Results. 210 urine samples were tested. After 3 hours of incubation on the BacteriOscan, 70 (33.3%) and 140 (67.7%) urine samples were reported as positive and negative for bacterial growth, respectively. 136/140 (97.1%) of the negative samples were either no growth (67.6%) or insignificant (32.4%) growth by culture. The remaining 4 (2.9%) were catheter (3) or surgical (1) samples that grew <10K CFU/ml. We sequenced plasma next-generation sequencing (plasma NGS) test to detect infections in SCT patients. Two cases highlight the potential of plasma NGS to detect pathogens in SCT patients early when used as a monitoring tool.

Conclusion. Karius has developed a novel NGS plasma test that can simultaneously identify pathogens in SCT patients. The test had 100% concordance with CMV qPCR above the lower level of quantitation. Further work is ongoing to determine the lower limits of detection for the plasma NGS test. Using NGS to monitor SCT patients for infection could permit earlier detection of pathogens, enabling earlier targeted therapy for this vulnerable population.

Disclosures. All authors: No reported disclosures.

2094. Futility of Centor Score (CS) for Predicting Group A Streptococcal (GAS) Pharyngitis in an Adult Hyper-endemic Native American (NA) Population

Background. Identification of Streptococcus pneumoniae (Spn) and its more than 90 serotypes is routinely conducted by culture and Quellung reactions. Quantitative (q)PCR was recently developed for molecular detection, including a pan-Spn and lytA assay, and assays targeting 78 serotypes. Reactions require genomic DNA from every target to prepare standards, which can be time consuming. In this study we developed a synthetic DNA molecule as a surrogate for genomic DNA and present new variable-plex (VP) qPCR reactions to increase molecular detection to 94 pneumococcal serotypes.

Methods. Single-plex qPCR reactions (N=11) that detect 16 pneumococcal serotypes/serogroups were developed and concentration of primer and probe optimized to obtain the best efficiency between 90 and 110%. Spectrally targeted serotype/serogroup of these new reactions was investigated using a collection of strains belonging to our laboratory and strains kindly donated by the “StrepLab” at CDS. A synthetic DNA NUversa (~8.2 kb) was then engineered to contain all available qPCR targets for serotyping and lytA, NUversa was cloned into pUC57. Amp-modified to generate pNUversa (~10.2 kb). Standards prepared from pNUversa and NUversa were compared against standards made out of genomic DNA.

Results. Specificity of these new reactions was confirmed, and after optimization, the obtained limit of detection (LOD) was between 2 and 20 genome equivalents/ reaction. Molecular studies demonstrated that linearity [NUversa (R² >0.992); pNUversa (R² > 0.991)] and efficiency of qPCR reactions using synthetic DNA were similar to those utilizing chromosomal DNA (R²~0.981). Quantification, however, with plasmid pNUversa (Y Int= 43.0 ± 1.12) was affected whereas using synthetic NUversa (Y Int= 48.3 ± 1.1.0) was comparable to genomic DNA (Y Int= 39.9 ± 0.62).

Conclusion. We validated single-plex qPCR reactions that, together with published qPCR reactions, now make possible to detect and quantify 94 pneumococcal serotypes/serogroups. NUversa can be utilized as a control in most, if not all, published single-plex qPCR reactions, for the identification (i.e., detection), and quantification (i.e., genome equivalents) of pneumococcal serotypes.

Disclosures. All authors: No reported disclosures.

2093. The DISCOVER Trial: Application of the Karius Plasma Next-Generation Sequencing Test for Pathogen Detection in Stem-Cell Transplant Patients

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Background. The diagnosis of infections in stem-cell transplant (SCT) patients is challenging. There is a need for improved diagnostics that can quickly and accurately detect a broad range of viruses, bacteria, and fungi that can infect these patients to guide aseptic therapy.

Methods. We enrolled 20 patients in a prospective study evaluating the Karius plasma next-generation sequencing (plasma NGS) test to detect infections in SCT patients. Patients had baseline plasma samples drawn prior to transplant followed by weekly collections during engraftment and at onset of febrile episodes. Samples were collected to the Karius CLIA/CAP Laboratory (Redwood City, CA) where cell-free DNA was extracted from plasma and NGS performed. Human sequences were removed and remaining reads were aligned against a curated pathogen database. Organisms present at a significance level above a predefined threshold were reported.

Results. Cytomegalovirus (CMV) was identified in 12/20 patients. Using a nearest-neighbor method, 61 pairs of observations were identified for a comparison of plasma NGS and CMV qPCR. Using the assay’s LOD, 33/37 (47.1%) samples were tested on the 216R AST System; 37/52 (72.3%) samples omitted by curve analysis showed no or questionable significant growth by culture. Comparator data were available for 26/33 samples. Amplification and ceftriaxone demonstrated categorical agreement of 100%, while ceftriaxone and ciprofloxacin had 96% and 88% agreement, respectively, with 4% major errors for cefazolin and 12% minor errors for ceftriaxone.

Conclusion. The 216R AST System could be utilized as a screening platform to rule out UTIs within 3 hours, with AST available after an additional 2-6 hours for suspect UTI positive samples. This could potentially prevent unnecessary antibiotic therapy. Preliminary data are promising but testing of additional clinical samples is warranted.

Disclosures. All authors: No reported disclosures.

2092. Development and Characterization of a Synthetic DNA, NUversa, to Be Used as a Standard in All Quantitative PCR Reactions for Molecular Pneumococcal Serotyping

Fumimori Sakai, MD, PhD1; Griffin Sonaty, MPH1; Keith Slukman, MD, PhD3; FIDSA2 and Jorge Vidal, PhD1;

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Background. Identification of Streptococcus pneumoniae (Spn) and its more than 90 serotypes is routinely conducted by culture and Quellung reactions. Quantitative (q)PCR was recently developed for molecular detection, including a pan-Spn and lytA assay, and assays targeting 78 serotypes. Reactions require genomic DNA from every target to prepare standards, which can be time consuming. In this study we developed a synthetic DNA molecule as a surrogate for genomic DNA and present new variable-plex (VP) qPCR reactions to increase molecular detection to 94 pneumococcal serotypes.

Methods. Single-plex qPCR reactions (N=11) that detect 16 pneumococcal serotypes/serogroups were developed and concentration of primer and probe optimized to obtain the best efficiency between 90 and 110%. Spectrally targeted assay for serotyping and lytA assay, and assays targeting 78 serotypes. Reactions require genomic DNA from every target to prepare standards, which can be time consuming. In this study we developed a synthetic DNA molecule as a surrogate for genomic DNA and present new variable-plex (VP) qPCR reactions to increase molecular detection to 94 pneumococcal serotypes.

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