# International Congress on Pathogens at the Human-Animal Interface (ICOPHAI)

## 4th International Congress on Pathogens at the Human-Animal Interface (ICOPHAI):

## Enviromental Changes and Impact on Global Health

Doha, Qatar Ritz Carlton, West Bay Lagoon

November 7-9, 2017

# ABSTRACT BOOK

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Dear Colleagues,

Fellow participants of the 4th International Congress on Pathogens at the Human Animal Interface (ICOPHAI):

On behalf of the Organizing team, composed of scientists and policy-makers from the host nation, Qatar and global partners including the United States, Africa, Asia, Latin America and Europe, we welcome you all to this congress. Thank you the government of Qatar and all associated agencies including the Qatar University (QU), Ministry of Public Health (MoPH), Hamad Medical Corporation (HMC), Qatar National Research Foundation (QNRF), Weill Cornell Medicine at Qatar and many others for your partnership and realizing this congress. The ICOPHAI global team greatly appreciates the partnership

As we mark the 4th congress in the heart of eastern Mediterranean region, Doha, the world population has reached more than 7 billion and with estimated trajectory of more than 9.6 billion by 2050. This means in a linear estimate, every day more than 200 thousand people are added to this defined planet. The increasing population and resulting global dynamics including deforestation, urbanization, climate change, migration, water crises and many others, all of which identified as major factors by the Global Risk Forum, have a direct impact on distribution of zoonotic diseases across the planet. It is with this reminder that the ICOPHAI 2017 Executive team decided to make the “Environmental Changes and Impact on Global Health” as the theme of the 4th ICOPHAI congress.

It is more than ever clear that biological agents at the interface of humans, animal and the environment including plants, zoonotic, vector-borne, food and water-borne diseases impose a major burden more than ever before globally and with a much higher burden on tropical regions. Among the most recent outbreaks, we would like to remind all the recent outbreaks of Zika virus in Latin America as well as Middle-eastern Respiratory Syndrome (MERS) and many others. In addition, antimicrobial resistant bacterial pathogens have become a major burden in the world with estimated mortality of 10 million people per year in the world by 2050, particularly in the developing region. Unfortunately, in these same regions where the impact of pathogens at the human animal interface is much larger, the skilled manpower and infrastructure capacity is, ironically, much lower. The constantly present zoonotic epidemics and pandemics, are stark reminders of the constant need of scientists and policy-makers to work together collaboratively to prevent and control them and build the knowledge equity and capacity of developing regions to be able to tackle them effectively, establish sustainable infrastructure and make the planet a better place for everyone.

The increasing population and paralleling industrialization in the developing region, also brought additional risks. We also should not forget the increasing significance of chemical hazards and their resulting non-communicable and chronic diseases such as cancer.

It is with this rationale that the International Congress on Pathogens at the Human Animal Interface (ICOPHAI) was established in 2011 by a consortium of institutes across the globe that aim to utilize the GLOBAL ONE HEALTH approach to operationalize, build capacity and thereby contribute to the global efforts to tackle zoonotic, foodborne and vector-borne infections. As we prepare to launch this congress, the organizing team is pleasantly surprised by the regular flow of interested and committed scientists who showed interest to take part at ICOPHAI. We have more than 1211 subscribers to our online system that originated from 80 countries (among the 924 who declared their national origin) and close to 304 research, academic, regulatory and intergovernmental organizations world-wide. In this 4th congress, we have 164 abstracts and more than 30 countries confirmed participation as of this moment and we anticipate more on-site registrations as we kick-off the congress.

The Local, international Organizing teams as well as the Scientific Program committees and the Secretariat offices both in Qatar and the U.S. (at Ohio State Global One Health initiative) worked hard to make this congress successful and we are grateful to everyone. Our team is also humbled by the commitment of several sponsoring agencies, who stepped up to the plate to support this congress financially. We are grateful to the support of all sponsors, which are listed on the back of this congress program document. These committed sponsors, not only enabled us to organize the congress and pay for the venue and organization expenses, In addition, they enabled the organizing team to support travel, accommodation and meal expenses to close to 70 participants with full expenses covered.  The sponsored participants were primarily from developing regions. We would also like to thank the commitment of the organizing partners particularly the academic institutes in Qatar again and the U.S., Canada, Africa and Latin America. Finally, we are very much grateful to our keynote, special and plenary speakers and other dignitaries who have a proven leadership in their respective scientific disciplines, who are here to share their knowledge, strengthen scientific networking and help us all together achieve our goals in the short or long-term.

Finally, to all ICOPHAI 2017 patrons, colleagues and scientists, we would like to ask and encourage you all to take the three days congress period as an opportunity to: 1) promote the science you are doing; 2) to engage in scientific networking; 3) maximize the scientific inputs you receive from all and further 4) appreciate the value and need for unconventional partnership across diverse disciplines and sectors to achieve the complex issues of out breaks caused by pathogens at the human, animal and ecosystem interface and 5) upon your return to your home, we ask you to actively advocate to operationalize One Health globally in your respective capacities, be it in small district in sub-Saharan Africa (Borana or Masai Mara)  or the Caatinga region of North–eastern Brazil, at Ministries of Public health, Agriculture  or at head-quarters of intergovernmental agencies.

Again, on behalf of the organizing body of ICOPHAI 2017, I wish you the best time in Doha.

