1177. Meteorology-driven Prediction of RSV/RHV Incidence in Rural Nepal
Anna Scott, MS1, Janet Englund, MD, FIDSA2, Helen Chu, MD MPH3, James Tielsch, PhD4, James Tielsch, PhD5, Subarna Khatry, MBBS, DOMS5, Steven C Leclerc, MPH6, Laxman Shrestha, MBBS, MD7, Jane Kuypers, PhD7, Mark C. Steinhoff, MD, FIDSA8 and Joanne Katz, ScD9; Johns Hopkins University, Baltimore, Maryland, 1University of Washington/Seattle Children's Hospital, Seattle, Washington, 2Global Health, George Washington University, Washington, DC, 3NNIPS, Kathmandu, Nepal, 4NNIPS, Baltimore, Maryland, 5Pediatrics and Child Health, Institute of Medicine, Tribhuvan University, Kathmandu, Nepal, 6Laboratory Medicine, University of Washington, Seattle, Washington, 7Division of Infectious Diseases, Global Health Center, Cincinnati Children's Hospital Medical Center, Cincinnati, Ohio

Session: 145. Diagnostics: Viral
Friday, October 6, 2017: 12:30 PM

Background. Incidence of respiratory syncytial virus (RSV) and rhinovirus (RHV) varies throughout the year. We aim to quantify the relationship between weather variables (temperature, humidity, precipitation, and aerosol concentration) and disease incidence in order to quantify how outbreaks of RSV and RHV are related to seasonal or sub-seasonal meteorology, and if these relationships can predict viral outbreaks of RSV and RHV.

Methods. Health data were collected in a community-based, prospective randomized trial of maternal influenza immunization of pregnant women and their infants conducted in rural Nepal from 2011–2014. Adult illness episodes were defined as fever plus cough, sore throat, runny nose, and/or myalgia, with infant illness defined similarly but without fever requirement. Cases were identified through longitudinal household-based weekly surveillance. Temperature, humidity, precipitation, and fine particulate matter (PM 2.5) data came from reanalysis data products NCEP, Era-Interim, and Merra-2, which are produced by assimilating historical in-situ and satellite-based observations into a weather model.

Results. RSV exhibits a relationship with temperature after removing the seasonal cycle (r = -0.16, N = 208, P = 0.02), and RHV exhibits a strong relationship to daily temperature (r = -0.14, N = 208, P = 0.05). When lagging meteorology by up to 15 weeks, correlations with disease count and weather improve (RSV: r_max = 0.45, P < 0.05; RHV: r_max = 0.15, P = 0.05). We use an SIR model forced by lagged meteorological variables to predict RSV and RHV, suggesting that disease burden can be predicted at lead times of weeks to months.

Conclusion. Meteorological variables are associated with RSV and RHV incidence in rural Nepal and can be used to drive predictive models with a lead time of several months.

Disclosures. J. Englund, Gilead: Consultant and Investigator, Research support Chimerix: Investigator, Research support support Ailios: Investigator, Research support support Novavax: Investigator, Research support Mediumimmune: Investigator, Research support GlaxoSmithKline: Investigator, Research support

1178. Feasibility and Validation of Viral Respiratory Disease Surveillance in a Combat Theater Using the FilmArray Respiratory Panel
Ryan Maves, MD, FCFP, FIDSA1,2; Derek Larson, DO2; Michael Dempsey, PhD2,3, Benjamin Connors, MS2, James Baldwin, PhD2,3, Richard Thomas, MS2, and Clarise Stare, PhD2,3; Division of Infectious Diseases, Naval Medical Center San Diego, San Diego, California, 1NATO Role 3 Multinational Medical Unit, Kandahar Airfield, Afghanistan, 2Applied Technology Center, USAF School of Aerospace Medicine, Wright-Patterson AFB, Ohio

Session: 145. Diagnostics: Viral
Friday, October 6, 2017: 12:30 PM

Background. Viral respiratory infections are a significant threat to deployed military units. Pathogen-based surveillance may be hampered by limitations in trained personnel in theater, difficulty with specimen shipment, and technical issues with equipment maintenance. In this project, we evaluated the performance of the FilmArray respiratory panel at military clinics in Afghanistan and compare results to testing performed in the United States.

