2024. Modeled Impact of Rapid Diagnostics on the Treatment of Gram-Negative Bacteremia at a Tertiary-Care VA Medical Center

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Session: 229. Diagnostics: Biomarkers and Novel Approaches

Saturday, October 6, 2018: 12:30 PM

Background. Gram-negative pathogens take 24–72 hours to be identified (ID) and antibiotics are dosed empirically (AE), based on blood cultures. Rapid molecular diagnostic tests (RDT) can shorten time to pathogen identification and antibiotic optimization. We compared our current processes with the predicted impact of an RDT system, to assist with an institutional decision to invest in RDT. The Accelerate PhenoTest™ BC Kit, which provides pathogen ID within 90 minutes of positive growth and AST within 7 hours, was selected as an example of a commercially available system for study purposes.

Methods. A retrospective review of adult patients between January 2016 and September 2017 with positive blood cultures at a tertiary-care VA hospital was performed. The 95th percentile upper refer-
cive cutoff was calculated at 0.08 ng/mL. This 95th percentile cutoff seemed to be much lower than the self-reported healthy individuals, the 95th percentile, upper reference range limit was calculated at 0.3 ng/mL to indicate invasive bacterial infection in our institution. In the 10-year study period, 258 S. maltophilia isolates were identified, 94.0, 75.3, 28.6, 17.2% and 0.0% of isolates, respectively.

Conclusion. This result confirmed that a procalcitonin clinical cutoff of 0.3 ng/mL is appropriate in our patient population. It also showed that both plasma and serum specimens can be used for procalcitonin measurement.
PBMC, HZ cases had higher %FOXP3+CD25+(CD4+) Treg compared with controls (P = 0.08). Cases generally had lower responses to ex vivo VZV-restimulation of mock compared with controls, including %perforin+(CD8+) CTL (P = 0.07) and %IL10+(CD4+) (P = 0.04) and %TGFb+(CD4+) Treg (P = 0.07). %FOXP3+CD25+(CD4+) Treg in unstimulated PBMC did not correlate with VZV-specific or non-specific response in T cells, but the VZV-specific effector T cell percentages correlated with each other (r = 0.24, P = 0.05).

Conclusion. Although limited by small numbers, this study showed that before development of HZ, PLWH had marginally increased number of Treg in blood and decreased VZV-specific responses. VZV-specific Treg and CTL were equally low in cases compared with controls, suggesting that a general low VZV-specific T cell responsiveness precedes HZ in PLWH. The lack of association between circulating Treg and VZV-specific T cell responses suggests independent mechanisms of action.

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2028. ID Consultant EMR Hyperlinked Recommendation as a Tool to Curb “Routine” Following of Inflammatory Markers
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Background. “Routine” daily inpatient labs are ineffective at improving patient outcomes and are associated with antibiotic overuse and delayed hospital discharge. Despite recommendations from the ABIM in the “Choosing Wisely” program, limited progress has been made in curbing inappropriate testing. In particular, admonitions from ID consultants that daily measurement of inflammatory markers is unnecessary have gone largely unheeded. Since online messaging tools are helpful in areas such as medication reconciliation, we hypothesized that EMR-based “clickable” hyperlinks to “Choosing Wisely” recommendations within the ID consultant daily progress note might provide a psychologically stronger “nudge” toward appropriate use.

Methods. In a community teaching hospital, from September 1, 2017 through March 31, 2018, 38 stable patients with requested ID consultation and three or more sequential daily measurements of CBC and/or CRP were sequentially assigned to receive either standard ID advice including that daily testing was unnecessary, or additionally a hyperlink to the URL for the Choosing Wisely recommendation. At 48 hours, patient data were analyzed for whether daily labs continued or stopped. Significance was assessed with 2 x 2 contingency testing. In addition, relevant provider comments in the daily progress notes were assessed.

Results. Of 19 consultations with hyperlinked recommendations, 10 showed cessation of daily CBC/CRP testing. Of 19 without the hyperlink, only 4our showed discontinuation by 48 hours (P = 0.04 Fisher exact). Comments ranged from appreciative to defensive, with the former more common from House Officers compared with attending physicians.

Conclusion. Inclusion of a clickable hyperlink in the EMR progress note from an ID consultant may provide a more effective psychological nudge away from inappropriate testing compared with text advice alone. Physicians in training may be more receptive to this messaging.