**Wondwossen A. Gebreyes**
The Ohio State University
Chair

**Asmaa Al-Thani**
Qatar University
Co-chair

**Walid Al-Ali**
Hamad Bin Kalifah University
Secretary General

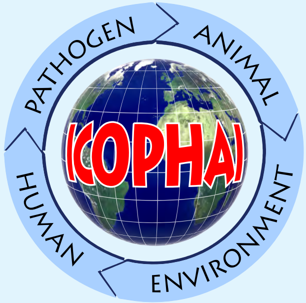
**Hadi Yassine**
Qatar University
Local Organizing Co-chair

**Sylvain Quessy**
University of Montreal
Scientific Program Chair

**Laith Abu-Raddad**
Weill-Cornell Medicine at Qatar
Scientific Program Co-chair

# Scientific Program

November 7-9, 2017



| Monday November 6, 2017 | |
|---|---|
| Qatar University Biomedical Research Center | **Pre-congress workshop:**<br>Exposure and Toxicological Characteristics of Chemical Agents in the Environment<br>**Lead Instructors:**<br>Michael Bisesi PhD Sr. Associate Dean of Academic Affairs and Professor, The Ohio State University;<br>Jeff Obbard, PhD Director of Environmental Sciences, Biomedical Research Center, Qatar University |
| Ministry of Public Health | **Pre-congress workshop:**<br>One Health Approach to Combat Antimicrobial Resistance (AMR)<br>**Lead Instructors:**<br>Dr. Nahla Sharaf & Dr. Eman Radwan Ministry of Public Health<br>Dr. Jameela Ali A.A. Al Ajmi |

| **Tuesday November 7, 2017 (Day One)**<br>4th ICOPHAI Main Congress Program<br>Master of Ceremonies- Hadi Yassine - Qatar Univ.<br>Mistress of Ceremonies - Ashley Bersani- Ohio State Univ. | |
|---|---|
| 07:30- 5:00 | On-Site Registration |
| 08:15 -09:00 | Welcome/Opening Address<br>QU leadership- Dr. Hassan Al-Derham( QU president)<br>Misistry of Public Health- Dr. Hamad Al Romaihi<br>OSU representative- Prof. Rustin Moore (Dean, CVM)<br>ICOPHAI leadership- Chair (Prof. Wondwossen Gebreyes) |
| 09:00-10:00 | Keynote moderator- Hadi Yassine/ Asmaa Al Thani<br>Keynote Address by Roberto Bertollini, MD, MPH, Advisor for the Minister of Public Health, Government of Qatar<br>Title: Environmental Changes and their Impact on Global Health |
| 10:00- 10:30 | Refreshments and Networking |
| 10:30-12:15 | Special Session:<br>Zika Virus, Emerging and Re-emerging Infectious Diseases<br>Session chairs: Laith Abu-Raddad (Weill Cornell Medicine Qatar) and Mohammed Mohammed Al-Hajri (Ministry of Public Health, Qatar) |
| 10:30-11:15 | Lead special session speaker: Larry Schlesinger, MD President and CEO Texas Biomedical Institute, San Antonio, TX, USA<br>Title: N/A |
| 11:15-11:30 | Oral Presentation 0.1<br>Title: Crimean Congo Hemorrhagic Fever among the One-Humped Camel (Camelus dromedaries) in Central Sudan.<br>Presenter: Imadeldin Aradaib, aradaib@uofk.edu, Molecular Biology Laboratory (MBL), Department of Clinical Medicine, University of Khartoum, Khartoum North, Sudan |
| 11:30-11:45 | Oral Presentation 0.2<br>Title: Dengue and Chikungunya in the Middle East and North Africa: A Systematic Review.<br>Presenter: John Humphrey, john.m.humphrey@gmail.com, Indiana University School of Medicine, Indianapolis, United States |
| 11:45-12:00 | Oral Presentation 0.3<br>Title: Challenges to Control Ebola in West Africa: A Review<br>Presenter: Tadesse Delele, PhD; tadeguade2@gmail.com, Associate Professor of Public Health, Gondar, Ethiopia |

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| 12:00-12:15 | Oral Presentation 0.4<br>Title: Corona viruses detected in bats of Rwanda: diversity at human–wild life interfaces and a call for one health approach.<br>Presenter: Julius Nziza, DVM, nzizavet@gmail.com, Gorilla doctors, Rwanda program, Musanze, Rwanda |
| 12:15-01:30 | Lunch and Networking |
| 1:00-1:30 | Poster Discussions- Zika Virus, Emerging and Re-emerging Infectious Diseases |
| 01:30-03:15 | Plenary Session 1: Parasitic and Environmental Zoonoses<br>Session Chairs: Marawan A.M. Abou Madi (Assoc. Prof. Parasitology, Head of Dept. of Biomedical Sciences, Qatar University) and<br>Marty Kress (Director Global Water Institute, Ohio State University) |
| 01:30-02:15 | Lead Speaker: Filipe Dantas-Torres, MV, MSc, DSc, PhD, FRES, Dipl. EVPC; Oswaldo-Cruz Foundation, Brazil<br>Title: Climate change, biodiversity, ticks and tick-borne diseases: The butterfly effect |
| 02:15-02:30 | Oral Presentation 1.1<br>Title: Molecular characterization of Echinococcus granulosus s.l. cysts from cattle, camels, goats and pigs in Ethiopia<br>Presenter: Benti Deresa Gelalcha, bentijc@gmail.com, Jimma University, Ethiopia, Jimma, Ethiopia |
| 02:30-02:45 | Oral Presentation 1.2<br>Title: A rapid, sensitive and low-cost real-time PCR assay for the detection of Leishmania infantum and Leishmania braziliensis kinetoplast DNA in canine blood samples<br>Presenter: Kamila Sales, kamilasalesg@gmail.com, Department of Immunology, Aggeu Magalhães Institute, Oswaldo Cruz Foundation, Recife, Brazil |
| 02:45-03:00 | Oral Presentation 1.3<br>Title: Role of Cattle in the Epidemiology of Echinococcus granulosus sensu lato in Central Sudan<br>Presenter: Imadeldin Aradaib, aradaib@uofk.edu, Echinoccosis Research Center, Al-Neelain Institute for Medical Research (NIMR),Faculty of Medicine, Al-Neelain University, Khartoum, Sudan \| Center of Tropical Medicine and Travel Medicine, University of Amsterdam, Amsterdam, Netherlands |
| 03:00-03:15 | Oral Presentation 1.4<br>Title: Understanding the Risk of Bat-Borne Zoonotic Diseases<br>Presenter: Nesreen Alhmoud, Nesreen.Alhmoud@rss.jo Director of Biosafety and Biosecurity Center \| Royal Scientific Society, Amman, Jordan (N/A) |
| 03:15-03:45 | Refreshments and Networking Break / Poster Discussions<br>(Parasitic & Environmental Zoonoses/ One health and impact on climate change) |

