found to be associated with use of BS antibiotics on day 4. Both total and IV antibiotic duration were longer in the BS group (10 vs. 8 days, P = 0.002, and 4 vs. 3 days, P < 0.001, respectively). On adjusted analysis, there were no differences in patient outcomes (Figure 2).

Conclusion. Among patients with HCAP started on empiric MRSA and PSA coverage without microbiological diagnosis, clinical outcomes were similar in patients switched to an NS antibiotic and those maintained on BS antibiotics. Our findings suggest a potential role for antimicrobial stewardship in promoting antibiotic de-escalation in this population.



Figure 2. Comparison of Outcomes in Patients with Healthcare-Associated Pneumonia and No Microbiological Diagnosis Maintained on Broad-Spectrum Antibiotics versus Switched to Narrow Spectrum Antibiotics

Variable	Broad-Spectrum Antibiotics (n=290)	Narrow-Spectrum Antibiotics (n=73)	Adjusted OR (95% CI)	Adjusted P-value
All-cause mortality at 30 days1	15 (5.2%)	3 (4.1%)	0.63 (0.20, 1.96)	0.4274
Pneumonia-related mortality at 30 days1	1 (0.3%)	0 (0.0%)		
All-cause readmission within 30 days1	69 (23.8%)	21 (28.8%)	0.80 (0.37, 1.74)	0.5697
Clostridium difficile infection ²	3 (1.0%)	0 (0.0%)		
Allergic reaction or adverse drug event ^{3,4}	11 (3.8%)	2 (2.7%)	3.41 (0.56, 21.01)	0.1852
Length of stay ³	5.00 (4.00-7.00)	4.00 (3.00-5.00)	1.09 (0.90, 1.32)	0.3665

Mortality and readmissions are adjusted for age, length of stay, Charlson, discharge to nursing home, insurance, days on IV therapy, CKD, antibiotic duration

(KD), antibotic duration (Costridium difficile rates are adjusted for age, history of antibiotic use (and number of antibiotics), transfer from skilled nursing facility, prior hospitalization, length of hospital stay, proton-pump inhibitor use, Charlson comorbidity index, days on IV therapy, CKD, antibiotic duration 2.3 down dwa sent and IOS are adjusted for are Charlson comorbidity index, used et due on IV therapy, CKD, antibiotic duration

antibitoti duration 7Ådverse drug events and LOS are adjusted for age, Charlson comorbidity index, gender, days on IV therapy, CKD, antibiotic duration ⁴Adverse drug events defined as rash, diarrhea, acute kidney injury, neutropenia, thrombocytopenia, allergic reaction

Disclosures. All authors: No reported disclosures.

871. Symptomatic Respiratory Syncytial Virus and Adenovirus Upper Respiratory Tract Infections Increase the Risk of Invasive Aspergillosis After Allogeneic Hematopoietic Cell Transplantation

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Session: 87. Respiratory Infections: An Update Thursday, October 4, 2018: 2:00 PM

Background. Invasive aspergillosis (IA) is a serious infectious complication following hematopoietic cell transplantation (HCT). Few studies have reported respiratory viral infections (RVIs) as a risk factor for developing IA, and data regarding specific viruses is sparse. We examined whether specific respiratory viruses were associated with increased risk of developing IA post-HCT.

Methods. In a longitudinal surveillance study of RVIs among allogeneic HCT recipients conducted 2005-2010, weekly post-HCT nasal washes were collected through 100, then every 3 months, and whenever respiratory symptoms occurred through 1 year post-HCT. Nasal and bronchoalveolar lavage (BAL) samples were tested by multiplex PCR for respiratory syncytial virus (RSV), parainfluenza viruses (PIV)1-4, influenza A/B, human metapneumovirus, adenovirus (ADV), and human rhinoviruses, and coronaviruses. Only respiratory virus detections with symptoms were counted as RVI. Separate Cox proportional hazards models were used to examine adjusted associations between each RVI and the development of first proven/probable IA by 1-year post-HCT.

Results. Among 437 patients who survived >28 days following HCT, 39 patients developed IA by 1-year post-HCT (median 87 days, range 5–283). After adjusting for age at HCT, neutropenia, high-grade CMV viremia, and HLA status (matched related vs. others) or severe acute graft-versus-host disease (GVHD Grade 0–2 vs. 3–4), RSV and ADV upper respiratory tract infections (URTI) were associated with increased risk of developing IA (figure). Detection of any respiratory virus in the BAL was associated with IA (P < 0.001).

