Figure 2.

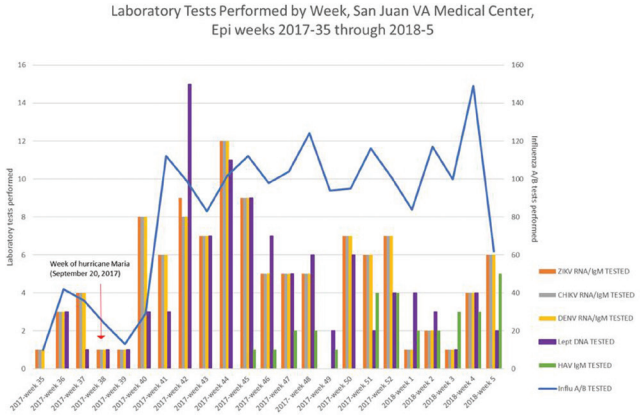
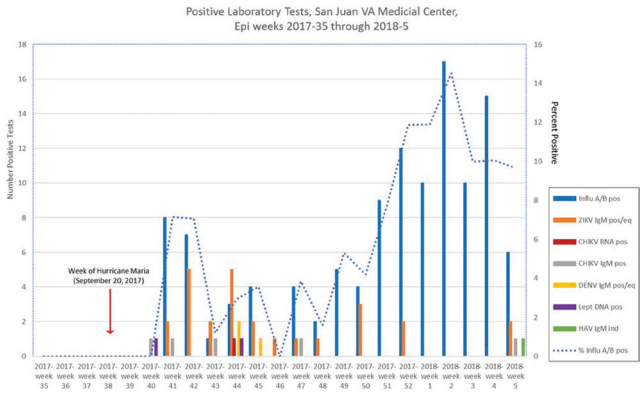


Figure 3.



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

450. Using Geographical Information Systems to Interpret the Efficacy of Mass Drug Administration for Soil-Transmitted Helminthiasis in Rural Madagascar

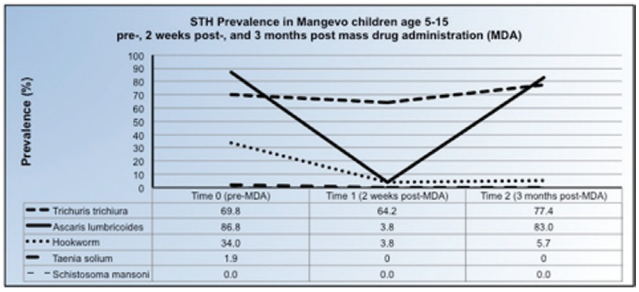
Emile Redwood, BA, MD Candidate[1]; Liana Langdon-Embry, BA, MD Candidate[1]; Annabelle Jones, BS, MD Candidate[1]; Benjamin Schwarz, BS, MD Candidate[1]; Ando Lvasoa Rakotoniaina, MD[2]; Fara Nantenaina Rakotoarison, Midwife, Mobile Health Team[2]; Andry Andriamiadanarivo, Cartographer[2]; Patricia Wright, PhD[3]; Ines Vigan-Womas, PhD[4]; Peter Small, MD[5] and Luis A. Marcos, MD, MPH[6]; [1]Stony Brook School of Medicine, Stony Brook, New York, [2]Centre Val Bio, Ranomafana, Madagascar, [3]Anthropology, Stony Brook University, Stony Brook, New York, [4]Institut Pasteur de Madagascar, Antananarivo, Madagascar, [5]Global Health Institute, Stony Brook School of Medicine, Stony Brook, New York, [6]Infectious Disease, Stony Brook University Hospital, Stony Brook, New York

Session: 57. Global Health and Travel Medicine
Thursday, October 4, 2018: 12:30 PM

