Conclusion: Point of care multiplex PCR panel test might be useful in the acute care of patients with unknown infectious disease syndromes and negative standard test methods.

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UMP. 167

Standardization of gut microbiota analysis: Variability in samples taken at different times from single case and the effect of the freezing the sample

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Background: Gut microbiota analysis can help understand many diseases some of which, like inflammatory bowel diseases, obesity and diabetes are already established and the others are to be determined. Using this test for diagnostic purposes and establishing personalized care seems to become a routine procedure that needs standardization protocols. The aim of this study was to analyze the changes in gut microbiota communities in samples taken from single case at different times and the effect of storing the samples in -20 °C before processing them.

Methods & Materials: On the day 1 and the day 8, two stool samples were obtained from a single case, 40-year-old woman using insulin for the control of her Type 1 Diabetes Mellitus. The first sample were processed in 2 hours and part of it was kept in -20 until day 8. The second stool sample was processed together with the frozen sample in 2 hours. DNA was obtained with fecal DNA extraction kit (QIAGENE). The microbiota was determined using Ion 16S rRNA Metagenomic Kit on Ion Torrent platform. The extraction were done as mentioned above and metagenomic studies were done for all samples in a single run and chip. The comparison of the results was done using t-test with SPSS (IBM) software.

Results: Six phyla were determined: Bacteriodetes, Firmicutes, Proteobacteria, Tenericutes, Actinobacteria and Verrucomicrobia. Bacteriodetes and Firmicutes formed the majority of the bacterial population studied. Bacteriodetes were 57% in the 1st day fresh sample and 28% in the frozen one. Bacteriodetes ratio in 8th day sample was 44%. Firmicutes formed 35% in 1st day fresh sample, 38% and 19% in frozen and 8th day samples respectively. Proteobacteria ratios were high in frozen and 8th day samples: 31% and 36%. Proteobacteria formed 7% of bacterial population in the 1st day fresh sample. Tenericutes, Actinobacteria and Verrucomicrobia were below 1% in all samples.

Conclusion: Gut microbiota analysis results although being variable, showed a basic level consistency. Microbiota testing can be a part of routine work up when standard protocols for sample preparation and processing are established.

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UMP. 168

Incorporation of MALDI TOF technology into the daily routine of positive blood cultures in a clinical microbiology laboratory

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Background: To evaluate the performance of the MALDI TOF MS technology in the processing of positive blood cultures in the clinical microbiology laboratory of a high complexity hospital.

Methods & Materials: The blood cultures that the BACT Alert® system identified as positive in a period of 18 months were analyzed. Samples that showed unique morphology to gram staining was inoculated into agar sheep blood plate and incubating at 37 °C in aerobiosis. Each hour, visual inspection was carried out until microbial development was observed and the spot was made to be analyzed by VITEK MS® according to the manufacturer's instructions. Identification correlation was performed by VITEK 2C® from isolated colony.

The incubation time necessary to obtain a mass spectrum of good quality that was associated with identification with high confidence level (> 99.8%) was evaluated.

Results: A total of 200 positive blood cultures were included. The minimum incubation times obtained were: 3, 5, 5, 5, 4 and 6 hours for the enterobacteria (EN), nonfermenting gram-negative bacilli(NFGNB), staphylococci, streptococci, enterococci and yeasts. respectively. Within EN, streptococci and enterococci, no statistically significant differences were observed between the different species. In the NFGNB, Acinetobacter baumanii showed shorter incubation times than Pseudomonas aeruginosa. In staphylococci, there was a statistically significant difference ($p < 0.01$) between Staphylococcus aureus and Staphylococcus haemolyticus (3 hs) and other coagulase-negative staphylococci (5 hs). The yeasts were required a longest incubation time.

The concordance in the identification at the genus and species level between the rapid and final identification was 98% for gram-negative bacilli, 95% for gram-positive cocci and 99% for yeasts. Those identification discrepancies that required a third methodology for definitive taxonomic assignment were not considered in the analysis.

Conclusion: By comparing the usual identification workflow with the MALDI TOF MS technology, the latter showed excellent overall performance and great flexibility to be incorporated into the daily routine of the microbiology laboratory. This processing modality provides identifity of microorganisms with a high level of certainty, decreases turnaround time and provides the physician with a significant improvement in antibiotic therapy if it is adjusted to local and institutional epidemiology.

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