Background. Biomarkers (C-reactive protein [CRP], procalcitonin [PCT]) have been used in patients with systemic inflammatory response syndrome (SIRS) to identify those with and without bacterial infection. However, their performance in immunocompromised (IC) children is not well studied.

Methods. Retrospective chart review of episodes of SIRS in IC children <19 years old admitted to the PICU August 2012–June 2016 with: (a) blood culture, PCT, and CRP obtained within 6 hours of SIRS; (b) no recent SIRS episodes (> 30 days), and (c) no positive blood culture in 2 days preceding SIRS. We defined IC as neutropenia (ANC < 500), solid-organ transplant (SOT), hematopoietic cell transplant (HCT), and other (immunosuppressive medications or primary immunodeficiency). To identify a comparator group, we additionally reviewed a previously published cohort of non-IC children with SIRS (Downes, et al, JPIDS 2018), applying the same inclusion criteria. For each episode (first 48 hours after SIRS), we determined the presence of bacterial infection using NHSN definitions and viral infection as symptoms with positive PCR. We compared biomarkers in IC children with and without bacterial infection, and in IC and non-IC children, using Wilcoxon rank-sum tests.

Results. We identified 108 SIRS episodes in 94 IC children (neutropenia = 35, SOT = 18, HCT = 22, other = 33) and 278 episodes in 250 non-IC children. Age (P = 0.15) and gender (P = 0.70) were similar among IC and non-IC groups. 41% of episodes in both IC and non-IC children had bacterial infections (P = 0.96). PCT and CRP were significantly higher in IC children with bacterial infection than those without (Figure 1). Biomarkers did not differ significantly among episodes in IC and non-IC children with bacterial infection; however, among episodes without bacterial infection, biomarkers were higher in IC than non-IC children (Table 1). Detection of a viral infection did not affect biomarker values in IC or non-IC children when bacterial infection was absent (Table 2).

Conclusion. In IC children with SIRS, PCT and CRP were higher when bacterial infection was present. Meanwhile, in the subset of non-bacterial SIRS episodes, biomarkers were higher in IC compared with non-IC children. PCT and CRP may be valuable markers to discriminate bacterial from non-bacterial causes of SIRS in IC children.

1334. Performance of C-Reactive Protein and Procalcitonin in Immunocompromised Children with SIRS
Leila C. Posch, MD1; Craig L. K. Boge, MPH2; Jeffrey Gerber, MD, PhD2; Julie Fitzgerald, MD, PhD2; Scott L. Weiss, MD, MSCE3; Ebbing Lautenbach, MD, MPH, MSCE3; Susan E. Coffin, MD, MPH1; Kevin J. Downes, MD3; Kevin J. Downes, MD3; The Children’s Hospital of Philadelphia, Philadelphia, Pennsylvania; 2The University of Pennsylvania Perelman School of Medicine, Philadelphia, Pennsylvania; 3University of Pennsylvania, Philadelphia, New York

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1335. A Translational Nephrotoxicity Model to Probe Acute Kidney Injury with Vancomycin and Piperacillin–Tazobactam
Gwendolyn M. Pias, PhD1; Iaijun Liu, PharmD2; Sean N. Avedissian, PharmD, MS3; Danielle Hiner, BS4; Thodoros Xanthos, MD, PhD5; Anna Khouri, PharmD6; Ernesto d’Alia, MD, PhD6; Emanuela Locci, PhD1; Annette Gilchrist, PhD1; Walter Prozialeck, PhD1; Nathanial J. Rhodes, PharmD, MS7; APQ ID8; Thomas Lodise, PharmD, PhD1; Julie Fitzgerald, MD, PhD2; Kevin J. Downes, MD3; Kevin J. Downes, MD1; Athena Zuppa, MD, MSCE1; Marc H. Scheetz, PharmD, MSc2; Midwestern University, Downers Grove, Illinois; Midwestern University, Northwestern Memorial Hospital, Downers Grove, Illinois; College of Pharmacy, University of Michigan, Ann Arbor, Michigan; European University Cyprus, Nicosia, Cyprus; School of Medicine, University of Thessaly, Athens, Attiki, Greece; Cagliari University, Cagliari, Sardegna, Italy; The University of Cagliari, Cagliari, Abruzzi, Italy; Albany College of Pharmacy and Health Sciences, Albany, New York; The University of Pennsylvania Perelman School of Medicine, Philadelphia, Pennsylvania; The Children’s Hospital of Philadelphia, Philadelphia, Pennsylvania