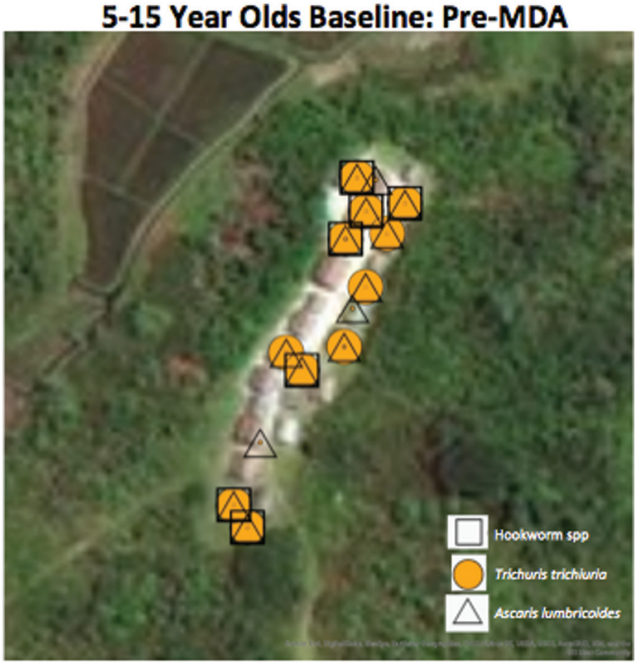
Background. In Madagascar, mass drug administration (MDA) of anti-parasitics is administered every 6 months to combat soil-transmitted helminthiasis (STH) in school-aged children, although little information exists as to its efficacy. In recent years, geographical information systems (GIS) have been used for visualization of patterns in disease epidemiology. This inexpensive technology may be leveraged to aid in education of local health workers toward a more integrated approach to control STH.

Methods. Baseline questionnaires and stool/blood samples were collected from participants of Mangevo, a rural village in southeast Madagascar. GPS coordinates and qualitative descriptions were collected from all village homes, common latrines, and animal pens. All children 5–15 years old were given MDA per WHO protocol. Stool was again collected from these children 2 weeks later and 3 months later. Parasitological examination of stool samples for STH eggs was performed using Spontaneous Sedimentation Technique. Results were overlaid onto GIS maps and used to further educate the local mobile health team.

Results. A total of 183 participants were eligible for the study. Analysis found 89% of adults >15 years old were infected with one or more parasite and 100% of children 5–15 were infected with one or more parasite at time 0. *Trichuris trichuria* prevalence fell 8% ($P < 0.5$) in 2 weeks and climbed 17% ($P < 0.05$) by 3 months follow-up. *Ascaris lumbricoides* prevalence fell 96% ($P < 0.0001$) in the 2 weeks and climbed 95% ($P < 0.0001$) by 3 months follow-up. Hookworm prevalence dropped 89% ($P < 0.0001$) in 2 weeks and climbed 5% ($P < 0.5$) by 3 months follow-up. Prevalence data, descriptive results, and GPS coordinates of village homes were integrated into a GIS maps pre- and post-MDA of children, and pre-MDA for adults.



	Time 0 (pre-MDA)	Time 1 (2 weeks post-MDA)	Time 2 (3 months post-MDA)
Trichuris trichiura	69.8	64.2	77.4
Ascaris lumbricoides	86.8	3.8	83.0
Hookworm	34.0	3.8	5.7
Taenia solium	1.9	0	0
Schistosoma mansoni	0.0	0.0	0.0



Conclusion. While GIS has been used to yield insights into the ecology of infection, this study examined the efficacy of the current MDA through the lens of small scale GIS mapping. This may be an ideal and inexpensive technology to help in the implementation of future interventions of the government-mandated STH treatment protocol and work toward the strengthening of local health teams.

