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The prevalence of norovirus in the MAL-ED cohort

M. McGrath¹, J. Seidman^{1,*}, M. Nelson², D. Lang³, J. Gratz⁴, S. Knobler¹, J. Platts-Mills⁴, E. Houpt⁴

¹ Fogarty International Center, Bethesda, USA² National Institutes of Health, Bethesda, USA³ Foundations of the National Institutes of Health, Bethesda, USA⁴ Division of Infectious Diseases and International Health, Charlottesville, USA

Background: Norovirus (NRV) is an important cause of gastroenteritis in children in developed countries. The genus NRV has extensive genetic diversity and is divided into at least two genogroups, I (GI) and II (GII) based on sequence analysis of genes encoding structural and nonstructural proteins. The MAL-ED Study is a longitudinal study at eight geographically diverse sites to describe the pattern of nutritional, enteric disease and other factors influencing childhood growth and development from birth to two years of age. We determined the prevalence of NRV GI and GII in diarrheal and non-diarrheal stool samples among children enrolled from 2009 to 2012.

Methods & Materials: Non-diarrheal stool samples were collected on the monthly anniversary of the child's birth, and diarrheal stool samples were collected for each diarrhea episode experienced by a child for two years. RNA extraction and a real-time PCR assay were used for the identification of NRV. In a pilot study, the whole genomes of 94 NRV-positive samples from Bangladesh were sequenced (~7.5 kb) to identify the genetic diversity of the virus circulating within a defined human population.

Results: 7,819 diarrhea and 4,300 non-diarrhea stool samples were tested for NRV: 20.3% of non-diarrhea samples tested positive for NRV; 5.7% tested positive for NRV GI and 15.6% tested positive for NRV GII. Among diarrheal stool samples, 23.3% tested positive for NRV with 5.8% testing positive for NRV GI and 18.6% testing positive for GII. The mean cycle number for GI positivity was 31.7 (SD 6.0) for non-diarrhea samples, and 32.8 (SD 5.8) for diarrheal samples. For NRV GII, the mean cycle number for positivity for non-diarrhea samples was 29.6 (SD, 5.3) and 29.0 (SD, 6.0) for diarrheal samples. Among 12 month old children with complete microbiology testing, NRV ranked in the top 5 pathogens identified in diarrheal samples for 7 of 8 sites, and in the top 5 for 6 of 7 sites contributing data for non-diarrheal stool samples with complete data.

Conclusion: Norovirus is a significant contributor to pathogen burden among MAL-ED children. This data provides an estimate of the exposure and frequency of identification of the virus in non-diarrheal and diarrheal stools.

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Investigation of a suspected tuberculosis outbreak in a long-term care facility, KwaZulu-Natal, South Africa, July-October 2013

C. Mugero^{1,*}, C. Atchison², S. Machingaidze³, B. Maphosa⁴, A. Takalani⁴, M. Beery⁴, P. Kweza⁴, G.M. Ntshoe⁵, J. Thomas⁵, S. Fynn⁶, O. Matuka⁷, T. Singh⁸, G. Sekobe⁹

¹ National Institute for Communicable Diseases, Johannesburg, South Africa² Public Health England, London, United Kingdom³ National Institute of Communicable Diseases, Johannesburg, South Africa⁴ National Institute for Communicable Diseases, Johannesburg, South Africa⁵ National Institute for Communicable Diseases (NICD) of the National Health Laboratory Service (NHLS), Johannesburg, South Africa⁶ eThekweni Department of Health, Durban, South Africa⁷ National Institute for Occupational Health, Johannesburg, South Africa⁸ National Institute of Occupational Health, Johannesburg, South Africa⁹ National Institute for occupational Health, Johannesburg, South Africa

Background: In August 2013, eThekweni Department of Health (DoH) in KZN was notified of an increase in TB cases among residents at a local long-term care facility (LTF). Following initial assessment and implementation of TB-specific infection control measures, eThekweni DoH requested support from the National Institute of Communicable Diseases (NICD). In October 2013, an outbreak response team from NICD, NIOH, eThekweni DoH and eThekweni municipality conducted an investigation at the LTF.

Methods & Materials: A cross-sectional survey was conducted among all staff and residents of the LTF in order to detect suspected cases of active TB using a structured screening questionnaire. Individuals with symptoms suggestive of TB were defined as suspected cases of active TB. For these cases, sputum specimens were collected for Gene Xpert, culture and drug susceptibility testing. Medical record reviews were performed to obtain more information. NIOH performed the environmental assessment.

Results: The initial assessment in August by eThekweni DoH identified 11 clinically-diagnosed TB cases and one laboratory-confirmed multi-drug resistant TB case. In October, the outbreak team were able to screen 96% (330/345) of residents, 59% (153/259) of staff and 67% (217/324) of nursing students. Of those screened, 23% (76/330) of residents, 21% (32/153) of staff and 26% (57/217) of nursing students were identified as suspected active TB. The team obtained sputum or gastric aspirate samples on 83% (137/165) of all screen-positive individuals. One resident was positive for TB and Rifampicin resistant on Gene Xpert.