Methods. Participants were recruited after presenting at military clinics at Bagram Airfield (BAF), Afghanistan, in 2013–2014 with fever (≥38° C) and respiratory symptoms (cough, dyspnea, chest pain, and/or sore throat). General medical laboratory staff at BAF were trained to operate the FilmArray; nasopharyngeal swabs were obtained and tested in-theater using the FilmArray respiratory panel (Biofire Diagnostics, Salt Lake City, UT). Samples were then shipped to the USAF/AF Hospital Technology Center in 50% RNA Later (Qiagen, Valencia, CA) without dry ice and then retested using the same panel. Selected influenza isolates then underwent sequencing to evaluate for potential novel circulating strains.

Results. 29 specimens underwent testing. A virus was identified on FilmArray 22/29 specimens at BAF and 24/29 specimens at USAFSAM, of whom 17/29 had influenza A. Positive results between BAF and USAFSAM were concordant in all cases; 2 of the negative results at BAF were identified as having influenza A and rhinovirus respectively. Among those with influenza A, one BAF specimen exhibited a strong seasonal influenza vaccination 5 influenza isolates then underwent sequencing; 2 were A(H1N1pdm09) consistent with the predominant 2012–2013 strain, while 3 were A(H3N2) viruses with HA mutations that differed from those in the 2013–2014 vaccine strain. No resistance-associated neuraminidase mutations were identified.

Conclusion. Surveillance using the FilmArray system is effective and feasible in theater by general laboratory staff. H1N1 and H3N2 influenza A viruses predominated in this sample of acute respiratory infections in a deployed military setting despite high vaccination rates. The use of the RNA Later preservative is an effective method for specimen transport without requiring a cold chain and may facilitate biosurveillance in remote settings.

Disclosures. All authors: No reported disclosures.

1179. Experience of Sublingual Microcirculation Evaluation in Adults Patients with Severe Dengue
Fernando Rosso, MD, MSc1, Gustavo Osponsa, MD, PhD2, Edgardo Quiñones, MD3 and Ana María Sanz, MD4; ID Service, Fundación Valle del Lili, Cali, Colombia, 2CCM Service, Fundación Valle del Lili, Cali, Colombia, 3Fundación Valle del Lili, Cali, Colombia

Session: 145. Diagnostics: Viral
Friday, October 6, 2017: 12:30 PM

Background. Severe microcirculatory changes are involved in the pathophysiological mechanisms that lead to irreversible final stages of dengue shock. We report our experience of the evaluation of sublingual microcirculation in adult patients with severe dengue

Methods. Adults patients with severe dengue (by WHO 2009 criteria) were included. Sublingual microcirculatory imaging was made by positive serology for IgM / IgG, antigen NS1 or PCR. Sublingual Microcirculation (SM) was evaluated by Sidestream Dark Field imaging. Microvascular flow index (MFI), proportion of small-perfused vessels (%MVP), heterogeneity index (HI) and Total Vascular Density were calculated. All patients received Fluids Challenge (FC) at hospital admission.

Results. 5 patients were included. The median age was 65 years [IQR: 34–70], 60% were male. Eight patients were admitted to the ICU, of which 63% required invasive ventilatory and vasosupportive. One patient died. After the fluid challenge, the median of the %MVP was 94 [IR: 86 – 97], the median of the MFI was 2.82 [IR: 2.45 – 2.14]. There were not significant differences in %MVP and MFI among the patients who survived. In the deceased patient, the %MVP with continuous flow was 59, 18% and the MFI was 1, 45; these values were significantly decreased compared with patients who survived. A significant negative correlation between hematocrit and %MVP and MFI was found.

Conclusion. Initial fluid challenge, that identifies and treats volume depletion, could correct microcirculation abnormalities evaluated by SDF imaging. However, in the patient who did not respond to this challenge, significant alterations of the MFI and the %MVP were evidenced. There is a need for more studies to improve our understanding of the role of microcirculation evaluation in these patients.

Disclosures. All authors: No reported disclosures.

