially examined for stx1, stx2, eae, lt, st, Pcvd435, O157:H7, α-hly and Shigella spp., Salmonella spp. and Campylobacter spp. genes via Polymerase Chain Reaction (PCR) approach. Shiga-toxin producing Escherichia coli strains were isolated from 41% of meat, 64% of cattle feces and 24% of children's fecal samples. PCR analysis indicated that 16 samples in total were positive for O157:H7. Also, 14% of human children and 0.85% of cattle species were Shigella spp. positive. The most commonly isolated STEC bacteria were from the O146, O112a and O44 serogroups for all 3 sources. Remarkably, none of the STEC strains proved to be from the O145, O111 and O26 serogroups. In conclusions, high levels of Shiga toxin producing E. coli in cattle and raw beef samples were observed at high rates and STEC colonization is widespread amongst healthy cattle in Iran. These observations provide strong evidence that STEC is one of the major causes of diarrhea in developing countries, mainly in children. The panel of assays employed offer simple strategies for the widespread detection and characterization of diarrheagenic E. coli isolates from a range of sources. DEC detection in this manner facilitates our understanding of their prevalence, clinical characteristics and epidemiology and will serve to support the future development of further food safety control strategies which target all STEC serotypes.

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Plant derived pharmaceuticals

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Plant made biologics have elicited much attention over recent years for their potential in assisting those in developing countries who have poor access to modern medicine. Additional applications such as the stockpiling of vaccines against pandemic infectious diseases or potential biological warfare agents are also under investigation. Plant virus expression vectors represent a technology that enables high levels of pharmaceutical proteins to be produced in a very short period of time. Recent advances in research and development have brought about the generation of superior virus expression systems which can be readily delivered to the host plant in a manner that is both efficient and cost effective. The following presentation describes recent innovations in plant virus expression systems and their uses for producing biologics from plants.

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Detection of uncommon enteric bacterial pathogens from human diarrheal specimens by SYBR-Green real time PCR

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A cute diarrheal disease is still a major health problem and second most common cause of death worldwide in children under five years of age. Most of the morbidity occurs in low-income countries, where the etiologies and epidemiology of gastroenteritis remain incompletely understood. Diarrhea can be caused by a range of pathogens, including several bacteria. Conventional diagnostic methods, such as culture, biochemical tests and enzyme-linked immunosorbent assay (ELISA) are laborious and time consuming. We used SYBR-Green real time PCR assay targeting 10 uncommon diarrheagenic bacterial pathogens (*S. aureus, Enterotoxigenic* B. *cereus*, C. *perfringens*, C. *difficile*, L. *monocytogenes*, P. *shigelloides*, Y. *enterocolitica*, *Enterotoxigenic* B. *fragilis*, A. *hydrophila* and P. *alcalifaciens*) directly in fecal specimens from patients admitted infectious diseases hospital with acute diarrhea in Kolkata, India. The products formed were identified based on melting point temperature (Tm) curve analysis. The assay was first validated with reference strains or isolates and exhibited a limit of detection of 103 to 105 CFU/gm of stool for each pathogen. A total of 1184 clinical fecal specimens from individual with diarrhea, previously cultured for enteric pathogens were evaluated. Enterotoxigenic *B. fragilis* was detected highest number about 80 (6.75%) followed by enterotoxigenic B. *cereus* 60 (5.06%), C. *perfringens* 46 (3.88%), A. *hydrophila* 45 (3.80%), P. *alcalifaciens* 44 (3.71%), P. *shigelloides* 39 (3.29%), C. *difficile* 39 (3.29%), L. *monocytogenes* 38 (3.20%), *S. aureus* 23 (1.94%) and Y. *enterocolitica* 14 (1.8%) respectively. We found SYBR-Green real time PCR assay for simultaneous detection of 10 target pathogens to be comprehensive, rapid, inexpensive and accurate, of high selectivity and is well suited for surveillance or clinical purpose.

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Comparison of virological and serological findings on Moroccan bluetongue virus 1 and 4 infected sheep

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The bluetongue (BT) virus has been reported in Morocco in 2004. To investigate the involvement of BTV 1 and BTV4 infections, on immunity of sheep and to provide a basis for interpretation of serological and virological data, experimental infections were conducted with BTV-1 and BTV-4 strains. Antibody responses to BTV infections were evaluated using two enzyme linked immunosorbent assays and microtiter serum neutralization tests (mSNTs) in addition to virological monitoring based on RT-PCR. Large variation was observed between the three groups in clinical signs, showed variation in immune responses between animals. Viremia for BT virus was readily detected in sheep following BTV-1 infection, but was not detected following exposure to BTV-4 in group B and C. The high manifestation of clinical signs caused by BTV1 serotype compared to those caused by BTV4 could likely be due to BTV strains antigenicity and could probably be responsible in suppressing or manifesting BT symptoms and viremia for this serotype.

