

obtained from a centralized, enterprise data warehouse. The study was approved by the University of Tennessee Health Science Center Institutional Review Board.

Results. A total of 1,005,377 patients on antibiotics from 136 facilities were included. Procalcitonin levels were evaluated for 103,913 of these patients. Within the procalcitonin group, 96% had their first procalcitonin drawn within 36 hours of the first antibiotic dose and 70% of patients had a single procalcitonin level drawn. Of those with multiple levels, 23% had levels drawn 24–72 hours apart. Only 32% had antibiotic therapy discontinued within 36 hours of meeting threshold.

Conclusion. There is wide variability among facilities regarding procalcitonin use and monitoring. Baseline procalcitonin levels were drawn appropriately for most patients. Opportunities exist to standardize monitoring and encourage discontinuation of antibiotics when thresholds are reached. The findings of this analysis will be used to aid efforts to establish a health-system wide procalcitonin monitoring protocol to support antibiotic and laboratory stewardship.

Disclosures. All authors: No reported disclosures.

2014. TLDA Validation of a Host Response Signature to Discriminate Bacterial, Viral, and Non-infectious Causes of Illness

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Background. Bacterial and viral infections are difficult to clinically distinguish, leading to antibiotic overuse and resistance. Host response signatures are an alternative to traditional pathogen-detection methods to differentiate these etiologies. Several gene expression signatures have been described although performance in ambiguous clinical phenotypes is unknown. Here, we validate a host response signature and explore its performance in microbiology-negative and co-infection cases.

Methods. RT-PCR taqman low-density array (TLDA) was used to measure 87 gene targets in a training cohort of 151 samples from patients with microbiologically confirmed and clinically adjudicated phenotypes (48 bacterial; 54 viral; 49 non-infectious illness [NI]). This data were used to construct three distinct classifiers: bacterial vs. nonbacterial; viral vs. nonviral; and non-infectious vs. infectious. This model was then applied to 75 subjects with co-infection and 40 suspected bacterial cases without microbiological confirmation.

Results. Leave-one-out cross validation on the training cohort demonstrated AUC values of 0.85, 0.89, and 0.88 for bacterial, viral, and NI, respectively. In 40 subjects with microbiology-negative bacterial infections, a bacterial or co-infection signature was present in 72%. Of 75 subjects with co-infection, 53 included a bacterial infection following recent viral infection and 22 were bacterial infections in patients with chronic viral infection (e.g., HCV, HIV). Bacterial infection and co-infection were successfully identified in these varied scenarios.

Conclusion. This gene expression signature distinguished bacterial, viral, and noninfectious causes of illness. The host response was able to confirm the majority of suspected bacterial infection without confirmatory microbiology but also highlighted a viral response in many. Furthermore, the use of distinct viral and bacterial signatures was capable of identifying co-infection. Such a host gene expression strategy, when translated to a clinically useful platform, can offer new insights into the etiology of both simple and complex cases that are not currently available.

Disclosures. G. S. Ginsburg, Host Response Inc.: Board Member, Founder, Scientific Advisor and Shareholder, Stock (currently worth <\$100). C. W. Woods, Host Response: Founder, Licensing agreement or royalty; Qvella: Collaborator, Research support; BioFire: Collaborator, none. E. L. Tsalik, Host Response, Inc.: Founder, Equity.

2015. Host Gene Expression Identifies Infectious Triggers of Asthma Exacerbation

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Background. Asthma exacerbations often occur due to infectious triggers. However, determining whether an infection is present and whether it is bacterial or viral remains clinically challenging leading to antibiotic overuse. A diagnostic strategy that clarifies these uncertainties can enable personalized asthma treatment and mitigate antibiotic resistance. Host gene expression is a promising alternative to pathogen-detection methods.

Methods. Forty-six patients presenting to the emergency department with asthma exacerbations were enrolled. Cases were clinically adjudicated as having bacterial, viral, or non-infectious etiologies. RT-PCR taqman low density array (TLDA) was used to quantify 87 gene targets, followed by logistic regression modeling to define

class. Etiologies were correlated with clinical information including symptoms and antibiotic prescriptions.