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| 03:45-05:30 | Plenary Session 2: One health and impact on climate change<br>Session chairs- Michael Bisesi PhD Sr. Associate Dean of Academic Affairs and Professor, The Ohio State University;<br>and Walid Alali Associate Professor of Epidemiology, College of Food and Agriculture, United Arab Emirates University |
| 3:45-4:00 | Oral Presentation 2.1<br>Title: The Influence of Weather Patterns on Biodiversity and Health in Uganda<br>Presenter: Fredrick Kabbale, MSc, fredrickkabbale@yahoo.co.uk, Makerere University, Kamuli, Uganda |
| 4:00-4:15 | Oral Presentation 2.2<br>Title: Epidemiology of hepatitis C virus among hemodialysis patients in the Middle East and North Africa: systematic syntheses, meta-analyses, and meta-regressions<br>Presenter: Manale Harfouche, MPH, mah2064@qatar-med.cornell.edu, Infectious Disease Epidemiology Group, Weill Cornell Medicine-Qatar, Cornell University, Qatar Foundation - Education City, Doha, Qatar, Doha, Qatar |
| 4:15-4:30 | Oral Presentation 2.3<br>Title: Why is Environmental Risk Assessment and Environmental Risk Management lagging behind?<br>Presenter: Salome Margaret Molefe, molefe.mabunda@gmail.com, National Department of Environmental Affairs, Pretoria, South Africa |
| 4:30-4:45 | Oral Presentation 2.4<br>Title: Influenza viruses in backyard poultry, pigs, and people in pig rearing communities in northwestern Bangladesh, 2014-2016<br>Presenter: Shamim Sarkar, shamim.sarkar08@gmail.com, Programme for Emerging Infections, Infectious Diseases Division, icddr,b, Dhaka, Bangladesh |
| 04:45-05:30 | Panel Discussion: “Environmental Challenges and Impact on Global Health”<br>Panel moderator: Nicole Kraft (USA)<br>Panelists: Lauro Santos (Brazil), Salome Margaret Molefe (Republic of South Africa), Walid Alali (UAE), Sylvain Quessy (Canada) |
| 05:30 | End of scientific session- Day One |
| 6:30-8:30 | GALA DINNER<br>Introduction by featured sponsor- Hamad Medical Corporation (HMC)<br>Dr. Muna Al Maslamani, Medical Director of the Communicable Disease Center<br>Speaker: William Brustein, Vice President, West Virginia University, USA.<br>Title: Immigration and Nativism in America: Opened and Closed Doors |

| **Wednesday November 8, 2017 (Congress Day Two)** | |
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| 08:00-08:30 | On-Site Registration |
| 08:30-10:15 | Plenary Session 3: Innovative Capacity Building, e-Learning and Outreach approaches.<br>Session chairs: Joshua Amimo (University of Nairobi, Kenya)<br>and Essam Abdelalim (Hamad Bin Khalifa University, Qatar) |
| 08:30-09:15 | Lead Speaker: Nicole Kraft, Clinical Assistant Professor, School of Communication, The Ohio State University<br>Title: Global One (Tech) Health: How technology guides education, research and outreach. |
| 09:15-09:30 | Oral Presentation 3.1<br>Title: Bovine Tuberculosis infection in pastoral cattle and wildlife at livestock-wildlife interface of the Greater Ruaha ecosystem, Tanzania<br>Presenter: Julius Medardus, juliusjhn@yahoo.com, College of Veterinary and Medical Sciences, Sokoine University of Agriculture, Morogoro, Tanzania. |
| 9:30-9:45 | Oral Presentation 3.2<br>Title: Gastro-intestinal parasites infections in mountain gorillas (Gorilla beringei beringei) of Rwanda Volcanoes National Park: One Health Implications<br>Presenter: Richard S. Gashururu, gasirich@yahoo.fr, University of Rwanda, school of veterinary medicine, Nyagatare, Rwanda |
| 9:45-10:00 | Oral Presentation 3.3<br>Title: In vitro antimycobacterial activity and cytotoxicity of selected medicinal plants against pathogenic and non-pathogenic mycobacterial strains<br>Presenter: Joseph Mwanzia Nguta, joseph.nguta@uonbi.ac.ke, Department of Public Health, Pharmacology and Toxicology, Faculty of Veterinary Medicine, University of Nairobi, Nairobi, Kenya, Nairobi, Kenya |
| 10:00-10:15 | Oral Presentation 3.4<br>Title: Diversity and antibiotic resistance profiles of Escherichia coli strains from migratory bird (Branta leucopis) and Reindeer (Rangifer tarandus) reveals dissemination of multi drug resistant (MDR) E. coli to pristine arctic environment<br>Presenter: Hatha Mohamed Abdulla, mohamedhatha@gmail.com, Department of Marine Biology, Microbiology and Biochemistry, Cochin University of Science and Technology, Cochin, India |
| 10:15-10:45 | Refreshments and Networking<br>(Poster Discussions- Innovative Capacity Building) |
| 10:45-12:30 | Plenary Session 4: Antimicrobial Resistance and Drug Related Issues<br>Session Chairs: Lauro Filho Santos (Brazil)<br>and Nahla Sharaf (Ministry of Public Health, Qatar) |