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

451. High-Frequency of Multi-Drug-Resistant Organisms (MDRO) at University Teaching Hospital (UTH), Lusaka, Zambia

Brenna Roth, MD, MPH[1]; Alexandra Laps, BS[2]; Kristen Stafford, PhD, MPH[3]; Emily Heil, PharmD, BCPS-AQID[4]; Lottie Hachaambwa, MBChB[2]; Kaunda Yamba, MD, MSc[5]; Mox Kalumbi, MSc[5]; Devang Patel, MD[2]; J. Kristie Johnson, PhD[2]and Cassidy Claassen, MD, MPH[2]; [1]Institute of Human Virology, University of Maryland School of Medicine, Baltimore, Maryland, [2]University of Maryland School of Medicine, Baltimore, Maryland, [3]Department of Epidemiology and Public Health, University of Maryland School of Medicine, Baltimore, Maryland, [4]Division of Infectious Disease, University of Maryland Medical Center, Baltimore, Maryland, [5]University Teaching Hospital, Lusaka, Zambia

Session: 57. Global Health and Travel Medicine
Thursday, October 4, 2018: 12:30 PM

Background. Antibiotic resistance is a worldwide problem. Prior studies on patterns of resistance in Zambia depended on laboratory methods that lacked standardization. UTH is a 1,655-bed quaternary care hospital and the primary teaching hospital of Zambia. Since 2015, the microbiology laboratory has used Vitek 2 Compact (bioMerieux, Inc., France) for standardized detection of resistance.

Methods. We conducted a retrospective cross-sectional study of data collected on bacterial isolates analyzed from July 2015 to April 2017. We entered the data into WHONET 5.6 and aggregated it to develop hospital antibiograms. Due to high levels of resistance, we defined susceptible, intermediate, and resistant as >70%, 40–70%, and <40% of isolates sensitive to a drug, respectively. To improve usability, a version replacing the percent susceptible with these categories was developed.

Results. We analyzed 2,019 isolates to identify susceptibility patterns to commonly used antibiotics at UTH. *Escherichia coli* and *Klebsiella pneumoniae*, the most commonly isolated Gram-negative (GN) organisms, were resistant to most drugs including ceftriaxone, indicating high rates of extended-spectrum β-lactamase production. Methicillin-resistant *Staphylococcus aureus* (MRSA) made up 37% of *S. aureus*

isolates. MRSA and methicillin-susceptible *S. aureus* were resistant to trimethoprim/sulfamethoxazole, a commonly used drug at UTH. *S. pneumoniae* was resistant to most drugs against which it was tested.

Conclusion. MDROs were common at UTH with carbapenems indicated for empiric GN therapy. Further research should assess the extent and depth of antibiotic resistance in Zambia. Antibiograms provide critical information for clinicians to strategically use antibiotics.

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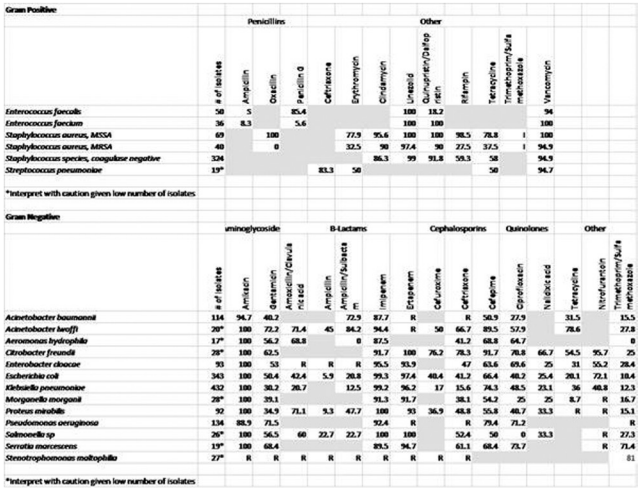
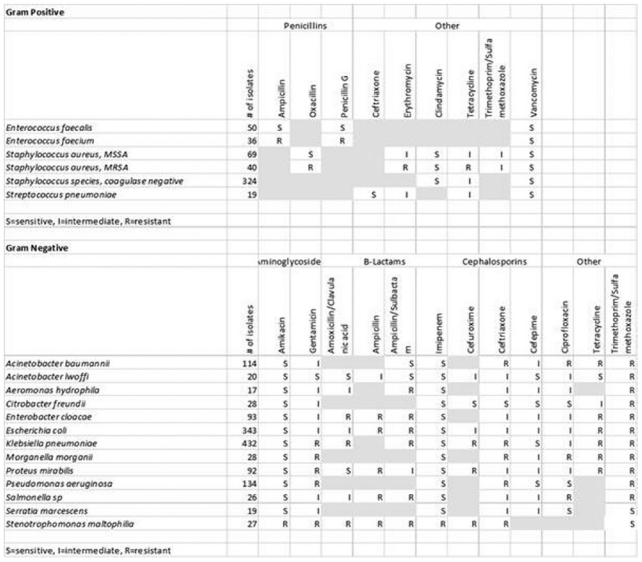