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Delivery of Mycobacterium tuberculosis lipids using chitosan nanoparticles induce potent cytokine and antibody response through activation of $\gamma\delta$ T-cells in mice

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A ctivation of cell mediated and humoral immune responses to *Mycobacterium tuberculosis* (Mtb), the causative agent of tuberculosis (TB), are critical for protection. For decades, most studies regarding immunity to TB are focused mainly on proteins. In recent years, increasing evidences have shown that Mtb cell wall lipids act as potent adjuvants as well as antigens capable of activating specific T-cells through their presentation by CD1 molecules and also induce IgM, IgA and IgG antibody responses. However unlike proteins, delivery and presentation of lipid antigens is a major challenge. Herein, we have used chitosan nanoparticles (NPs) as Mtb lipid delivery system and showed that chitosan NP mediated delivery of Mtb lipids induce potent cytokine and antibody responses in immunized mice. Chitosan NP delivered Mtb lipids induced the release of most prominent cytokines associated with Th1 (TNF- α , IFN- γ , IL-2) and Th2-type (IL-4, IL-5, IL-6, IL-13) immune responses in mice lymphatic and spleen cells as compared to immunogenic Mtb purified protein derivative (PPD) and chitosan NPs alone. Moreover, mice immunized with Mtb lipid coated chitosan NPs showed significantly higher levels of IgG, IgG1 and IgM and a moderate increase in IgG2a antibodies as compared to Mtb lipid liposomes and chitosan NP immunized mice. In conclusion, this study represents a promising new strategy for efficient delivery of Mtb lipids to trigger enhanced cell mediated and antibody response against Mtb infection.

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Questionnaire triaging model adopted in rapid screening patients who are suspected to have Ebola infection

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Introduction & Aim: Ebola disease (EVD) is a fetal viral infectious disease with case fatality as high as 90%. Early discriminating patients on admission into high risk or low risk are of extremely important, thus the patients can be delivered to corresponding isolation areas to avoid Ebola viral cross transmission. However, diagnostic lab results of patients are difficultly obtained at first, especially during the early period of outbreak. A questionnaire triaging model was designed and then applied in a holding center in Sierra Leone successfully during the outbreak 2014.

Methodology: Medical histories of the patients were collected on admission according to case investigation form made by 'WHO', including 21 symptoms. The patients were diagnosed to have or not to have EVD 2 to 3 days after admission based on results of RT-PCR. Symptoms between the EVD and non-EVD patients were analyzed and compared. A criterion of screening the patients was made based on the results of date analysis.

Results: The total symptoms of EVD patients were significantly higher than those of non-EVD patients (9 vs. 5.5; p<0.001). Cutoff value was 6, the sensitivity, specificity, positive predictive value and negative predictive value were 70.4, 76.1, 87.4 and 52.2 % respectively. We assigned suspected patients to high risk area if the amount of their symptoms were equal or greater than 6; or to low risk area if less than 6. Patients were separated by space in both quarantine areas according to the Sierra Leone Emergency Management Program Standard Operating Procedures for Managing Ebola Virus Disease in Holding Centers. By the end of our work in Sierra Leone, there was no patient of cross transmission reported under this triaging model.

Conclusions: Questionnaire triaging model is efficient in screening suspected EVD patients in highly epidemic regions, which could be reference in patient management for other fetal infectious diseases. Even though clinical manifestations of EVD patients are generally non-specific, the amount of all symptoms could be of more diagnostic value.