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**Background.** Chronic obstructive pulmonary disease (COPD) exacerbation and community-acquired pneumonia (CAP) are major drivers of antibiotic overuse, primarily due to challenges in pathogen identification. Pneumococcal OPAs are used as a marker that assists in distinguishing bacterial infection from other causes. The purpose of this study was to determine whether the use of a pneumococcal OPA guided algorithm in patients diagnosed with COPD exacerbation and/or CAP can reduce antibiotic exposure without negatively impacting clinical outcomes.

**Methods.** This was a quasi-experimental study conducted at Mercy Medical Center in Canton, Ohio. The patient data for the retrospective cohort (control group) was collected from the months of September 2017 through January 2018. The prospective phase (POA group) took place during the months of September 2018 through January 2019. Physicians utilized a pneumococcal OPA algorithm to determine appropriate initiation and duration of antibiotic use in patients admitted with a primary diagnosis of COPD exacerbation and/or CAP. The primary outcome was the duration of antibiotic therapy, measured in days. Secondary outcomes included all-cause hospital readmission within 30 days of discharge, cardiovascular-related hospital readmission within 30 days of discharge, 30-day mortality, hospital length of stay, and adverse events to antibiotics.

**Results.** A total of 76 patients were included in the study, 43 in the control group and 33 in the POA group. Baseline characteristics were similar between groups. The use of a POA algorithm significantly decreased duration of antibiotics by 2.7 days in comparison to the control group (2.6 vs 3.3 days; P < 0.001; 95% CI). Secondary safety outcomes between the POA and control group were similar, including all-cause hospital readmission within 30 days of discharge (30.3% vs. 25.6%; P = 0.648), respiratory-related hospital readmission within 30 days of discharge (80.0% vs. 81.8%; P = 0.731), and 30-day mortality (no incidence in either group).

**Conclusion.** The use of a pneumococcal OPA algorithm significantly reduced duration of antibiotics by 2.7 days without negatively impacting clinical outcomes in patients being treated for COPD exacerbation and/or CAP.

**Length of Antibiotic Therapy**

| Mean Antibiotic Days (SD) | 95% CI (p<0.001) |
|---------------------------|------------------|
| Control (n=43)            | 5.3 (3.51)       |
| PCT (n=33)                | 2.6 (2.55)       |

**Disclosures.** All authors: No reported disclosures.

1338. Development of a Novel Application for Differential Diagnosis of Tick-borne Diseases
Corey Meyer, PhD; Jalal Sanjik, PhD; Audrey Cerles; Christian Garnier; Laurel MacMillan, MS; Gryphon Scientific, Takoma Park, Maryland
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**Background.** Early diagnosis and treatment of tick-borne diseases (TBDs) is critical for mitigating their adverse health outcomes, but the differential diagnosis of TBDs is challenging because many symptoms are nonspecific and commonly used diagnostic assays have significant shortcomings. Furthermore, although the local incidence of TBDs is recognized as an important factor in diagnosis, tools to help clinicians formally consider surveillance data in their decision-making are not available. To address these gaps, Gryphon Scientific developed a differential diagnosis application (app) for TBDs that calculates a patient’s likelihood of infection with specific TBDs based on their symptoms, risk factors, and state of suspected tick exposure.