Results. Most clinical parameters were similar between groups including duration of symptoms, presence of sick contacts, and severity of nasal symptoms, cough, headache, throat discomfort, and malaise. Only fever/chills ($P = 0.006$) and a composite of all symptoms ($P = 0.02$) were significantly different. In contrast to clinically adjudicated phenotypes, host response signatures identified very few bacterial triggers. Notably, none of the adjudicated bacterial cases had positive confirmatory microbiology. Instead, 29 and 57% were identified as having a viral infection or no infection, respectively. Despite the absence of bacterial infections identified using host gene expression, antibiotics were prescribed in 47.8% of all cases.

Conclusion. Host response signatures indicated that asthma exacerbation is infrequently caused by bacterial infections, even when clinical adjudications suggest this to be the case. Instead, most are either of viral or non-infectious etiologies. Despite most cases being classified as nonbacterial, empiric antibiotics were prescribed nearly half the time. A host gene expression approach can offer clinically useful diagnostic information to guide more appropriate antibiotic use among patients with asthma exacerbation.

Disclosures. G. S. Ginsburg, Host Response Inc.: Board Member, Founder, Scientific Advisor and Shareholder, Stock (currently worth <\$100). C. W. Woods, Host Response: Founder, Licensing agreement or royalty; Qvella: Collaborator, Research support; BioFire: Collaborator, none. E. L. Tsalik, Host Response, Inc.: Founder, Equity.

2016. TaqMan Multiplex PCR of a Seven-Gene Host Biomarker to Discriminate Bacterial from Viral Infections

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Background. Acute infections are among the most frequent diagnoses in outpatient care settings. Early, accurate and rapid differentiation between viral and bacterial infections is critical to guide the choice of antimicrobial treatment, improve patient outcome, and to ensure antimicrobial stewardship. Current microbiological offerings rely on direct pathogen detection, which is limited by insufficient accuracy. Recently, host response-based molecular diagnostics have been considered as a novel alternative or complementary approach. We have previously developed and validated a seven-gene signature set (higher in viral infections (*IFI272*, *JUP*, and *LAX1*) and higher in bacterial infection (*HK3*, *TNIP1*, *GPAA1*, and *CTSB*) that accurately discriminated between viral and bacterial infections (in six validation cohorts, summary ROC AUC of 0.91 (95% CI, 0.82–0.96). We here describe the development of a rapid multiplex HostDx™ Fever, a seven-gene host response biomarker PCR assay that discriminates bacterial from viral infections.

Methods. To translate the microarray-derived gene set into a rapid and easy to use assay to be run on an automated PCR instrument, TaqMan assays were designed, multiplexed and optimized for each of the seven targets. Data were then compared with NanoString and an ultrafast qPCR platform, respectively.

Results. Seven TaqMan assays were divided into two multiplex reactions, one 5-plex and one 4-plex. KPNA6 was included as housekeeping control in each of the two multiplexes. Ten clinical samples from healthy subjects (3) or patients with confirmed viral (4) or bacterial (3) infections were tested in parallel on three platforms: regular qPCR, an ultrafast qPCR and NanoString platform. We found a high degree of concordance with $R > 0.95$ between TaqMan and NanoString platforms, and $R > 0.94$ between TaqMan and the ultrafast qPCR platform. Ultrafast qPCR results were obtained in 12 minutes.

Conclusion. The discovered seven-gene set was validated and allows for robust discrimination between bacterial and viral infections. Multiplexing permits are more cost-effective method of testing. As a rapid test, HostDx™ Fever could assist in improved decision making for outpatients with suspected acute infections.

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2017. Improving Timely Diagnosis of Meningitis and Encephalitis: The Effectiveness of Online CME

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Background. Timely and accurate diagnosis of meningitis and encephalitis not only guides the patient care strategy, but can reduce inappropriate antibiotic use, support antimicrobial stewardship, shorten hospital stays, and decrease morbidity and mortality.

Methods. To address knowledge and competence gaps among ID specialists, a CME/CE-certified. Thirty-minute, video-based, multidisciplinary panel discussion