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Assessment of pathogenicity and tissue distribution of infectious bronchitis virus strains (Italy 02 genotype) isolated from Moroccan broiler chickens

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A vian infectious bronchitis (IB) is one of the most important viral diseases of poultry, affecting chickens of all ages and causing major economic losses in poultry flocks. The aim of this study is to evaluate pathogenicity and tissue distribution of Moroccan Italy 02 genotype of infectious bronchitis virus (IBV). Total 40 one day old specific pathogen free chickens were divided randomly into four groups. Group-1, 2 and 3 were inoculated intra oculo-nasally with 103.5 EID50 of virus and Group-4 was kept as control. Chickens in each group were monitored for 14 days post-infection (dpi). Chickens in all infected groups showed severe respiratory signs which most of them have been reproduced on 2 dpi with varying times of appearance and disappearance. The infected birds appeared lethargic, reluctant to move with specific respiratory signs and macroscopic lesions. The specific histological lesions developed in all infected birds, confirm the ability of the three tested strains to induce severe respiratory disease. The results at 14 dpi also revealed that all strains were able to induce serological response. Virus re-isolation from infected organs and amplification of the viral RNA by real-time PCR proved the presence of the virus in lung and trachea of infected chicks. Neither re-isolation nor significant viral RNA detection were detected in the kidney. These results demonstrated that the three strains Italy 02 genotype emerging in Moroccan poultry farms have a wide distribution for respiratory system without kidney damage and without causing mortality.

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Ulceroglandular tularemia: Clinical course and outcome in 5 cases

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Introduction: Tularemia is an acute febrile zoonosis, which is potential life threatening disease. The most popular clinical form is ulceroglandular.

Materials & Methods: In a period of 8 months (December 2014-July 2015) through the Clinic of Infectious diseases of University Hospital Stara Zagora, Bulgaria, 5 patients with ulceroglandular form of Tularemia were passed; they were 4 men and 1 woman, aged from 52 to 73 years. Clinical, epidemiological, laboratorial and serological investigations were provided.

Results & Discussion: Three of patients were hunters, fired wild rabbits and the rest two took part in breaking up and cooking the game. After an incubation period mean 4.8±1.4 days in all was appeared a primary affect in region of the fingers. Three had redness in eyes, on face and oropharynx. Later on the toxic syndrome a regional painful lymphadenitis was appeared. Two patients had dyspeptic syndrome with vomiting and diarrhea, no appetite. All had enlarged liver, two had scanty maculopapular rash. The diagnosis was proved by degree agglutination type Vidal at the Referent Laboratory of Particularly Dangerous Infection, National Center of Infectious, Parasite Diseases, Sofia. The antibacterial treatment was a combination of 4-quinolones and aminoglycosides. The outcome was favorable in all patients.

Conclusion: Because tularemia is not so common disease, it could be easy left out. It must be suspected when there were unusual temperature, redness in eyes and glandular syndrome with corresponding epidemiological situation.

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Surveillance systems for nosocomial infections: Principles and challenges

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Nosocomial Infections (NIs) are considered to be serious public health problems around the world. The NI-related burden is unknown because of lack of access to reliable data, lack of surveillance systems and the complexity of corresponding NI outcomes. Health care systems use different approaches for monitoring NIs. Generally, surveillance methods are categorized under the umbrellas of active, passive and sentinel surveillance methods. At present, hospitals implement passive surveillance approaches because of feasibility and low cost. However, the quality of this methodology is in question; under reporting and lack of timeliness are the main challenges. In contrast to the passive approach of NI surveillance systems, active ones do not face the challenge of real-time detection of hospital-acquired infection and provide high quality data on the trends and burdens of NIs. This approach needs extensive resources. Lessons learnt from the implementation of passive approaches to NI surveillance, especially in low and middle income countries, have revealed the necessity of implementation of integrated sentinel surveillance methods using active approaches at selected hospitals/health care facilities. Selecting representative hospitals can contribute to an appropriate understanding of NI-related burden.

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A study of antibiotic susceptibility of clinical strains of *Pseudomonas aeruginosa* in University Hospital Center in Batna, Algeria

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P seudomonas aeruginosa is an important opportunistic pathogen that plays an important role in hospital and causes a wide spectrum of nosocomial infections that can lead to sepsis, pneumonia, endocarditis and urinary tract infections. The development of resistance of *P. aeruginosa* to antibiotics is increasing globally due to the overuse of antibiotics. This study examines the antibiotic resistance in clinical isolates of *P. aeruginosa* that was carried out in the Central Bacteriology Laboratory, University Hospital Center in Batna from January 2015 to December 2015. All samples received in the laboratory were processed according to Clinical and Laboratory Standards Institute (CLSI, 2014) guidelines. Identification of P. aeruginosa was done by conventional (Api 20 NE) techniques and antimicrobial susceptibility pattern to 14 antimicrobial agents was determined by disc diffusion method and total of 199 patients with mean age of 24.15±22.15 (50.25% males and 49.75% females). The resistance was seen with Levofloxacin 21.6%, Ceftazidime 9.55%, Piperacillin 38.68%, Colistin 6.03%, Gentamicin 30.15%, Ciprofloxacin 9.04% Aztreonam 8.54% and Imipenem was 14.07%. The most frequent mechanisms of resistance were OprD2 (2.01%) and metallo-b-lactamase M β L (1%). The most affected departments were: Burned (29.14%), Neurosurgery (17.58%) and the Medical-ICU (11.55%). Specimens' frequency according to the isolation rate was: Pus (53.77%) and cerebrospinal fluid (12.56%). In the present study Aztreonam, Ceftazidime, Ciprofloxacin and Colistin were found to be the most effective drugs against *P. aeruginosa*.