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| 10:45-11:30 | Lead Speaker: Satoru Suzuki, PhD Ehime University, Matsuyama, Japan Professor of Microbiology Division of Aquatic Biosciences Center for Marine Environmental Studies (CMES)Laboratory of Marine Molecular Ecology (MME)<br>Title: Aquatic environments as a reservoir of antibiotic resistance genes (ARGs) |
| 11:30-11:45 | Oral Presentation 4.1<br>Title: Global trends in antimicrobial consumption in food animals<br>Presenter: Thomas Van Boeckel, thomas.vanboeckel@env.ethz.ch, ETH Zurich, Zurich, Switzerland I Princeton, Princeton, United States |
| 11:45-12:00 | Oral Presentation 4.2<br>Title: National Action Plan to Combat AMR in the State of Qatar Using “One health” Approach<br>Presenter:Nahla Sharaf nsharaf@moph.gov.qa, Eman Radwan, Ministry of Public Health - Healthcare Quality and Patient safety Department, Doha, Qatar |
| 12:00-12:15 | Oral Presentation 4.3<br>Title: Identification of potential drivers for antimicrobial resistance and screening for genetic basis of resistance in E. coli strains obtained from people with a recent history of diarrhea and/or fever residing along the Lake Victoria basin of Western Kenya<br>Presenter: John Kiiru, kyirow@gmail.com, Kenya Medical Research Institute (KEMRI), Nairobi, Kenya |
| 12:15-12:30 | Oral Presentation 4.4<br>Title: Detection of BLAKPC-2 and fosA genes in Enterobacteriaceae isolated from urban river in Paraiba, Brazil.<br>Presenter: Lauro Filho Santos, lauro.santos@superig.com.br, Federal University of Paraiba, João Pessoa, Brazil I Department of Pharmaceutical Sciences; João Pessoa, Brazil |
| 12:30-02:00 | Lunch and Networking<br>1:30-2:00 Poster Discussions: Antimicrobial resistance and Drug Related Issues |
| 02:00-04:00 | Plenary Session 5: Biosecurity, Biodefense, and Disaster Response<br>Session Chairs: Tahra El-Obeid<br>(Prof. College of Health Sciences, Qatar University)<br>and Getnet Yimer (Global One Health initiative, Ohio State University) |
| 02:00-02:30 | Lead speaker: Barbara Kowalcyk, kowalcyk.1@osu.edu, The Ohio State University, Columbus, OH, I RTI International, Research Triangle Park, United States I Food and Agriculture Organization of the United Nations, Rome, Italy<br>Title: Ranking food safety risks: a guided approach |
| 02:30-03:00 | Plenary Speaker 5: Douglas T. Shinsato, JD, MBA, Board of Regents, University of Hawaii, Hawaii, USA.<br>Title: Bio-Security, Silos and Solutions |

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| 03:00-03:15 | Oral Presentation 5.1<br>Title: Promoting “One Health” approach implementation governance and response capacity approaches against emerging zoonotic threats and outbreaks in Africa<br>Presenter: Ernest Tambo, tambo0711@gmail.com, Africa Disease Intelligence and Surveillance, Communication and Response Institute, Yaounde, Cameroon, Yaounde, Cameroon I Higher Institute for Health sciences,Universite des Montagnes, Bangangte, Cameroon |
| 03:15-03:30 | Oral Presentation 5.2<br>Title: High Mortality from Blood Stream Infection in Addis Ababa, Ethiopia, Is Due to Antimicrobial Resistance<br>Presenter: Tewodros Ayele, teddyts2000@yahoo.com, Gondar University, Gondar, Ethiopia |
| 03:30-03:45 | Oral Presentation 5.3<br>Title: How South Africa respond to environmental risks of concern with acute and long-term chronic risks<br>Presenter: Margaret Salome Molefe, Molefe.Mabunda@gmail.com, National Department of Environmental Affairs, Directorate: Hazardous Chemicals Management, South Africa I Paraclinical Science: Faculty of Veterinary Science, University of Pretoria, South Africa |
| 03:45-04:00 | Oral Presentation 5.4<br>Title: Assessment of KAP, economic and public health burden of Anthrax in selected outbreak hit areas of Jimma zone<br>Presenter: Feyissa Begna Deressa, feyissa.begna@yahoo.com, Jimma University College of Agriculture and Veterinary Medicine, Jimma, Ethiopia |
| 04:00- 05:00 | Refreshments and Networking Break<br>Poster Discussions (Biosecurity and Biodefense and Pathogenesis, Vaccine Development and metagenomic Technologies) |
| 05:00 | End of Day 2- Scientific session |
| 6:00-9:00 | Cultural Outing in Doha |

