2014 APHL Annual Meeting
Little Rock, AR – June 1-4, 2014

Poster Winner and Honorable Mentions

Poster Winner

Building DNA Sequencing Capacity for Hepatitis C Virus: Application to a Hepatitis C Outbreak at a Local Hospital Cardiac Catheterization Laboratory in New Hampshire, 2012

F. Gao[1], JC. Mahoney[1], S. Alroy-Preis[2], J. Forbi[3], J. Li[1], J. Dionne-Odom[2], G. Xia[3], C. Loring[1], E.A. Talbot[2], Y. Khudyakov[3], E.R. Daly[2], A. Vazquez[1], J. Drobeniuc[3], E.E. Metcalf[2], S Kamili[3], C. Adamski[2] , C. Teo[3], C. Bean[1]; [1]Public Health Laboratories, [2]Bureau of Infectious Disease Control, New Hampshire Division of Public Health Services, Concord, NH, [3]Division of Viral Hepatitis Laboratory, Centers for Disease Control and Prevention, Atlanta, GA

Background: DNA sequencing of specific targets in the hepatitis C virus (HCV) genome can identify linked cases during an outbreak. On May 15, 2012, a potential HCV outbreak associated with a hospital Cardiac Catheterization Laboratory (CCL) was reported.
Methods: Patients who received care and hospital employees who worked in the CCL between October 1, 2010 and May 25, 2012 were tested for anti-HCV by EIA and HCV RNA by RT-PCR. Sequencing of HCV NS5b region and hypervariable region 1 (HVR1) was performed at the New Hampshire Public Health Laboratories (NH PHL). Quasispecies analysis of HVR1 was conducted at the Division of Viral Hepatitis Laboratory, CDC.
Results: A total of 1142 individuals including 1066 patients and 76 employees were screened for HCV infection; of these 52 individuals (50 patients and two employees) were HCV RNA positive. Phylogenetic analysis of HVR1 sequences and quasispecies analysis of HVR1 confirmed that 32 patients and one employee were associated with the outbreak. The epidemiological investigation indicated that the HCV transmission was through drug diversion by one HCV-infected CCL employee.
Conclusion: DNA sequencing of HCV HVR1 is a useful tool to confirm HCV transmission. Building this capacity at the state levels is crucial for early identification and control of HCV outbreaks.

Presenter: Fengxiang Gao, MD, MS, MPH, Microbiologist V, Chief, Virology and Molecular Diagnostics Section Public Health Laboratories New Hampshire Department of Health and Human Services, 29 Hazen Drive, Concord, NH 03301, Phone: 603.271.2497, Email: Fgao@dhhs.state.nh.us

Honorable Mention

Classifying Picornavirus-Positive Specimens from Unexplained Deaths in Minnesota

R. Reneau, L. Carroll, E. Cebelinski and S.Vetter, Minnesota Department of Health, St. Paul, MN

Objective: The Unexplained Death Program (UNEX) tests specimens from patients with unexplained deaths of which an infectious agent is the suspected etiology. A picornavirus detection assay is often performed in cases involving respiratory symptoms. However, since the picornavirus family encompasses many species, it was unknown what proportion of positive specimens are from significant pathogens.

Study Design: 110 UNEX upper respiratory specimens from 2005-2013 that previously tested positive for picornavirus RNA by PCR were further characterized for rhinovirus, enterovirus, and parechovirus. Viral RNA was re-extracted from the UNEX specimens and was tested using rhinovirus, enterovirus, and parechovirus-specific reverse transcriptase real-time PCR (rRT-PCR) assays. Specimens negative for all three types of viral RNA were tested using a conventional picornavirus-specific PCR assay to confirm the presence of picornavirus RNA. The picornavirus PCR products were then purified, sequenced, and identified using the Basic Local Alignment Search Tool (BLAST).

Results: Of the 110 specimens, 70% (77) had detectable RNA for at least one virus; rhinovirus RNA was found in 50% (55), 4% (5) were positive of enterovirus, and 3% (3) were positive for parechovirus. 8% (9) were positive for both rhinovirus and enterovirus, 4% (4) were positive for both rhinovirus and parechovirus, and 1% (1) was positive for rhinovirus, enterovirus, and parechovirus. 11% of the specimens were either negative or not tested. 19% (21) were negative for all three viral types but were confirmed picornavirus positive. Preliminary sequence data of PCR products from the uncharacterized picornavirus PCRs suggest the unknown specimens could be rhinoviruses.

Conclusions: 70% of specimens were classified into at least one of three significant pathogens. Though, since 19% of these specimens are yet unknown picornaviruses, these data demonstrate limitations in the current assays used for testing and suggest that updated rRT-PCR methods and testing algorithms should be developed to improve the quality and accuracy of the data produced. Improved testing will help bolster surveillance efforts and define the viral types causing morbidity and mortality in Minnesota.

Presenter: Rachelle Reneau, APHL-CDC EID Training Fellow, Public Health Laboratory Division, Minnesota Department of Health, Phone: 651.201.5033, Email: rachelle.reneau@state.mn.us

Honorable Mention

Awareness and Opportunities in Public Health Laboratory Careers – Value of a Laboratory System Improvement Program (L-SIP) in Bridging Workforce Development Gaps among Stakeholders

S. Gradus, K. Owusu-Ofori, J. Becker and S. Bhattacharyya, Milwaukee Public Health Laboratory, Milwaukee, WI

Objective: This APHL grant-funded study aimed to engage the L-SIP community in the Greater Milwaukee Area in activities that raise the awareness of laboratory careers and develop strategies for workforce development in our local public health laboratory (LPHL) system.
Study Design: We hosted a one-day career fair for local college and high school students to gather information about their current awareness levels of careers in the LPHL system. Students from high school, local colleges and universities were invited to attend a series of 15 minute presentations by 15 local professionals and educators from a wide variety of laboratory fields. Surveys were taken before and after the career fair to determine the immediate impact of the event. Also an L-SIP Workforce Development (WFD) committee met to further analyze the career forum data and identify key gaps in laboratory career awareness and training that may hinder a student's transition from college graduation to a career in the laboratory sciences.
Results: Students attending the career fair reported a low initial awareness of viable career options in the Milwaukee LPHL system. However, after a "round robin" of short talks held by local laboratory professionals (e.g. medical examiner, crime lab, clinical and environmental microbiologists), students showed a significant increase in their knowledge and awareness of public health laboratory science careers. Students' surveys measured positive feedback regarding the career opportunities that were presented. The WFD committee meeting further addressed the need for transition from college to career through informational presentations, brainstorming sessions, and affinity diagrams that identified access to internships as a key gap in laboratory training and career option awareness. The career fair and WFD committee meeting outcomes resulted in MHDL efforts to standardize internship programs for the local emerging laboratory workforce.
Conclusions: A career fair can be used to identify and address gaps in awareness about laboratory career options in the LPHL system. Additionally, L-SIP can be used to understand and address gaps in laboratory training in a PHL system.

Presenter: Stephen Gradus, PhD, City of Milwaukee Health Department, Public Health Laboratory, Milwaukee, WI, Phone: 414.286.3909, Email: sgradu@milwaukee.gov