1180. Identifying Enteropathogens in Children with Acute Gastroenteritis Presenting with Isolated Vomiting–Appetite Study
Bonita Lee, MD MSc (Eps)1; Xiao-Li Fang, PhD2; Ran Zhou, PhD3; Brendan Parsons, PhD4; Linda Chui, PhD2; Janilong Xie, MD, MPH1, Karen Lowerison, AHT5; Lara Osterreicher, RN6; Samina Ali, MDCM2; Stephen Freedman, MDCM2 and
APPETITE (Alberta Provincial Pediatric Enteric Infection Team); 1Pediatrics, University of Alberta, Edmonton, AB, Canada; 2University of Alberta, Edmonton, AB, Canada; 3Laboratory Medicine and Pathology, University of Alberta, Edmonton, AB, Canada; 4Alberta Children’s Hospital, Calgary, AB, Canada; 5University of Calgary, Calgary, AB, Canada; 6Alberta Health Services, Calgary, AB, Canada; Session: 146. Enteric Infections and Diagnostics
Friday, October 6, 2017: 12:30 PM

**Background.** As diarrheal stool samples are the recommended specimen for test-
ing in acute gastroenteritis (AGE), etiological investigations are rarely performed in children presenting with isolated vomiting. This study identifies enteropathogens in children with AGE presenting with isolated vomiting.

**Methods.** Children <18 years old with ≥3 episodes of vomiting/diarrhea in 24 hours and <7 days of symptoms were recruited in 2 pediatric emergency departments, a public health clinic and via Health Link, a provincial nurse advice phone line. Rectal swabs and stool samples were collected and tested using the Luminox xTAG GPP, an in-house 5-virus RT-qPCR panel and enteric bacterial culture. Vomiting and diarrhea data were collected at enrollment (day 0) and at day 14.

**Results.** Between Dec 9, 2014 and Apr 14, 2016, 2,184 children were enrolled and tested; 784 (36%) presented with isolated vomiting, 250 (11%) with isolated diarrhea (ID), 1,138 (52%) with both vomiting and diarrhea (V&D), 12 had missing data. The detection of enteropathogens was 56% when presenting with isolated vomiting, 55% with ID and 83% with V&D. Of the 784 children with isolated vomiting, 54% (n = 424) had one or more viruses: the most common was norovirus (NoV) (n = 244, 50%), followed by adenovirus (Adv) (91, 19%), rotavirus (Rot) (35, 12%), sapovirus (84, 17%) and astrovirus (10, 2%). Fifty-eight cases had >1 virus; co-infection with NoV and Adv was the most common (n = 23). Ten of these 424 patients also had enteric bacteria (2 Aeromonas, 2 ETEC, 2 Salmonella, 2 Verminia, 1 Campylobacter, 1 E. coli O157) and 8/9 (89%) of these patients reported development of diarrhea at day 14. In comparison, 212/383 (55%) of patients with virus only reported diarrhea at follow up. Enteric bacteria with no virus was detected in 11 patients (3 Aeromonas, 2 ETEC, 2 Salmonella, 2 verminia, 2 Campylobacter, 1 E. coli O157) and 3/10 of these patients reported diarrhea.

**Conclusion.** Over 50% of AGE presented with isolated vomiting had enteric virus identified in stool or rectal swabs, representing a significant pathogen-based disease burden not previously included in healthcare planning (e.g., Rota vaccine). NoV was the predominant agent followed by Adv and Rot. Finding enteric bacteria in these cases is novel and requires further study.

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

### 1181. Enteropathogen Identification by Multiplex PCR in Guatemalan Children with Acute, Non-bloody Diarrhea

**Mario Melgar, MD**; 1Molly Lamb, PhD; 1Diva M Calvimontes, MD; 1Edwin J Asturias, MD; 2Ingrid Contreras-Roldan, MD; 3Samuel Dominguez, MD, PhD; 4Christine C. Robinson, PhD; 2Stephen Berman, MD; 2James Gaensbauer, MD, MSCHP; 3Centro De Estudios En Salud, Universidad del Valle de Guatemala, Guatemala City, Guatemala; 4Hospital Roosevelt, Guatemala City, Guatemala; 5Center for Global Health and Department of Epidemiology, Colorado School of Public Health, Aurora, Colorado; 6Department of Epidemiology, Colorado School of Public Health, Aurora, Colorado; 7Department of Pediatrics, University of Colorado School of Medicine, Aurora, Colorado; 8Universidad del Valle de Guatemala, Guatemala City, Guatemala; 9Department of Pathology and Laboratory Medicine, Children’s Hospital Colorado, Aurora, Colorado; 10Infectious Diseases, Department of Pediatrics, University of Colorado School of Medicine, Aurora, Colorado; 11Pediatric Infectious Disease, Denver Health and Hospital Authority, Denver, Colorado; Session: 146. Enteric Infections and Diagnostics
Friday, October 6, 2017: 12:30 PM

**Background.** Diarrhea is a leading cause of morbidity and mortality in children in low and middle income countries (LMICs). Assessing diarrhea etiology in LMICs is of great importance in order to better develop both therapeutic and public health strategies, but is hampered by the complexity of potential diarrheal pathogens, and diverse methodology needed for pathogen identification.