**Methods.** A differential diagnosis model for TBDs was developed using data on:

1. TBD symptom and risk factor prevalence in TBD patient populations, collected from clinical studies; and
2. Human TBD incidence data from notifiable disease surveillance systems and tick infection prevalence data from reports and public databases, which were combined to develop an environmental risk measure. These data were used to build a Bayesian Belief Network (BBN) model that predicts TBD infection probabilities based on a patient’s symptoms, risk factors, and state of suspected tick exposure. Performance of the model was validated using case studies from the biomedical literature. The model was incorporated into an app developed using R-shiny, called TBD-DDx (Figures 1 and 3).

**Results.** A pilot application was developed that includes 10 states (AR, CT, MA, ME, MN, MO, NH, RI, VT, and WI) and the 11 TBDs endemic to those states. The differential diagnosis model identified the patient’s true disease as the top-predicted TBD in 56% of cases and within the top three predicted TBDs in 84% of cases. The inclusion of incidence factors in the model improved performance (Figure 4).

**Conclusion.** These results demonstrate that the TBD-DDx app is a promising tool for informing clinical diagnoses of TBDs to guide selection of diagnostic testing and treatment. This study represents the first use of a BBN modeling approach that incorporates an environmental risk measure to improve the ability to conduct a differential diagnosis of other diseases with environmental or other exposure risks.

**Disclosures.** All authors: No reported disclosures.

1337. Development, Maintenance, and Application of Ospomophagocytic Assays to Measure Functional Antibody Responses to Support a 20 Valant Pneumococcal Conjugate Vaccine
Ingrid L. Scully, PhD1; Mark W. Cutler, PhD2; Seema Gangolli, MS3; Todd Belanger, MS1; David Cooper, PhD3; Thomas Jones, PhD3; Andrew McKeen, MS3; Charles Tan, PhD3; Wendy Watson, MD3; Annalisa S. Anderson, PhD2; Kahrun U. Jensen, PhD2; Michael W. Pride, PhD3; 1Pfizer Vaccine Research and Development, Pearl River, New York; 2Pfizer, Inc., Pearl River, New York
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**Background.** Ospomophagocytic assays (OPAs) are an important tool for assessing vaccine-induced functional antibody responses. OPAs are complex assays composed of many biological components (e.g., serum, complement sources, bacteria, and human phagocytes) which contribute to assay variability and may result in titr dilution if not carefully controlled. Rigorous development and validation coupled with routine monitoring of assay performance are required to ensure that high-quality OPA serological data are generated throughout the lifetime of existing and next-generation pneumococcal vaccines.

**Methods.** OPA specificity was demonstrated by competing functional antibody responses, such as OPAs, is critical for mitigating their adverse health outcomes, but the differential diagnosis of TBDs is challenging because many symptoms are nonspecific and commonly used diagnostic assays have significant shortcomings. Furthermore, although the local incidence of TBDs is recognized as an important factor in diagnosis, tools to help clinicians formally consider surveillance data in their decision-making are not available. To address these gaps, Gryphon Scientific developed a differential diagnosis application (app) for TBDs that calculates a patient’s likelihood of infection with specific TBDs based on their symptoms, risk factors, and state of suspected tick exposure.

**Results.** A differential diagnosis model for TBDs was developed using data on:

1. TBD symptom and risk factor prevalence in TBD patient populations, collected from clinical studies; and
2. Human TBD incidence data from notifiable disease surveillance systems and tick infection prevalence data from reports and public databases, which were combined to develop an environmental risk measure. These data were used to build a Bayesian Belief Network (BBN) model that predicts TBD infection probabilities based on a patient’s symptoms, risk factors, and state of suspected tick exposure. Performance of the model was validated using case studies from the biomedical literature. The model was incorporated into an app developed using R-shiny, called TBD-DDx (Figures 1 and 3).

**Conclusion.** These results demonstrate that the TBD-DDx app is a promising tool for informing clinical diagnoses of TBDs to guide selection of diagnostic testing and treatment. This study represents the first use of a BBN modeling approach that incorporates an environmental risk measure to improve the ability to conduct a differential diagnosis of other diseases with environmental or other exposure risks.

**Disclosures.** All authors: No reported disclosures.