Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.
Microbiological assessment of a rapid diagnostic assay for blood stream infections

F. Alturki
Kfu

Background and Purpose Early recognition of sepsis and subsequent initiation of effective targeted therapy are crucial steps in the patient outcome as each hour of delay increases the mortality. Currently, only few testing tools can rapidly identify the pathogen and provide the antimicrobial susceptibility testing (AST) results in forms of phenotypic MICs directly from positive blood culture vials. Here, we are presenting a model of how to evaluate a potential platform for Antimicrobial stewardship program “Accelerate PhenoTM system”.

Methodology This is a prospective study performed on 24 positive blood cultures of suspected Blood stream infection (BSI) cases at King Fahad Hospital of the University over 4 months in 2018. The system was compared to the conventional methods (MALDI-TOF and VITEK2). Categorical agreement, rates of errors and sensitivity/specificity at both genus and species levels were calculated. The time reduction to final identification (ID) and AST was calculated by Wilcoxon Signed Rank, test and paired T-test, respectively.

Results and Discussions The Accelerate PhenoTM system correctly identified 95.24% of the isolates to the genus level and 90.47% to the species level. At a genus level, it demonstrated sensitivity and specificity of 80% (95% CI: 59.3–93.2) and 100% (95% CI: 86.3–100) respectively. At a species level, it gave sensitivity and specificity of 59.3% (95% CI: 38.8–77.6) and 100% (95% CI: 87.2–100) respectively. It was able to generate AST for 78.9% of the isolates with an overall categorical agreement of 98.06%. The system reduced the time to final ID and AST by 17.26 hr. (P value 0.001) and 30.08 hr. (P value < 0.001), respectively.

Conclusions The Accelerate PhenoTM system provides rapid and accurate results for the organisms included in the panel. Implementation of this diagnostic tool along with routine microbiology work-up could be useful to optimize sepsis management.

References

https://doi.org/10.1016/j.jiph.2020.01.129

PP099

Interactions of bacterial infections with latent cytomegalovirus in patients in critical condition

S. Yahorau∗, V. Harbachou
Vitebsk State Medical University

Severe bacterial infection in patients in critical condition can lead to reactivation of latent cytomegalovirus infection affecting the clinical outcomes, which was the subject of our research.

A prospective observational study included 61 ICU patients (Vitebsk Regional Hospital) aged 29 to 90 years: 47 men, average age 56.2 years (95% CI 52.2...60.3). Inclusion criteria were diagnosed sepsis (following Sepsis-3 criteria) or verified severe bacterial infection, absence of primary immunodeficiency. The results of a common, biochemical and immunological blood tests, microbiological culture were taken into account in assessing the clinical condition.

In order to quantify cytomegalovirus DNA, a real-time PCR kit was developed, tested and licensed in the Belarus. Samples were stored at –80 °C. qPCR was performed on Bioread CFX96 thermocycler according to the kit recommendations. The methods of descriptive and nonparametric statistics (Mann-Whitney U test) were used for analysis in Statistica 10.

Cytomegalovirus DNA was detected in 18 of 52 samples (34.6%) in plasma: range = 22–13274 IU/ml, Me (25%; 75%) = 1093 IU/ml (154.8; 3011). 8 of 20 sputum samples (40%) were cytomegalovirus DNA positive: range = 21–58636 IU/ml, Me (25%; 75%) = 4519 IU/ml (1525.5; 21823).

In group of cytomegalovirus positive patients sepsis was diagnosed in 14 of 28 cases versus 12 of 33 in the group of non-septic patients (OR = 1.75). Also, statistically significant connection was found between cytomegalovirus persistence and decreased number of T-suppressors CD-8 and increased immunoregulatory index (CD4+ /CD8+ ; p = 0.01). Among 11 patients who died in the study, 5 revealed cytomegalovirus reactivation.

Thus, the relationship between the presence of severe bacterial infections (sepsis), immunological changes and reactivation of cytomegalovirus was found. Monitoring of the cytomegalovirus viral load can be used in assessing the state of the host’s immune status and its clinical prognosis.

References

https://doi.org/10.1016/j.jiph.2020.01.131

PP100

The clinical significance of filmarray pneumonia panel plus in diagnosing pneumonia due to MDRO

T. Alsalmi, S. Aljohani∗
KAMC

Background The FilmArray Pneumonia Panel plus (PPPlus) is an in vitro multiplex nucleic acid diagnostic test for the simultaneous detection and identification of multiple lower respiratory viral and bacterial Nucleic acids, as well as select antimicrobial resistance genes. It is a rapid test (~60-min) detect 28 pathogens directly from bronchoalveolar lavage (BAL), endotracheal aspirates and sputum samples.

Methods A total of 60 clinical specimens were tested by microbiology cultured as well as Biofire Filmarray. all samples were lower respiratory, 13 Sputum (including Tracheal Aspiration and Endotracheal aspirate).

In the (PPplus), the organisms identified are classified in to 4 groups:
a. Bacteria are reported semi-quantitatively: Acinetobacter calcoaceticus-baumannii complex, Klebsiella oxytoca, Serratia marcescens, Enterobacter cloacaee complex, Klebsiella pneumoniae group, Staphylococcus aureus, Escherichia coli, Moraxella catarrhalis, Streptococcus agalactiae, Haemophilus influenzae, Proteus spp. Streptococcus pneumoniae, Klebsiella aerogenes, Pseudomonas aeruginosa and Streptococcus pyogenes.

b. Atypical Bacteria: Chlamydia pneumonia, Legionella pneumophila and Mycoplasma pneumoniae.

c. Viruses: Adenovirus, Human Rhinovirus/Enterovirus, Middle East Respiratory Syndrome Coronavirus (MERS-CoV), Coronavirus, Influenza A, Parainfluenza Virus, Human Metapneumovirus, Influenza B and RSV.

d. Antimicrobial Resistance Genes: CTX-M, NDM, mecA/C and MREJ, OXA-48-like, KPC and VIM. In this study, we are evaluating the performance and accuracy of (PPplus) in comparison to our clinical Microbiology standard procedure Respiratory Culture.