**Methods.** Subjects 6 to 35 months old with acute, moderate severity, non-bloody diarrhea were enrolled in a diarrheal treatment trial, conducted at one rural (N = 172) and two urban sites (N = 144) in Guatemala. Diarrheal pathogens were determined in stool by multiplex PCR (FilmArray GI™ Biofire) which allows simultaneous identification of 23 bacterial, viral, parasitic pathogens. Descriptive statistics on demographics, pathogen load, and differences in pathogen occurrence by site were performed; differences were assessed with t-test and chi² test.

**Results.** Nearly all (96.6%) subjects had pathogens identified, and most had multiple potential pathogens identified (mean pathogen count: 2.7 urban and 4.8 rural, P < 0.001 (Figure 1). Notable pathogen differences were observed between rural and urban populations. Bacteria (particularly E.coli pathotypes and Campylobacter) and protozoa (particularly giardia) were more common in the rural population (Figure 2). Viral pathogens were either similar or more common (norovirus; P = 0.04) in the urban population; rotavirus was uncommon in both sites (10 rural and 12 urban cases). A similar pattern of pathogen evolution with patient age was noted in both settings, with a decrease in the relative number of viral and increase in parasitic pathogens (Figure 3). Important demographic and socioeconomic differences between rural and urban noted: rural subjects had poorer nutritional status, underdeveloped water and sanitation facilities and more domestic animal exposure.

**Conclusion.** Acute diarrheal episodes in Guatemalan children were associated with a complex spectrum of pathogens when determined by multiplex PCR, with distinct patterns in rural and urban populations. Future studies to precisely determine diarrheal etiologies in LMICs will need to incorporate controls to sort causative organisms from those colonizing the intestine.

### 1182. Appropriateness of a Rapid Multiplex Gastrointestinal Panel in the Investigation of Suspected Infectious Diarrhea After Implementation at an Academic Medical Center

**Norman Beatty, MD**; 1David Nix, PharmD; 2Jessica August, MD; 2Roberto Swazo, MD; 2Janame Kottry, MD; 3Kyle Mceown, MPH; 4Mohammad Alshibani, PharmD; 5Wanda Fety, BS; 5Kathryn Matthias, PharmD and 5Mayar Al Mohajer, MD, MBA, CAQ, FACP; 6Internal Medicine, University of Arizona College of Medicine at South Campus, Tucson, Arizona; 7Department of Pharmacy Practice and Science, University of Arizona College of Pharmacy, Tucson, Arizona; 8University of Arizona College of Medicine, Tucson, Arizona; 9College of Pharmacy, King Abdullah University of Science and Technology, Jeddah, Saudi Arabia; 10Department of Pathology; Banner University Medical Center, Tucson, Arizona; 11Department of Medicine, Division of Infectious Diseases, Baylor College of Medicine, Houston, Texas; Session: 146. Enteric Infections and Diagnostics
Friday, October 6, 2017: 12:30 PM

**Background.** The BioFire FilmArray™ Gastrointestinal (GI) Panel is a 1 hour multiplex real-time PCR test that can detect the presence of 22 GI pathogens (viral, bacterial, and parasitic) known to cause infectious diarrhea. Our tertiary-care academic medical center implemented the GI Panel for all cases of suspected infectious diarrhea replacing the previous conventional testing once utilized to detect GI pathogens. Since its implementation we have not had any criteria for ordering this test to aid healthcare providers.

The aim of this IRB approved, retrospective investigation was to determine the appropriateness of ordering the GI panel at our academic institution. Cases were randomly selected, stratified by age group and result (specific pathogens or negative result) from May 2015 through April 2016 in the post-implementation period (n = 400 of 1117 total tests). We developed appropriateness criteria for ordering the GI panel which included: passage of at least 3 unformed stools in 24 hours plus one