Conclusion. RSV and ADV URTI are significant risk factors for development of IA post-HCT; the association between PIV URTI and development of IA approached statistical significance. Viral lower respiratory tract infection was associated with IA. Our data provide a rationale to assess IA as an endpoint in preventive studies of novel agents for respiratory viruses and further emphasize the importance of effective infection practices for RVIs after HCT.





Figure. Respiratory virus variables with p=0.2 in univariable analysis were evaluated as candidate risk factors for development of mostive apergalicis in reparted adjusted models. With 30 advances events, 5 aconatate were included in each adjusted models (including the virus) of interest). All models are adjusted for age at transplantation (~40 vs. >40), neutropenia (neutrophi court <900mm3 as time-dependent) and high-grade CMV viremia (viral lace) 1.000 UIIIn (FCP) or 10 p055-antigen politive esite perzy 2000 leuko/cyte k interesting time-dependent]. HLA status (matched related vs. others) (<u>A</u>) and severe acute graft-versus-host disease (Grade 0-2 vs.3-4 as timedependent).

Disclosures. J. Chien, Gilead Sciences, Inc.: Employee and Shareholder, Salary and stocks. A. Waghmare, Ablynx: Investigator, Research support. J. Englund, Gilead: Consultant and Investigator, Consulting fee and Research support. Novavax: Investigator, Research support. GlaxoSmithKline: Investigator, Research support. Alios: Investigator, Research support. MedImmune: Investigator, Research support. M. Boeckh, Asun Biopharma: Consultant and Investigator, Consulting fee and

This abstract has been withdrawn at the author's request.

Research support. Gilead Sciences: Consultant and Investigator, Consulting fee and Research support. Chimerix Inc.: Consultant and Investigator, Consulting fee and Research support. Humabs: Consultant, Consulting fee. GSK: Investigator, Research support.

872. PROPHETIC: Predicting Pneumonia in Hospitalized Patients in the ICU—A Model and Scoring System

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Session: 87. Respiratory Infections: An Update

Thursday, October 4, 2018: 2:00 PM

Background. Prospectively identifying patients at highest risk for hospital-acquired and ventilator-associated bacterial pneumonia (HABP/VABP) by implementing a risk assessment scoring tool may help focus prevention efforts, optimize the screening process to improve clinical trial feasibility, and enhance development of new antibacterial agents.

Methods. Within the intensive care units (ICU) of 28 US hospitals, between February 6, 2016 and October 7, 2016, patients hospitalized >48 hours and receiving high levels of respiratory support were prospectively followed for meeting the definition of HABP/VABP recommended in US FDA draft guidance. Patient demographics, medical comorbidities, and treatment exposures were recorded. The association between candidate risk factors and odds of developing HABP/VABP was evaluated with a multivariable logistic regression model. Risk factors were selected using backward selection with $\alpha = 0.1$ for model inclusion. A webbased scoring system was developed to estimate the risk of HABP/VABP from the risk factors identified.

Results. A total of 5,101 patients were enrolled, of whom 1,005 (20%) developed HABP/VABp. 4,613 patients were included in the model, excluding 488 (10%) with HABP/VABP at or before enrollment. There are 15 variables included in the model. APACHE II admission score >20 (P < 0.001, OR 2.14, 95% CI 2.00–2.29), admission diagnosis of trauma (P < 0.001, OR 3.31, 95% CI 1.90–5.74), frequent oral or lower respiratory tract suctioning (P < 0.001, OR 2.33, 95% CI 1.69–3.16) were the key drivers of increased pneumonia risk. The model demonstrated excellent discrimination (bias-corrected C-statistic 0.861, 95% CI 0.843–0.880). The web-based scoring system can be accessed via this link: https://ctti-habpvabp.shinyapps.io/web_based_tool/.

Conclusion. Using a web-based scoring system, ICU patients at highest risk for developing HABP/VABP can be accurately identified. Prospective implementation of this tool may assist in focusing additional prevention efforts on the highest risk patients and enhance new drug development for HABP/VABP.