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Effect of interruption on treatment outcome of drug resistant tuberculosis patients at the Indus Hospital

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The treatment of drug resistant TB (DR TB) is complicated and lengthy. Sometimes patients fail to appear on each month follow up and the treatment is interrupted. We explored whether the number of months patient has missed follow up during duration of treatment has any impact on the treatment outcomes. We conducted a retrospective data analysis of the patients enrolled on drug resistance tuberculosis (DR TB) from 2009 to February, 2016 at the Indus Hospital, Karachi. The number of enrolled patients till the time of analysis was 895. Still under treatment and transferred out patients were exluded. Hence 623 patients were included in the analysis. The treatment interruption was defined as the discontinuation of treatment for at least for 30 consecutive days. Median age of the patients was 27 years (6 months to 85 years) 298 (46%) were females. 489 (79%) were MDR, 31 (5%) were XDR, 36 (6%) were PDR, 12 (2%) were resistant to Rifampicin only, 55 (9%) were reported to be Rifampicin resistant on GeneXpert. Number of patients who were declared as treatment failure was 51 (8%), 90 (15%) patients died. Overall success rate was 70% and default rate was 7%. Number of patients whose treatment was interrupted for at least 30 consecutive days was 110 (18%). Mean number of days treatment was interrupted was 15 days (0-6 months). Mean number of days treatment was interrupted in the patients who successfully completed the treatment was 16 days and for those with the poor outcomes it was 24 days. After controlling for age, SLD history, gender, presence of co morbid diseases and resistance patterns the multivariate logistic regression showed that the number of months treatment was interrupted was directly associated with poor treatment outcomes (OR 2, 95% CI 1.5-2.2). For this population overall compliance (% of patients who never miss drugs) is 71%.

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Situation of Crimean Congo hemorrhagic fever in last 15 years in Iran

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Crimean Congo Hemorrhagic Fever (CCHF) is a zoonotic viral disease caused by infected tick bite, contact with blood or tissues of infected livestock and nosocomially. CCHF is a life-threatening virus with a 5-50% fatality rate. CCHF in Iran was reported by Chumakov in 1970. Since establishment of the Arboviruses and Viral Hemorrhagic Fevers Laboratory in Pasteur Institute of Iran in 2000 till now, 3104 human sera were submitted from different provinces and tested serologically and molecularly. Of 3104, we had 960 confirmed cases and 135 deaths. Males with 747 confirmed cases were the most affected gender. Geographically, Sistanva Baluchistan, Khorasan and Isfahan provinces had the highest rate of CCHF confirmed cases. Slaughterers (240 cases) and farmers (176 cases) were the most high-risk occupation. The results of our phylogenetic studies showed that Pakistani, Iraqi and Russian strains are the circulating in Iran. CCHF is one of the most important viral emerging zoonotic diseases in Iran. CCHF has been mainly seen in certain professions and regions, as it is mainly related to imported livestock from neighboring countries. Data with respect to the gender acquired infection shows that CCHF infection in male is more than female, which seems due to male implication in high risk professions. To establish preventive strategies for CCHF, firstly awareness and training programs for high risk professions and secondly conducting joint projects with neighboring countries on ticks can play a critical role in the control of disease.