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2029. Comparison of Primers Amplifying Two Different Regions of the 16S Ribosomal RNA Gene for Microbiologic Diagnosis of Cardiovascular Implantable Electronic Device Infection
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Session: 229. Diagnostics: Biomarkers and Novel Approaches
Saturday, October 6, 2018: 12:30 PM

Background. Bacterial cultures are negative in over 13% of cases of Cardiovascular Implantable Electronic Device (CIED) Infections. Broad-range PCR and Sanger sequencing could potentially establish a microbiologic diagnosis in these patients. We aim to evaluate and compare detection and sequencing performance of primers targeting two different hypervariable regions of the 16s ribosomal RNA (rRNA) gene on sonicated fluid from extracted CIEDs.

Methods. Samples of sonicate fluid from extracted cardiac devices of patients with suspected CIED infection have been collected in our laboratory from 2012 through 2017. We selected 39 of these samples and classified them as culture-positive or culture-negative based on the results of conventional culture. ZytoBIOIMICS DNA miniprep kit was used to extract DNA from all samples. PCR was performed on a Roche LightCycler 1.0 instrument. Annealing temperature of 65°C was used for the primers targeting the V3–V4 16s rRNA hypervariable region and 62°C for the V1–V3 primers according to previously published protocols. Samples with crossing point (Cp) of <32 or <3 Cps below the negative control were sent for bidirectional Sanger sequencing. Sequences were aligned and edited using Sequencher 5.0 software. Contiguous assemblies were queried using the NCBI BLAST database and results interpreted using CLSI guidelines. The organism identified by sequencing was compared with the results of conventional culture.

Results. Of the 39 samples, 23 were culture-positive and 16 were culture-negative. Of those 23 culture-positive, 19 were PCR-positive using both sets of primers and sequencing of these samples identified the same organism reported on conventional culture. Two out of the 23 samples were only PCR-positive using the V1–V3 primer set. In the culture-negative group, no PCR-positive results were obtained using both sets of primers, identifying Staphylococcus aureus in both. The remaining samples were PCR-negative.

Conclusion. Our results suggest that primer set amplifying the V1–V3 region of the 16s rRNA gene leads to slightly better detection results compared with the V3–V4 primer set used. Molecular testing performed on sonicate fluid from extracted devices may identify pathogens in cases of culture-negative CIED infection.

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2030. How Machine-Learning Technique Using Artificial Neural Network Determines Whether the Fever Is Actually Related to the Bacteria
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Background. By applying machine-learning-based algorithm using artificial intelligence to massive medical data, we are trying to build a real-time monitoring system for prediction of diseases to support accurate and efficient clinical decision making in time. In the previous study, we presented a model for predicting bacteremia using Bayesian statistical approach. Now, we have developed various machine-learning technique-based prediction models to achieve better prediction performance.

Methods. We retrospectively analyzed 13,402 febrile patients who were admitted to Gangnam Severance Hospital, a tertiary center in Seoul, South Korea. The training data were 11,661 patients with admission date from July 2008 to August 2011, and validation data were 2,341 patients from September 2011 to February 2012. The primary outcome was bacteremia, and the training data were analyzed to make prediction model with conventional Bayesian approach, Support Vector Machine (SVM), Random Forest (RF) and multi-layer perceptron (MLP), a representative artificial neural network (ANN) model. The performance of prediction was assessed based on the area under the curve (AUC) and sensitivity from validation data. We used 20 clinical variables for predictors of bacteremia same as Bayesian approach. The difference from the previous model was that each variable had been stratified, but in this study, they were trained as a full number.

Results. A total of 1,538 bacteremia episodes were identified from 13,402 febrile patients. The AUC of bacteremia prediction performance in SVM model was lowest with the result of 0.699 (95%CI 0.667–0.700), even though it was 0.7 in conventional Bayesian statistical method. The highest results were 0.732 (95% CI 0.722–0.733) in RF model and in MLP with 128 nodes of hidden layer model, the AUC was 0.719 (95% CI 0.712–0.728) and in MLP with 256 nodes, it was 0.727 (95% CI 0.713–0.727). In comparison with sensitivity, MLP models (0.810, 95% CI 0.772–0.747 in 128 nodes, 0.810, 95% CI 0.782–0.837 in 256 nodes) were the highest but in RF model, the sensitivity was the lowest.

Conclusion. Compared with conventional statistical model, ANN-based bacteremia prediction model-MLP showed better prediction value. In order to improve the performance of prediction, further larger amount of clinical data is needed to be analyzed.

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2031. False-positive Serologic Results attributable to IVIG therapy
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Poster Abstracts • OFID 2018:5 (Suppl 1) • S591