| Thursday November 9, 2017 (Day Three) | |
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| 08:30-10:15 | Plenary Session 6: Pathogenesis, Vaccine Development and metagenomic Technologies<br>Session Chairs: Shu-Hua Wang (Dept of Internal Medicine, Infectious Disease Unit, Ohio State University)<br>and Hadi Yassine (Qatar University) |
| 08:30– 09:15 | Lead Speaker: Barney S. Graham, M.D., Ph.D. Vaccine Research Center, Viral Pathogenesis Laboratory and Translational Science Core, The National Institutes of Health, USA<br>Title: Anti-Viral Vaccine Development: Preparing for the Next Pandemic |
| 09:15-09:30 | Oral Presentation 6.1<br>Title: Point-of-Care Lionex and Lipoarabinomannan (LAM) antigen tests and rapid Tuberculosis detection in cattle using non-invasive samples<br>Presenter: Sarah Waibel, waibel.15@osu.edu, Department of Preventive Medicine, The Ohio State University, Columbus, United States |
| 09:30-09:45 | Oral Presentation 6.2<br>Title: Characterization of diverse novel porcine astroviruses in East African smallholder piglets<br>Presenter: Joshua Amimo, jamimo@uonbi.ac.ke, University of Nairobi, Kenya I Biosciences east and central Africa - International Livestock Research Institute (BecA-ILRI) Hub, Kenya |
| 09:45-10:00 | Oral Presentation 6.3<br>Title: Tumor Necrosis factor -308 gene polymorphism and risk of Plasmodium Falcifarum malaria infection among poeple living in Denbia wereda, Northwest Ethiopia<br>Presenter: Nega Berhane Tessema tesnega@yahoo.com, Department of Biotechnology, College of Natural and computational Sciences, University of Gondar, Ethiopia |
| 10:00-10:15 | Oral Presentation 6.4<br>Title: Detection and Phylogenetic Genotyping of Epstein Barr Virus (EBV) Among Blood Donors in Qatar<br>Presenter: Maria Smatti Khalid, msmatti@qu.edu.qa, Biomedical Research Center, Qatar University, Doha, Qatar |
| 10:15-10:45 | Refreshments and Networking<br>Poster Discussions- Food-borne and Water-borne Diseases |
| 10:45-12:30 | Plenary Session 7: Food-borne and Water-borne Diseases<br>Session Chairs: Barbara Kowalcyk and Sylvain Quessy |
| 10:45 -11:30 | Lead Speaker: Manon Racicot DVM, PhD; Adjunct Professor, University of Montreal, St. Hyacinth, Canada.<br>Title: Food Safety from Farm to Fork: A Behavioral Perspective |

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| 11:30-11:45 | Oral Presentation 7.1<br>Title: Comparative Genotypic Analysis of Major Virulence Factors of Salmonella Strains Isolated Along the Beef Chain in Mexico<br>Presenter: Enrique Delgado Suárez, enriquedelgado.suarez@gmail.com, Faculty of Veterinary Medicine and Zootechnics, National Autonomous University of Mexico, Mexico City, Mexico |
| 11:45-12:00 | Oral Presentation 7.2<br>Title: Seroprevalence of Toxoplasma gondii infection among HIV-positive and HIV-negative Subjects in the Khartoum State, Sudan<br>Presenter: Abdalla Ibrahim, abdallami79772@gmail.com, Department of Parasitology, College of Veterinary Medicine, Abrar University, Mogadishu, Somalia |
| 12:00- 12:15 | Oral Presentation 7.3<br>Title: The Canadian Food Inspection Agency Establishment-based Risk Assessment model: How to allocate inspection resources to highest-risk areas?<br>Presenter: Sylvain Quessy, sylvain.quessy@umontreal.ca, Faculté de médecine vétérinaire, Université de Montréal, St-Hyacinthe, Canada |
| 12:15-12:30 | Oral Presentation 7.4<br>Title: A one year study of diversity/evolution of Listeria monocytogenes strains in slaughterhouses and meat facilities in province of Quebec: genomic characterization of virulence and resistance.<br>Presenter: Tamazight Cherifi, ctamazight@gmail.com, Chaire de recherche en salubrité des viandes, Faculté de médecine vétèrinaire, Université de Montréal, Saint-Hyacinthe, Qc, Canada |
| 12:30 -01:00 | CLOSING Ceremony and Bidding for ICOPHAI 2019<br>• 2019 Bidding presentation (10 min.)<br>• Closing remarks:<br>• Hamad Medical Corporation (HMC) - 10 min.<br>• Dr. Abdullatif Al Khal<br>• ICOPHAI Scientific and Organizing chairs (5 min each)<br>• Scientific planning - Prof. Sylvain Quessy<br>• Organizing committee - Dr. Hadi Yassine |
| **END OF ICOPHAI 2017** | |

# Pre-Congress Workshops

## November 6, 2017

**Workshop 1:** **Exposure and Toxicological Characteristics of Chemical Agents in the Environment**

**Workshop 2:** **One Health Approach to Combat AMR**

## Exposure and Toxicological Characteristics of Environmental Chemical Toxicants: An Expanded One Health Paradigm

Michael S. Bisesi, PhD, REHS, CIH

*College of Public Health*
*Ohio State University, Columbus, Ohio USA*

**Content:** The workshop will focus on modes and characterization of direct and indirect exposures to chemical toxicants present in various environmental settings. Examples of major categories and types of toxic organic and inorganic compounds will include solvents, metals and pesticides. Topics will address the general qualitative fate of these toxicants (i.e. absorption, distribution, biotransformation, elimination) in biological systems (i.e. human, animal, plant) and environmental matrices (i.e. air, water, soil, food). In addition, content will include related consequences of exposure, including bioaccumulation and biomagnification of toxic chemicals, general adverse impacts, and relation to risk of disease. The session will include short case scenarios to help contextually frame and apply the information.

