Fast, and Cost-Effective Fourier Transform-Infrared (FT-IR) – Spectroscopy-Based For Bacterial Typing

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Conventional microbiology tests are mainly dependent on time consuming culture and antibiotic susceptibility methods, putting patients and communities at risk of these infections. For epidemiological investigations, identified pathogens are usually subjected to further analyses to determine clonality and subtyping. Phenotypic methods (e.g., biochemical-typing, serotyping and antibiogram) do not produce high resolution typing results, and hence provide uncertainty to guide infection control. Consequently, molecular typing methods are able to distinguish between closely related bacteria and allow analyses of clonal diversity within single species to follow-up outbreaks. The ongoing advancements in next generation whole genome sequencing has increased accessibility and provided even higher-resolution typing. Results can help to identify the predominant genotypes existing within the community, which can direct interventions. Despite the great applications of molecular typing and next generation sequencing methods, the expertise and cost associated remains a challenge to most laboratories.

This presentation will demonstrate our experience in subtyping carbapenemase producing Klebsiella pneumoniae isolates from the Gulf States using the fast, and cost-effective Fourier Transform-Infrared (FT-IR) – Spectroscopy- based typing system named IR Biotyper (Bruker Daltonics, Inc.). The subtyping result generated by the IR Biotyper will be compare against the genotyping system DiversiLab® (bioMérieux), which was used against the same collection of isolates.

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Molecular Characterization of Multidrug-Resistant Gram-negative Bacilli in Egypt: A Snapshot Study

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Background: Infections due to multidrug-resistant Gram-negative bacilli (MDR-GNB) are increasingly reported worldwide. Many studies from the Middle East report a high prevalence of MDR-GNB. This high prevalence limits treatment options. We aimed to thoroughly characterize MDR-GNB from Egypt using Whole Genome Sequencing.

Materials/Methods: MDR-GNB associated with a range of clinical infections were collected from Egypt as part of a region-wide study. One isolate per patient was included. Species identification was performed using MALDI-TOF-MS. DNA. Paired-end reads were generated using Illumina. De novo assembly was performed using CLC-Genomics-Workbench and consensus sequences were compared to ResFinder. MLST were also assigned.

Results: Most isolates (47%) were Klebsiella pneumoniae of which two were ST-11, and the remainder were ST-15, ST-35, ST-307, ST-376 and ST-395. All isolates harboured ESBL genes blaCTX-M-15 except K.pneumoniae ST-376 which instead carried blaCTX-M-14b. Three K.pneumoniae (ST-11, ST-35, and ST-395) possessed the carbapenemase gene blaNDM-1 and ST-376 possessed blaOXA-48. All K.pneumoniae carried multiple genes encoding aminoglycoside resistance including aac(3)-IIa, aac(6′)lb-cr, aadA1, aadA2, aacA4, aph(3′)-VIa, strA, strB. All isolates possessed fluoroquinolone resistance genes aac(6′)lb-cr, oqxA, and oqxB, and all except ST-376 also possessed QnrB1, QnrS1, or QnrB66. Six isolates (40%) were Escherichia coli of which four were ST-410 and two were ST-167 and ST-405. All E.coli isolates carried blaCTX-M-15 while ST-405 additionally harboured blaCTX-M-14b. All isolates carried aminoglycoside resistance genes aac(6′)lb-cr, aadA5; ST405 additionally had aac(3)-IId and ST-167 also carried aac(3)-IId, strA, and strB. Two (13%) Acinetobacter baumannii isolates were included: ST-499 carried blaOXA-23 and blaGES-11; and ST-557 co-harboured blaOXA-23 and blaNDM-1. Both A.baumannii isolates had the aminoglycoside resistance determinants aph(3′)-VIa. ST-499 and ST-557 additionally possessed aacA4, or aph(3′)-Ic and armA, respectively.

Conclusions: This study identified resistance mechanisms and STs associated with MDR-GNB in Egypt. Raising awareness of MDR bacteria has important implications for controlling AMR in MENA.

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Comorbidities among HIV Adult Patients in King Abdulaziz Medical City, Western Saudi Arabia: 30 Years Retrospective Cohort Study

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Background: With successful medications, HIV is a lifelong condition. HIV-positive patients are considerably susceptible to encounter higher incidence of comorbidities related to normal aging, HIV infection and treatment.

Aim and objectives: This study aims to estimate incidence and assess pattern and factors associated with comorbidities among HIV patients in King AbdulAziz Medical City, Jeddah (KAMC-J).

Methods: This retrospective cohort study analyzed data on HIV positive cases diagnosed at KAMC-J from 1984 – July 2018. Duplicate files and files with no follow up were excluded. Descriptive statistics were used to measure occurrence of co-morbidities. Multivariate logistic regression analysis (Odds Ratio and 95% confidence interval) was applied to assess risk factors associated with multiple co-morbidities (> 3). Kaplan Meier curve with log-rank test was plotted to estimate survival. Level of significance was determined at p-value <0.05.

Results: Out of 198 HIV positive cases diagnosed at KAMC-J since 1984, 102 patients (51.5%) were included. All patients were Saudi with majority of them being males (73.5%). Mean ± SD of age was 49.0 ± 12.2 years. There were 15.7% deaths. Most common existing medical conditions were diabetes mellitus (29.4%), hypertension (24.5%), dyslipidemia (23.5%), tuberculosis (19.6%), pneumonia (18.6%) and lymphoma (16.7%). Pneumonia was the most common newly diagnosed disease (16.7%) followed by dyslipidemia (14.7%), TB (13.7%), candidiasis (13.7%) and lymphoma (10.8%). Infections were identified in 90.2%, followed by cardiovascular and endocrine/metabolic conditions (66.7% each). Patients with more than 3 comorbidities were 53.9%. Multivariate regression analysis identified age (≥50 years) and those received Raltegravir as more likely to have multiple comorbidities (OR = 4.56, 95%CI = 2.13, 15.68 and OR = 4.52, 95%CI = 1.15, 17.68; respectively).

Conclusion: This study highlights the substantially increased burden of chronic comorbidities among HIV patients. Patient coun-