Gram Positive		Penicillins				Other								
	# of isolates	Ampicillin	Oxacillin	Penicillin G	Ceftriaxone	Erythromycin	Clindamycin	Linezolid	Quinupristin/Dalfopristin	Rifampin	Tetracycline	Trimethoprim/Sulfamethoxazole	Vancomycin	
Enterococcus faecalis	58	S		85.4				100	18.2				94	
Enterococcus faecium	36	8.3		5.6				100	100				100	
Staphylococcus aureus, MSSA	69		100			77.9	95.6	100	100	98.5	78.8	I	100	
Staphylococcus aureus, MRSA	40		0			32.5	90	97.4	90	27.5	37.5	I	94.9	
Staphylococcus species, coagulase negative	324						86.3	99	91.8	59.3	58		94.9	
Streptococcus pneumoniae	19*				83.3	50					50		94.7	

*Interpret with caution given low number of isolates

Gram Negative		Aminoglycoside			B-Lactams				Cephalosporins			Quinolones		Other		
	# of isolates	Amikacin	Gentamicin	Amoxicillin/Clavulanic acid	Ampicillin	Ampicillin/Sulbactam	Imipenem	Ertapenem	Cefuroxime	Ceftriaxone	Cefepime	Ciprofloxacin	Nalidixic acid	Tetracycline	Nitrofurantoin	Trimethoprim/Sulfamethoxazole
Acinetobacter baumannii	114	94.7	40.2			72.9	87.7	R		R	50.9	27.9		31.5		15.5
Acinetobacter lwoffi	20*	100	72.2	71.4	45	84.2	94.4	R	50	66.7	89.5	57.9		78.6		27.8
Aeromonas hydrophila	17*	100	56.2	68.8		0	87.5			41.2	68.8	64.7				0
Citrobacter freundii	28*	100	62.5				91.7	100	76.2	78.3	91.7	70.8	66.7	54.5	95.7	25
Enterobacter cloacae	93	100	53	R	R	R	95.5	93.9		47	63.6	69.6	25	31	55.2	28.4
Escherichia coli	343	100	58.4	42.4	5.9	20.8	99.3	97.4	40.4	41.2	66.4	48.2	25.4	20.1	72.1	18.4
Klebsiella pneumoniae	432	100	30.2	20.7		12.5	99.2	96.2	17	15.6	74.3	48.5	23.1	36	40.8	12.3
Morganella morganii	28*	100	39.1				91.3	91.7		38.1	54.2	25	25	8.7	R	16.7
Proteus mirabilis	92	100	34.9	71.1	9.3	47.7	100	93	36.9	48.8	55.8	40.7	33.3	R	R	15.1
Pseudomonas aeruginosa	134	88.9	71.5				92.4	R		R	79.4	71.2				R
Salmonella sp	26*	100	56.5	60	22.7	22.7	100	100		52.4	50	0	33.3		R	27.3
Serratia marcescens	19*	100	68.4				89.5	94.7		61.1	68.4	73.7			R	71.4
Stenotrophomonas maltophilia	27*	R	R	R	R	R	R	R	R	R						81