**Result** In this study, 53 organisms were detected by (PPplus) ... see table...

The overall success rate for initial specimen tests in this study was 100% positive percent agreement with previous Microbiology results and the negative percent agreement was 95%.

**Conclusion** Rapid molecular test can identify the causative pathogens along with early detection of resistance gene.

The clinical impact of rapid bacterial identification and antimicrobial resistance gene could reduce the overuse of antimicrobial, lower mortality and major impact on outcome of hospitalized patient with infection.

https://doi.org/10.1016/j.jiph.2020.01.132

**PP101**

**Genomic analysis of chromobacterium haemolyticum causing near-drowning pneumonia and environmental investigation of river water as a source**

H. Kanamori1,2,∗, T. Aoyagi1,2, M. Kuroda3, T. Sekizuka4, M. Katsumi4, H. Baba5,6, K. Oshima1,2, K. Tokuda1,2, M. Kaku1,2

1 Department of Infection Control and Laboratory Diagnostics, Internal Medicine, Tohoku University Graduate School of Medicine
2 Department of Infectious Diseases, Internal Medicine, Tohoku University Graduate School of Medicine
3 Pathogen Genomics Center, National Institute of Infectious Diseases
4 Department of Laboratory Medicine, Tohoku University Hospital

**Background and purpose:** Very rare cases of Chromobacterium haemolyticum infections have been described, but environmental sources of this pathogen have not been well investigated. Here, we used whole-genome sequencing (WGS) to identify Chromobacterium species causing pneumonia associated with near-drowning and investigate molecular features of clinical and environmental isolates of C. haemolyticum.

**Methodology:** Two clinical isolates of Chromobacterium spp. detected from sputum and blood cultures and three environmental isolates taken from sites of drowning and upstream side in the river were analyzed using a next-generation sequencer. To comparative genomic analysis, publicly available genome sequences of Chromobacterium spp. on NCBI Assembly database were used. Metagenomic analysis of a river water sample collected from the site of drowning was also conducted.

**Results and discussions:** Nineteen strains of C. haemolyticum, including our 5 clinical and environmental isolates, were identified with 252,974 single nucleotide variation (SNVs) by core genome phylogenetic analysis. C. haemolyticum CH05-BL and other study isolates in this study possessed blaCHR-1 in the chromosome. Our study isolates also had type III secretion system (T3SS) encoded by Chromobacterium pathogenicity island 1 and 1a (Cpi-1/-1a). Metagenomic analysis of a river water sample collected from the site of drowning revealed that the relative abundance of Chromobacterium is 0.073%. Chromobacterium accounted for only a very small portion of bacterial class based on our metagenomics analysis of the river water, but its organism was isolated from our case and involved in human infection despite presence of other pathogens (e.g., Aeromonas, Pseudomonas, Legionella) in the river that can cause pneumonia associated with near-drowning.

**Conclusions:** WGS is a useful tool for accurate identification of Chromobacterium species. Our genomic and environmental study demonstrates that C. haemolyticum causing human infections is ubiquitous in the local river as a natural habitat of this pathogen in Japan.

https://doi.org/10.1016/j.jiph.2020.01.133

**PP102**

Investigation of the relationship between chronic spontaneous urticaria and gut microbiome

G. Yuksekål1, K. Yilmaz2, B. Dikicier1, M. Koroglu2, M. Altindis2,∗

1 Sakarya Unv School Of Medicine Dept of Dermatology
2 Sakarya Unv School Of Medicine, Dept of Microbiology

**Background and Purpose:** In this study, we aimed to determine the possible relationship between chronic spontaneous urticaria (CSU) disease and gut microbiome, to determine the pathogenesis of CSU and to help new diagnosis and treatment approaches.

**Methodology:** 20 patients with CSU and 10 age and sex-matched healthy individuals were included in this study. After nucleic acid isolation from fecal samples, bacterial 16S ribosomal RNA (rRNA) gene target sequencing was performed with the Illumina MiSeq system using universal bacterial 16S primers (V3–V4). Statistical analyses (LeSe, alpha, and beta diversity) were performed after bioinformatics. The default settings (p<0.05 and LDA score> 2) identified taxa that differed significantly between the groups.

**Results and Discussions:** Patients with CSU; Bacteroidetes phylum and Lachnospiraceae, Ruminococcaceae, Clostridiales family and Intestinibacter, Megasphaera, Sutterella genus member bacteria were significantly increased (p<0.05 and LDA score> 2). In healthy volunteers, Bifidobacteriaceae, Lachnospiraceae, Ruminococcaceae, Veillonellaceae, Prevotellaceae, Coriobacteriaceae family and Clostridiales order and Succinivibrio genus bacteria were found to be statistically significantly higher (p<0.05 and LDA score > 2) (Figure 1/2). The rate of Firmicutes/Bacteroidetes in CSU patients was found to be lower than in the healthy control group (0.95 in CSU patients, 1.69 in healthy volunteers). Beta diversity analysis showed a difference between the two groups (PC1 maximum variation rate; Bray–Curtis Plot; 22.23%, Bray Curtis Plot (Genus Level); 35.79%).