| **Thursday November 6**<br>One health approach to combat AMR | |
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| 08:00-08:30 | Opening session: AMR National action plan to combat AMR in the state of Qatar<br>Presenters: Dr. Nahla Sharaf & Dr. Eman Radwan Ministry of Public Health, Dr. Jameela Ali A.A. Al Ajmi |
| 08:30– 08:50 | Title: The current antimicrobial resistant pattern in the state of Qatar<br>Presenter: Dr. Dr. Emad Maghboul |
| 08:50-09:10 | Title: The Principles of Successful Stewardship Program<br>Presenter: Dr . Hisham Ziglam |
| 09:10-09:30 | Title: The role of the research in combating AMR - Academic perspective<br>Presenter: Dr. Mahmoud Hassan |
| 09:30-09:50 | Title: Current situation of AMR in animal sector and its impact on human health<br>Presenter: Dr. Mahmoud Hassan |
| 09:50-10:10 | Discussion |
| 10:10-10:30 | Break time |
| 10:30-12:00 | Group 1<br>• Establish a national governance mechanism,<br>• Increase awareness on AMR in public and HCW<br>• Strengthen AMR surveillance system<br>• Promote infection control programs<br>• Support research and development of one health<br>DR. Nahla Sharaf<br>DR. Eman Radwan<br>MS. Dhouha Hemdani<br>Group 2<br>• Role of Pharmacists in ASP<br>• Implementation of ASP in Outpatient setting<br>• Way of overcoming challenges in implementations of ASP<br>• Informatics and Stewardship<br>Dr. Hisham Ziglam<br>Dr. Yasser Eldeeb<br>Dr. hamad Abdel Hadi<br>Dr. Maliha Thapur<br>Dr. farah Jibril |
| 12:00-13:00 | Lunch Break |

Keynote Address

# Environmental changes and their impact on global health

**Roberto Bertollini, MD MPH**

Advisor to the Qatar Minister of Health

Diseases caused by pollution were responsible in 2015 for an estimated 9 million premature deaths - 16% of all deaths worldwide – three times more deaths than AIDS, tuberculosis, and malaria combined; and fifteen times more than all wars and other forms of violence. It kills more people than smoking, hunger and natural disasters. In some countries, it accounts for one in four deaths. Pollution is closely tied to climate change and loss of biodiversity.
Air pollution is one of the major problem. Fossil fuel combustion in higher-income countries and the burning of biomass in lower-income countries accounts for 85% of airborne particulate pollution. Major emitters of carbon dioxide are coal-fired power plants, chemical producers, mining operations, and vehicles. Accelerating the switch to cleaner sources of energy will reduce air pollution and improve human and planetary health.
Environmental degradation and pollution has a huge cost on societies. At the global scale, spending on pollution-related diseases accounts for up to 7% of health budgets in middle-income countries. Welfare costs from pollution are estimated to be $4.6 trillion per year – equivalent to 6.2% of global GDP.
These data will be illustrated in detail drawing from the results of the recently published report of the Lancet Commission on Pollution related diseases.
Policy option will be mentioned and their advantage for the environment, society and the economy underlined.

# Abstracts Day 1

## November 7, 2017

**Special Session: Zika Virus, Emerging and Re-Emerging Infectious Diseases**

**Session 1: Parasitic and Environmental Zoonoses**

**Session 2: One Health and Impact on Climate Change**

Lead special session: **Larry Schlesinger**, MD President and CEO Texas Biomedical Institute, San Antonio, TX, USA

Title: N/A

Lead Session 1: **Filipe Dantas-Torres**, MV, MSc, DSc, PhD, FRES, Dipl. EVPC; Oswaldo-Cruz Foundation, Brazil

Title: Climate change, biodiversity, ticks and tick-borne diseases: The butterfly effect

Session 2 Panel Discussion: “Environmental Challenges and Impact on Global Health”

Panel moderator: **Nicole Kraft** (USA)

Panelists: **Lauro Santos** (Brazil), **Salome Margaret Molefe** (Republic of South Africa), **Walid Alali** (UAE), **Sylvain Quessy** (Canada)

# Special Session:
# Zika Virus, Emerging and Re-Emerging Infectious Diseases

## Crimean Congo Hemorrhagic Fever in Sudan: Current Status and Future prospects

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**ABSTRACT:** Crimean Congo hemorrhagic fever (CCHF) virus (CCHFV) is the causative agent of a tick-borne disease with high mortality rates in humans. CCHFV strains represent a potential bioterrorism threat since infection can be acquired nosocomially. CCHFV has been detected in a wide geographic zone including most of Africa, southern Europe and Asia, extending from western China to the Middle East and Southern Russia, where focal endemic areas have been identified. Disease outbreaks and sporadic cases of CCHF have been recorded throughout these endemic areas, with several recent outbreaks occurring in the Sudan. In 2008, a nosocomial outbreak of CCHF occurred in a rural hospital in the Al-fulah District, Western Kordufan, Sudan ; two minor genetic variants, designated Al-fulah 3 and 4 (Genbank accession nos Q862371-2), were identified during that outbreak and were thought to be responsible for the emergence of the disease in the region. In 2009, a second CCHF outbreak involving approximately seven suspect cases of CCHF in Dunkop village, Abyei District, South Kordufan, Sudan, was reported reported. However, additional analysis revealed that the virus strains implicated in the June 2009 cluster was genetically distinct from that involved in the 2008 Al-fulah outbreak. In February 2010, a nosocomially acquired CCHF infections was reported in an attending physician in North Kordufan region as a result of medical referral of an index patient from an area of endemicity in Lagawa District, South Kordufan. This represents the third report of the disease in the same region of Sudan. In this paper, Viral RNA extraction and subsequent RT-PCR sequencing were used to generate the complete genome sequence. Phylogenetic analysis was constructed to determine the genetic lineage of the virus strains. Detection and genomic characterization of Sudanese CCHFV strain are discussed.

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## Crimean Congo Hemorrhagic Fever among the One-Humped Camel (Camelus dromedaries) in Central Sudan.