*Interpret with caution given low number of isolates



Gram Positive		Penicillins			Other					
	# of isolates	Ampicillin	Oxacillin	Penicillin G	Ceftriaxone	Erythromycin	Clindamycin	Tetracycline	Trimethoprim/Sulfamethoxazole	Vancomycin
Enterococcus faecalis	50	S		S						S
Enterococcus faecium	36	R		R						S
Staphylococcus aureus, MSSA	69		S			I	S	I	I	S
Staphylococcus aureus, MRSA	40		R			R	S	R	I	S
Staphylococcus species, coagulase negative	324						S	I		S
Streptococcus pneumoniae	19				S	I		I		S

S=sensitive, I=intermediate, R=resistant

Gram Negative		Aminoglycoside			B-Lactams			Cephalosporins				Other	
	# of isolates	Amikacin	Gentamicin	Amoxicillin/Clavulanic acid	Ampicillin	Ampicillin/Sulbactam	Imipenem	Cefuroxime	Ceftriaxone	Cefepime	Ciprofloxacin	Tetracycline	Trimethoprim/Sulfamethoxazole
Acinetobacter baumannii	114	S	I			S	S		R	I	R	R	R
Acinetobacter lwoffi	20	S	S	S	I	S	S	I	I	S	I	S	R
Aeromonas hydrophila	17	S	I	I		R	S		I	I	I		R
Citrobacter freundii	28	S	I				S	S	S	S	S	I	R
Enterobacter cloacae	93	S	I	R	R	R	S		I	I	I	R	R
Escherichia coli	343	S	I	I	R	R	S	I	I	I	I	R	R
Klebsiella pneumoniae	432	S	R	R		R	S	R	R	S	I	R	R
Morganella morganii	28	S	R				S		R	I	R	R	R
Proteus mirabilis	92	S	R	S	R	I	S	R	I	I	I	R	R
Pseudomonas aeruginosa	134	S	R				S		R	S	S		R
Salmonella sp	26	S	I	I	R	R	S		I	I	R		R
Serratia marcescens	19	S	I				S		I	I	S		S
Stenotrophomonas maltophilia	27	R	R	R	R	R	R	R	R				S

S=sensitive, I=intermediate, R=resistant

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452. Spectrum of Respiratory Pathogens Detected by Multiplex PCR in a Study of Respiratory Tract Infections Among Travelers

Satoshi Kutsuna, MD, PhD[1]; Maki Nagashima, PhD[2]; Yuta Toda, Dr[2]; Saho Takaya, MD, MSc[3]; Kei Yamamoto, MD[3]; Kayoko Hayakawa, MD, PhD[4] and Norio Ohmagari, MD, MSc, PhD[5]; [1]Disease Control and Prevention Center, National Center for Global Health and Medicine, Tokyo, Japan, [2]National Centre for Global Health and Medicine, Shinjuku-ku, Japan, [3]Disease Control and Prevention Center, National Center for Global Health and Medicine (NCGM), Tokyo, Japan, [4]c, Detroit, Michigan, [5]AMR Clinical Reference Center, National Center for Global Health and Medicine, Tokyo, Japan

Session: 57. Global Health and Travel Medicine

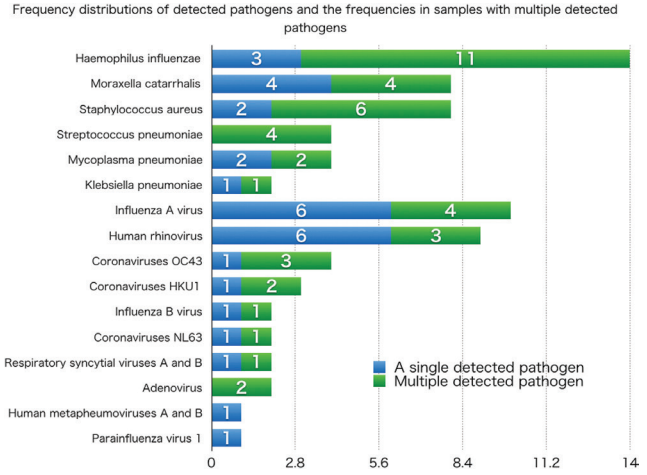
Thursday, October 4, 2018: 12:30 PM

Background. Respiratory tract infections (RTI) are a significant cause of health problems, accounting for about 10% of consultations in returning travelers. Nevertheless, the precise microbial etiology is not identified in many cases.