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Epidemiology status of cutaneous leishmaniasis in Morocco

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In Morocco, the number of cutaneous leishmaniasis (CL) cases is increasing over time and space with a total of 52 among 75 provinces. Both CL due to *L. major* and *L. tropica* are widespread in Morocco. CL due to *L. infantum* was sporadically represented in this country. However, the intersection of some clinical aspects between the three species of Leishmania and the possibility of polymorphism makes monitoring of the disease difficult which requires molecular studies. Therefore, the National Reference Laboratory of Leishmaniasis (NRLL) has performed epidemio-molecular studies to identify the circulating parasite species of leishmaniasis by PCR-ITS1-RFLP and to know its recent distribution. Results for these molecular studies have shown the presence none sporadic of *L. infantum* beside *L. tropica*. It is marked by an important number of cases and large geographical distribution in the north of country within foci of visceral leishmaniasis such as Taza, Sidi Kacem and Ouazzane provinces. Also, the NRLL has performed temporal and spatial distribution of CL due to *L. tropica* in endemic provinces and those recently affected by CL. This species was identified in several sectors and localities of the most affected provinces which prove the extension of the disease. These studies have shown that L. *tropica* which was limited to rural and semi-urban was extended to urban areas. Following the increase of CL cases due to *L. major* in 2010 with 6729, the national program has developed the response plan which allowed an important decrease of cases (460 in 2014). The molecular investigations showed the presence of *L. tropica* with low density beside some persistent cases of *L. major*. Finally, the molecular studies seem to be important since it allows the identification of new foci and the coexistence of multiple Leishmania species belonging to different provinces and sectors. These studies are the first step towards a better knowledge of disease evolution and consequently a better control and surveillance.

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Community acquired MRSA causing mediastinitis in a young girl: A case report

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ediastinitis is defined as acute or chronic inflammation of the mediastinal structures and generally has a low incidence. Invasive community acquired methicillin resistant *Staphylococcus aureus* (ca-MRSA) is a rare serious life threatening infection. The common conditions are cardiac revascularization procedures or esophageal perforation or a descending necrotizing mediastinits secondary to an odontogenic focus. We present a rare case of acute necrotizing mediastinitis in a healthy young girl about 1 week after diagnosis of influenza. An 18 year old female from Brooklyn with a past medical history of Gastroesophageal reflux disease and a recent diagnosis of influenza-A, 6 days back presented to the emergency room with fevers, weakness and chest pain for 4 days. Examination was pertinent for lethargy, ill looking female with tachycardia, tachypenia and decreased breath sounds bilaterally, subsequent work up revealed elevated white blood cell count, CRP and ESR. CXR revealed mediastinal widening with normal lung parenchyma. A CT scan of chest revealed diffuse confluent mediastinal adenopathy as well as diffuse thickening surrounding the esophagus with infiltration of surrounding mediastinal fat suggestive of diffuse esophagitis and mediastinitis. Patient was started on broad spectrum antibiotics. The progressive symptoms and imaging findings led to thoracotomy that revealed infected thymic tissue with surrounding induration and infection in the mediastinal and pretracheal space which was debrided. The bacterial cultures from the tissue as well as pleural fluid grew methicillin resistant Staphylococcus aureus. Pathology from the tissue revealed acute necrotizing fibrinopurulent inflammation and fibrinopurulent exudate. Patient was treated with Vancomycin and Piperacillin/ Tazobactam which was later targeted to MRSA patient was discharged home on IV Daptomycin and completed 5 weeks of therapy which was subsequently changed to PO Doxycycline. An MRI performed at 7 weeks of therapy revealed significant improvement in prior mediastinits with no residual fluid or stranding.

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Majocchi granuloma of the upper lip, a dermatophyte infection: A case report

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Background: Majocchi granuloma is an uncommon condition in which the dermatophyte invades the dermis and subcutaneous tissue. *Trichophyton rubrum* is the most frequent etiologic agent. The upper lip was chronically ulcerated and painless. Biopsy of the lesion on the upper lip exhibited fungal forms in the dermis. KOH preparation was negative.

Case presentation: A 28-years-old male from Agaw ethnicity, Ethiopia referred from rural health centre for the painless non healing ulcer of the upper lip of eleven years. It was reddish circular and indurated measuring 8 by 6 mm. The lower lip was also dry and peeling. He also had onychomycosis of the right thumbnail untreated for the past 18 years. After dermatologic consultation biopsy was taken and KOH was prepared from both lesions. KOH was done twice and were non-revealing from the lip lesion. Biopsy revealed different morphologic variations including yeast forms, bizarre hyphae, mucinous coatings and the Splendore-Hoeppeli phenomenon. After three weeks tissue culture results revealed *Trichophyton rubrum*. Terbinafine 250 mg/day for five weeks resulted in complete resolution of both the granuloma and the onychomycosis.

Conclusion: Varied presentation of such fungal diseases warrants early diagnostic intervention using biopsy and tissue culture to help detect such cases.

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