Genotype Analysis in Patients with Chronic Hepatitis C Infection in Saudi Arabia

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Background and Purpose: Hepatitis C infection affects 130 to 170 million people worldwide with chronic hepatitis C. HCV genotype is essential for diagnostic and therapeutic decision. The aim of this study is to identify HCV genotypes in patients referred to security forces hospital Riyadh (SFHR) in Saudi Arabia for chronic hepatitis C. Furthermore, genotype association with gender and age were studied.

Methodology: Laboratory test results of randomly selected 100 patients with chronic hepatitis C were reviewed. Patients were referred from all over Saudi Arabia regions to SFHR from 2010 to 2018. The patients' data were collected from electronic records. HCV genotyping was done by reverse transcription-polymerase chain reaction assay (Abbott RealTime HCV Genotype II) with Abbott m2000sp and m2000rt instruments. Statistical analysis was carried out using SPSS 20.0 software (SPSS Inc, USA) and P value less than 0.05 was considered significant.

Results and Discussions: In this study the frequency of genotypes 4, 1A, 1B and 2 were respectively 67%, 18%, 13%, and 2%. The gender ratio F/M was 0.69. The mean age at diagnosis was 59.28 years. 73% of patients were older than 50 years. No significant association was found between age at diagnosis, gender and virus genotypes.

HCV genotype 4 was predominant which confirms other studies in Saudi Arabia. The majority of patients were older than 50 years at diagnosis can be explained by the poor conditions of HCV prevention in 1960s in Saudi Arabia.

Conclusions: Our study confirmed the predominance of HCV genotype 4 in Saudi population. In order to achieve an accurate association of genotypes with age group and gender, a larger sample size is required.

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How to Successfully Manage Multi-drug-resistant Acinetobacter baumannii Trasnmissions in Intensive Care Unit?

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Background: Acinetobacter baumannii is a pathogen of considerable clinical importance that has been isolated worldwide. Few studies have evaluated the control of endemic multidrug-resistant Acinetobacter baumannii (MDR-ACB) in Intensive Care Unit (ICU). In this study, we assess the impact of comprehensive infection control interventions on the incidence of MDR-ACB in the ICU at a tertiary care hospital in Saudi Arabia.

Methods: A bundle of comprehensive infection prevention measures was introduced in ICU. The measured outcome was the MDR-ACB incidence density rate in ICU during the pre-interventions (from May 2016 to April 2017) versus the post-interventions phases (from May 2017 to April 2018). Rates were compared and analyzed using Z-test and a p-value of less than 0.05 was considered statistically significant.

Results: The MDR-ACB incidence density rate reached 4.7 per 1000 patient days after having a cluster of MDR-ACB cases in ICU during the pre-interventions phase through which the infection prevention practices were not optimal. The rate decreased to 1.6 per 1000 patient days throughout the post-interventions phase. The interventions resulted in a significant 66% decrease (p-value<0.05) in the MDR-ACB incidence density and included improving hand hygiene and use of personal protective equipment, enhancing cleaning and disinfection practices (both daily and post-patient discharge) of medical equipment and environmental surfaces (cleaning of high-touch areas at least 2 times per shift), monitoring of cleaning procedures, dedicating non-critical equipment, creating a MDR-ACB zone to cohort patients, cohorting staff, applying stringent contact isolation, implementing active surveillance for ICU admissions, applying patient decolonization by bathing with antiseptic agent, intensifying onsite education and implementing antimicrobial stewardship program (ASP).

Conclusion: Implementing a bundle of concomitant, comprehensive and rigorous infection control measures results in a significant decrease in the incidence of MDR-ACB and is crucial to control its spread in ICU.

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Rapid Identification of Bacterial Species with a Beam of Light

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Background: Testing of pathogens in traditional microbiology laboratories needs an instant revolution. Conventional microbiology tests mainly dependent on time consuming culture and antibiotic susceptibility methods, putting patients and the communities at risk of infection. Near Infrared Spectroscopy (NIRS) technique is a non-invasive detection method which involves a 3 second interaction of a beam of light with biological samples to produce a qualitative and quantitative diagnostic spectrum. NIRS is an easy to use non-ionizing technique that does not require access to medical facilities and reagents to operate and can be performed in the field. Recent research by (Lord Lab) demonstrated feasibility of using NIRS to detect, quantify and identify Malaria parasites at a density of 0.3 and 3 parasites/μL, well below the gold standard detection limit of 5–10 parasites/μL. NIRS has also been recently reported to noninvasively detect Zika virus in infected mosquitoes.

Methods: We tested NIRS to detect bacterial pathogens of multidrug resistance phenotypes in vitro. We collected the unique spectra signatures obtained by shining the light beam on bacterial culture of E. coli and K. pnemoniae. Using a machine learning algorithm, we processed the reads to create a prediction model based on the spectra generated by the spectrometer. Ongoing research will also test the potentiality of differentiating between resistance genotypes based on spectroscopy.

Results: Preliminary results demonstrated that the prediction model generated by measuring NIRS read, had successfully differentiated between the two bacterial species with 100% accuracy (N = 115).

Conclusion: Our preliminary results have demonstrated the utility of NIRS to detect and identify bacterial pathogens in vitro. This can potentially lead to a larger work that aims to test the application of NIRS in diagnosing infections in vivo. NIRS can potentially be a significantly rapid and non-invasive screening method for point of care use.

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