Disclosures. S. P. Bergin, CTTI: Investigator and Scientific Advisor, Research support and Travel to study related meetings. A. Coles, CTTI: Investigator and Scientific Advisor, Salary. S. B. Calvert, CTTI: Employee, Salary. M. J. Zervos, CTTI: Investigator, Research support. A. C. Bardossy, CTTI: Investigator, Research support. M. Kollef, CTTI: Investigator, Research support. M. J. Durkin, CTTI: Investigator, Research support. M. Sims, CTTI: Investigator, Research support. C. Greenshields, CTTI: Investigator, Research support. B. A. Kabchi, CTTI: Investigator, Research support. H. K. Donnelly, CTTI: Collaborator and Scientific Advisor, Research support and Salary. P. Tenaerts, CTTI: Employee, Salary. P. Gu, CTTI: Collaborator, Research support and Salary. V. G. Fowler Jr., CTTI: Investigator and Scientific Advisor, Research support and Salary. Merck: Consultant, Grant Investigator and Scientific Advisor, Consulting fee, Grant recipient and Research support. Cerexa/ Actavis/Allegan: Grant Investigator, Grant recipient. Pfizer: Consultant and Grant Investigator, Consulting fee and Grant recipient. Advanced Liquid Logics: Grant Investigator, Grant recipient. NIH: Investigator, Grant recipient, Research support and Salary. MedImmune: Consultant and Grant Investigator, Consulting fee and Grant recipient. Basilea: Consultant and Grant Investigator, Consulting fee and Grant recipient. Karius: Grant Investigator, Grant recipient. Contrafect: Consultant and Grant Investigator, Consulting fee and Grant recipient. Regeneron: Grant Investigator, Grant recipient. Genentech: Consultant and Grant Investigator, Consulting fee and Grant recipient. Achaogen: Consultant, Consulting fee. Astellas: Consultant, Consulting fee. Arsanis: Consultant, Consulting fee. Affinergy: Consultant, Consulting fee. Bayer: Consultant, Consulting fee. Cerexa: Consultant, Consulting fee. Cubist: Consultant, Consulting fee. Debiopharm: Consultant, Consulting fee. Durata: Consultant, Consulting fee. Grifols: Consultant, Consulting

fee. Medicines Co.: Consultant, Consulting fee. Novartis: Consultant, Consulting fee. Novadigm: Consultant, Consulting fee. Theravance: Consultant, Consulting fee and Speaker honorarium. XBiotech: Consultant, Consulting fee. Green Cross: Consultant, Speaker honorarium. **T. L. Holland**, CTTI: Investigator and Scientific Advisor, Research support and Salary.

873. Using the Host Immune Response to Identify Viral-Bacterial Coinfection in Children With Respiratory Syncytial Virus Infection

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Session: 87. Respiratory Infections: An Update Thursday, October 4, 2018: 2:00 PM

Background. A major challenge in the effective management of children with RSV infection is the clinical difficulty of distinguishing a simple viral from viral-bacterial coinfections. As a result, despite the low rates of viral-bacterial coinfection, RSV patients are often prescribed antibiotics with recent reports demonstrating more than 60% antibiotic overuse rates (Van Houten et al. 2018). Here, we examined whether a host-immune signature combining the viral-induced proteins TRALL and IP-10 with the bacterial-induced protein CRP (ImmunoXpert; Oved et al. 2015) can distinguish simple viral from viral-bacterial coinfection in RSV patients.

Methods. We studied 402 febrile children enrolled as part of "Curiosity," a prospective study designed to develop and validate the host-immune signature. Infection etiology—viral or viral-bacterial coinfection—was determined by a panel of experts following a review of patients' clinical, laboratory, radiological, microbiological, and follow-up data. RSV strains were detected using a respiratory multiplex PCR applied to nasal swabs (Seeplex-RV15).

Results. Out of the 402 children with suspected acute infection 29 had a positive RSV detection (Figure 1); of them, 27 had a unanimous expert panel etiology determination: 24 viral and 3 viral-bacterial coinfections. Out of the 24 patients unanimously assigned viral by the expert panel, 13 were given antibiotics, indicating a 54% antibiotic overuse rate. The host-immune signature correctly identified all 3 viral-bacterial coinfection cases, as well as 22 out of the 24 (92%) simple viral patients. This finding supports that the signature has the potential to reduce antibiotic overuse by 6.5-fold (from an overuse of 13/24 = 54% to 2/24 = 8%, P < 0.001).

Conclusion. Our results demonstrate high antibiotic overuse rates for RSV patients, consistent with previous reports. The host-immune signature correctly distinguished simple viral from viral-bacterial coinfection and therefore may have the potential to aid physicians in the correct management of children with RSV infection. Implementation studies are required to evaluate its utility in safely decreasing unnecessary antibiotic use for RSV patients.



Figure 1. Recruitment and flow of pediatric patients with positive RSV detection

Flow diagram is in line with the Standards for Reporting Diagnostic Accuracy (STARD); RSV – respiratory syncytial virus, Abx – antibiotic treatment, TP – true positive, PP – false positive, TN – true negative, FN – false negative. The index test is available in Europe as ImmunoXpert (CE-IVD), not yet cleared by the FDA.