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**ABSTRACT:** Crimean-Congo hemorrhagic fever (CCHF) is a tick-borne viral zoonotic disease caused by Crimean-Congo hemorrhagic fever virus (CCHFV), a member of the genus Nairovirus in the family Bunyaviridae. The disease is distributed worldwide and coincides with the global distribution of the tick vector. Whereas CCHF is typically asymptomatic in animals, the disease can be highly fatal in humans approaching mortality rate of 50%. In the present investigation, a cross sectional study was conducted to determine the prevalence of CCHF and to identify the potential risk factors associated with CCHFV seropositivity among the one-humped camel (Camelus dromedaries) in Khartoum State, Central Sudan. A total of 361 dromedary camels selected randomly from six localities were employed in this study. Sera sampled were tested for the presence of CCHFV-specific immunoglobulin G (IgG) antibodies using indirect enzyme-linked immunosorbent assay (ELISA). CCHFV seropositivity was recorded in 77 out of 361 animals accounting for a prevalence rate of 21.3 %. Age (OR = 3.6, CI= 1.72- 7.79, p-value = 0.026); locality (OR = 5.85, CI= 1.81-18.83, p- value = 0.003), tick number (OR = 4.6 , CI= 1.37-9.81, P-value 0.04); tick control (OR = 2.2 , CI, 1.11-4.35, P-value = 0.023 ) and breed (OR = 6.60 , CI=2.38-18.36, P-value = 0.001) were recorded as potential risk factors for contracting CCHF. Surveillance for CCHF should continue to include other susceptible ruminants and to study the distribution of the tick vectors in this region of Africa. Further molecular characterization studies such as complete viral genome sequencing and subsequent phylogeny would be necessary to determine the genetic lineages of CCHFV strains circulating in infected tick vectors in Sudan.

## Domestic cavies (Cavia porcellus) are reservoirs of zoonotic protozoa in rural areas of Cameroon.

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Domestic and pet animals are usually suspected to transmit infections to humans. Domestic cavies, currently massively adopted by farmers in rural areas of Cameroon as mini-livestock were investigated for their role as a reservoir of zoonotic protozoa in the Western Highland of Cameroon. The Giardia/Cryptosporidium Chek® immunoassay was used to detect both Giardia and Cryptosporidium antigens in cavy fecal samples. Giardia/Cryptosporidium antigens were detected in 12 out of 93 cavies (12.90%). Thus domestic cavies are host of Giardia/Cryptosporidium. Because these protozoa have a low infectious dose, have transmissive stages that are small in size and environmentally robust, and are insensitive to the disinfectants commonly used in the water industry, there is increased evidence that domestic cavies play a role in the transmission of Giardia/Cryptosporidium to human in rural areas of Cameroon. This implies that public health officials and veterinarians must collaborate for effective control measures against these protozoa.

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## Bovine Tuberculosis in Rwanda: Status, Challenges and Ways forward

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Despite the public and economic impact of bovine tuberculosis (BTB) in Rwanda, there is a paucity of information on its epidemiology and its true burden. The increased trend of zero grazing in many households in Rwanda has led to animals being in backyards forcing closer interaction of man and their animals. This scenario facilitates the transmission of zoonotic infectious diseases including BTB. Data collected from SABAN Nyabugogo over 5 consecutive years (2009-2013) show that the prevalence of BTB is fluctuating. In 2009 the prevalence of BTB-like lesions was 0.9% (n=16753) which slightly decreased in the following year 2010 with 0.7% (n=26708). The prevalence was slightly more than double in the following year with 1.7% (n=28005), and then varied between 0.5% (n=27508) and 1.5% (n=27391) in 2012 and 2013 respectively. The condemned meat prejudiced the nation of 11,174.5 kg of meat with attendant economic losses of FRW 22,349,000.00 (US$ 27,254.88) during this period. Considering its indirect public health consequences, BTB also contributed to the loss of animal protein that is already scarce. The condemned meat would have been enough to feed 122 adult men for a year. From the available baseline data, we can confirm that BTB is present in Rwanda. Considering the occurrence of BTB lesions in meat, it is likely that the risks for acquiring the infection through consumption of raw and/or undercooked meat exists. The increased prevalence of extra-pulmonary tuberculosis in humans calls for an investigation into the possibility of Mycobacterium bovis being the causative agent. At least surveillance programs should be put in place, focusing especially on high-risk animals from areas bordering national parks where the human-livestock-wildlife interaction is high and animals originating from neighbouring countries where BTB is present and its prevalence high.

## Informing hepatitis C virus screening strategies in the Middle East and North Africa: A pooled analysis for the risk of exposure

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**Background:** The drive towards hepatitis C virus (HCV) expanded treatment and eventual elimination is currently challenged by screening costs and logistics. The aim of this work is to quantify different populations' risk of being exposed to HCV and estimate the yields of screening programs targeting these populations across the Middle East and North Africa (MENA).

**Methods:** Our source of data was the MENA HCV Synthesis Project database, an extensive compilation of HCV prevalence studies identified through systematic literature searches and including tests for over 52 million individuals. Estimates for the mean risk of being exposed to HCV among different populations and for the mean relative risk (RR) of exposure across these populations were generated using DerSimonian-Laird random-effects meta-analyses. The yields of screening programs were subsequently derived assuming a spontaneous clearance rate of 25%.

**Results:** Compared to the general population, the mean RR (95% confidence interval-CI) was assessed at 55.5 (95% CI: 32.0-96.3) among people who inject drugs-PWID, 34.2 (95% CI: 19.4-60.3) among populations with high risk healthcare exposures, 4.8 (95% CI: 2.7-8.5) among populations at intermediate risk, 19.3 (95% CI: 11.7-32.0) among populations with liver conditions, and 15.8 (95% CI: 10.3-24.4) among special clinical populations. The yield of screening, that is number of screens needed to identify one HCV infected individual, was estimated at 2.8 (95% CI: 2.5-3.1) among PWID, 4.4 (95% CI: 4.1-4.8) among populations with high risk healthcare exposures, 20.3 (95% CI: 17.6-23.6) among populations at intermediate risk, 55.8 (95% CI: 53.5-58.5) among the general population, 4.0 (95% CI: 3.6-4.6) among populations with liver conditions, and 8.5 (95% CI: 6.8-11.1) among special clinical populations. The expansion path curve for countries with a generalized HCV epidemic showed a slow incremental increase from 2-3 screens among populations with liver conditions, PWID, and populations with high risk healthcare exposures up to 14 screens among the general population. Meanwhile, a sharper increase in the number of screens necessary to identify one HCV infected individual from 3 among PWID and 5 among populations with high risk healthcare exposures up to 242 screens among the general population was estimated in countries with concentrated epidemics.