The environmental assessment revealed poor adherence to infection control and TB management guidelines, including no TB screening for staff or residents, no training of staff on TB

prevention and inadequate use of personal protective equipment. Personal pump samples for only one staff member were positive for airborne MTB but sputum samples were Gene Xpert negative.

Conclusion: As neither Gene Xpert nor cultures were done on the clinically-diagnosed TB cases initially identified in August we could not determine whether there was an outbreak of TB with the same genotype in the LTF. Based on our findings, we recommend that the LTF and eThekweni DoH work together to implement national infection control and TB management guidelines.

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Molecular characterization of bacterial agents in asymptomatic bacteriuria diabetic patients in Trinidad & Tobago



P.E. Akpaka^{1,*}, P. Jayaratne², A.J. Vaillant¹, O.A. Onyegbule³

¹ *The University of the West Indies, Faculty of Medical Sciences, Champ Fleurs, Trinidad and Tobago*

² *St. Joseph's Healthcare, Hamilton, ON, Canada*

³ *St. Georges University, Grenada, Grenada*

Background: Trinidad & Tobago is a heterogeneous country of 1.3 million in population with people who have diverse ethnic, religious, cultural and socioeconomic activities. Great variations are seen in the prevalence of diabetes among several age and ethnic groups in the country. This study sought to perform molecular characterization of bacterial organisms prevalent among a cross section of diabetic patients with asymptomatic bacteriuria.

Methods & Materials: Over a 9 months period, two non-communicable chronic diseases clinics for adult patients were visited and after obtaining informed consent was obtained diabetic volunteers were recruited to participate in the study. Participants fulfilled study criteria that included absence of urinary symptoms, not catheterized, no history of UTI or any form of uropathy. Their blood samples were processed for HbA1c, serum electrolytes and urea values; and urine for microscopy, culture and sensitivity. *Enterobacteriaceae* from urine culture were subjected to screening for CTX, TEM, SHV, and VIM by amplification of gene fragments by conventional PCR and for KPC, NDM and OXA48 targets by real-time PCR using Sybergreen melting curve analysis.

Results: Four hundred and fourteen diabetics were surveyed. Significant bacteriuria was noted in sixty five subjects. Majority, 81.5% (53/65) of the positive urine cultures were in those with high HBA1c values. *Enterobacteriaceae* recovered most frequently were *Escherichia coli* 48.57% (34/70) and *Klebsiella pneumoniae* 25.7% (18/70). Most 87.1% (61/70) of the bacteria were recovered in urine samples from female 75.4% (49/65) subjects. Urine samples from males 24.6% (16/65) yielded mostly *Staphylococcus epidermidis* 14.3% (10/7) and the *Staphylococcus aureus* 5.7% (4/70) respectively. All *Enterobacteriaceae* isolates were negative KPC, NDM and OXA-48. Although the *bla*TEM and *bla* SHV were detected in both the *E. coli* and *K. pneumoniae* isolates these were nothing unusual.

Conclusion: *Escherichia coli* was the prevalent *Enterobacteriaceae* among the patients with asymptomatic bacteriuria. Poor diabetic control significantly is strongly associated with bacteriuria

that was more prevalent among female diabetics. Although none of the antimicrobial resistant targets were encountered among the *Enterobacteriaceae*, there is still the need to keep an eye on these targets and diabetic subjects in the country.

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Performance review of district and subdistrict hospitals in Punjab, Pakistan based on routine information systems



M.J. Syed^{1,*}, M.M. Syed²

¹ *NHIRC, Islamabad, Pakistan*

² *World Health Organization, Islamabad, Pakistan*

Background: District and sub district Hospitals play critical role in health care delivery system in a country. In Pakistan, each of the 140 districts in Pakistan has a 100–200 bedded District Hospital and two to three 50 bedded sub district hospital. Prior to launch of the nationally uniform District Health Information System in 2006, there was no standard mechanism for assessing the performance of the district hospitals. The health managers thus had very limited options to standard information that could lead to any analysis for regular managerial monitoring or for decision making.

Methods & Materials: This is the first analysis of its kind derived from Routine Health Information System working in the biggest province of Punjab. The performance of all the public sector District and sub District hospitals is measured on a uniform criteria. This analysis is derived from approximately 28.47 million visits made to 29 District and 84 sub district hospitals during 2011. This gives an overview of a range of selected health indicators pertaining to 43 priority health problems, on utilization of health services by departments, MNCH/EmONC, including diagnostics, laboratory services and human resource situation.

Results: This analysis has made some startling revelations. It is interesting to note that on average 796 visits are being made per day to the District Hospitals and 378 visits to the sub district hospitals. There existed visible variations across hospitals and districts. Another interesting finding is that more of male children were brought to the hospitals than their female counterparts. A high proportion of OPD patients belonged to respiratory diseases group. Next important reason for visits were for Diarrhea/Dysentery as about 1.75 million cases belonged to this group. Roughly 36% of pregnant women registered for ANC were found anemic. For deliveries/Caesarian Section about 42% of all deliveries were conducted through C-sections in DHQ hospitals. Tremendous inter district variations are also observed.

Conclusion: Early analysis and use of information collected through Routine Information Systems is cost effective and readily available for decision making.

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