Methods. Prospectively collected 63 respiratory specimens (sputum or throat swab) from patients presented with respiratory symptoms (cough, sputum, chest pain, dyspnea, tachypnea, or abnormal findings of chest auscultation) after travel were tested using multiplex real-time PCR. The FTD Respiratory pathogens 33 (Fast-track diagnostics, Ltd.) can simultaneously detect 33 different respiratory pathogens directly from respiratory specimens. This test ran in the PCR-Only mode on BD MAX™ (Nippon Becton Dickinson Company, Ltd.) and LightCycler480 System (Roche).

Results. Fifty-nine consecutive cases were included in the study. Thirty-nine cases were diagnosed as non-specific upper respiratory tract infections, five cases were influenza, bronchitis, pneumonia, threecases was acute sinusitis, and one case was acute pharyngitis, dengue fever. Twenty-four cases had returned from travel in Southeast Asia, nine from Africa, and 8 from Latin America, seven from South Asia, six from middle east, threefrom North America, threefrom East Asia, 2 from Oceania, and one from Europe. Of the 59 specimens analyzed, 48 (81.4%) tested positive for pathogens whereas 11 tested negative. Commonly detected pathogens were *Haemophilus influenzae* (14 cases; 23.7%), influenza A (10 cases; 17.0%), rhinovirus (9 cases; 15.2%), *Staphylococcus aureus* (8 cases; 13.6%), *Moraxella catarrhalis* (8 cases; 13.6%), *Streptococcus pneumonia*, coronaviruses OC43, and *Mycoplasma pneumoniae* (4 cases; 6.8%, respectively). Multiple pathogens were detected in 30.5% of the specimens. In 14 cases (23.7%), both virus and bacteria were detected from one specimen.

Conclusion. Not only viruses, bacterial pathogens were detected frequently than expected in the patients of RTI. Comprehensive molecular testing such as multiplex real-time PCR would change our understandings of epidemiology of RTI among travelers.



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

453. Understanding Travel Medicine Provider's Risk Assessment of Travel-Associated Diseases

Robert Ulrich, MD[1] and Scott Weisenberg, MD[2]; [1]Infectious Diseases, New York University School of Medicine, New York, New York and [2]New York University, New York, New York

Session: 57. Global Health and Travel Medicine

Thursday, October 4, 2018: 12:30 PM

Background. Pre-travel medical consultations attempt to reduce travel-associated risks by behavioral modification, vaccination, and medications. Provider understanding of quantitative risk of commonly discussed travel topics is poorly characterized. We investigated travel medicine provider understanding of quantitative risk of common travel-associated diseases, and explored how providers relay risk estimates to travelers.

Methods. After institutional review board (IRB) approval, an online anonymous survey was sent to the International Society for Travel Medicine Listserv. Travel medicine experience, practice patterns and demographics were recorded. Respondents estimated quantitative risk of various destination-specific diseases. Descriptive statistics were completed.

Results. Of 114 respondents, most were experienced travel medicine providers (79% saw >6 travel visits monthly). Overall risk estimates are in Table 1. Compared with published literature, providers gave accurate risk estimates for some diseases (yellow fever, traveler's diarrhea), but overestimated quantitative risk for others (Japanese encephalitis, hepatitis A, cholera). Interquartile range was greatest for Japanese encephalitis and cholera, reflecting a wider range of risk estimates. Most (81%) providers used general risk descriptions (high, low, none) and a minority (14%) discussed quantitative risk with travelers.