**Conclusions:** There is hierarchy in the risk of exposure to HCV, with PWID and clinical populations being most exposed to the infection. Screening yields must be factored in the design of screening programs to ensure cost-effective roll-out, notably in countries with concentrated epidemics.

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## Modeling the hepatitis C virus epidemic in Pakistan: Past trajectory and future trend

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**Background:** Pakistan is believed to have the second largest number of hepatitis C virus (HCV) infected people worldwide. Our aim was to assess the level and trend of the HCV epidemic in Pakistan.

**Methods:** We developed and analyzed an age-structured mathematical model that simulates HCV infection transmission in the population. The model was parameterized with current natural history data, and fitted to nationally-representative population-based HCV survey data and a comprehensive database of systematically-gathered HCV prevalence data in different risk populations.

**Results:** HCV antibody prevalence in Pakistan has been declining since 2000. While HCV prevalence was 5.3% in 2000, it was projected to decline to 4.4%, 3.5%, and 2.6% in 2017, 2030, and 2050, respectively. Number of prevalent chronic infections was 5,112,655 in 2000, and it was projected to increase, with the growing demographics, by 21.6%, 20.2%, and 5.7% in 2017, 2030, and 2050, respectively. Number of new HCV infections per year (HCV incidence) and incidence rate have been declining since 1989-1992, but will persist at considerable levels for decades unless controlled by interventions. While number of new infections was 285,891 in 2000, it was projected to decline by 37.5%, 51.6%, and 66.8% in 2017, 2030, and 2050, respectively. Although incidence rate per 100,000 person-year was 230.0 in 2000, it was projected to decline by 57.4%, 73.6%, and 80.3% in 2017, 2030, and 2050. Across age groups, the largest number of new infections and prevalent chronic infections in 2017 were in the age group 30-39 years at 47,930 and 1,242,357 infections, respectively.

**Conclusion:** Though HCV prevalence and incidence rate are declining, Pakistan is enduring a large epidemic that will persist for decades if not controlled. There is immediate need for rapid and mass scale-up of HCV prevention and treatment interventions to reduce transmission and decrease the burden of HCV disease sequelae.

## Rift Valley Risk Communication; a Possible Framework

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Rift Valley fever (RVF) is a mosquito-borne viral disease that affects both man and animals. It mainly affects sheep, cattle and goats, although the disease can also affect camels, buffaloes and many other mammalian species, including humans. The disease therefore poses a threat to human health animal health and production. Currently, RVFV is limited to Africa and the Arabian Peninsula, but the virus has demonstrated clear characteristics that might place nations outside its current borders at risk (WHO, 2009). Mosquito bites spread the disease in animals from where the virus is transmitted to humans through direct contact with raw animal products, aerosols, secretion or body fluids from infected animals. Human infections are common among virologists, veterinarians and slaughterhouse workers. These group therefore are at risk populations in an outbreak. Their risk perception index of the disease should be higher and this can be affected by the messages they receive about the disease. Risk communication is among the control interventions in the containment of RVF, others are strategic vaccinations and vector control. effective risk communication should serve to increase the RVF risk perception index among the at-risk population. However, it is also noted that risk communication is one of the challenges in the control of the disease. There is inadequate literature on RVF risk communication. This paper attempts to fill in the literature gap on RVF risk communication by looking at a possible risk communication framework build upon the Risk Information Seeking and Processing (RISP) Model.

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## Herpes Simplex Virus Type 2 Seroprevalence among Different Middle East and North Africa Men National Populations

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**Background:** There are very limited data on herpes simplex virus type-2 (HSV-2) infection in the Middle East and North Africa (MENA). We examined nationality- and age-specific HSV-2 seroprevalence among select MENA populations residing in Qatar.

**Methods:** Sera were collected from men blood donors attending Hamad Medical Corporation June 2013-2016. Specimens were screened for anti-HSV-2 antibodies following a two-test algorithm: HerpeSelect 2 ELISA was used to identify HSV-2 positive specimen, and Euroline-WB was used to confirm positive and equivocal specimens for final HSV-2 status. IgG kits. Trends and associations with HSV-2 seropositivity were assessed.

**Results:** Sera from 2,077 blood donors were tested for HSV-2. Of 122 eligible retested specimens, 61 were confirmed positive. The proportion confirmed positive increased steadily with HerpeSelect® 2 ELISA index value, ranging from 16.3% for index values 1.001-1.999 to 92.9% for index values ≥4. Nationality-specific HSV-2 prevalence was measured at 6.0% (95% confidence interval (CI), 4.1-8.8%) for Qataris, 5.3% (95% CI, 2.5-11.1%) for Iranians, 4.2% (95% CI, 1.8-9.5%) for Lebanese, 3.1% (95% CI, 1.2-7.7%) for Sudanese, 3.0% (95% CI, 1.4-6.4%) for Palestinians, 2.2% (95% CI, 1.1-4.3%) for Egyptians, 2.0% (95% CI, 1.0-5.0%) for Syrians, 1.0% (95% CI, 0.3-3.6%) for Jordanians, 0.7% (95% CI, 0.1-3.7%) for Yemenis, and 0.5% (95% CI, 0.1-2.8%) for Pakistanis. Age-specific HSV-2 prevalence was estimated for Egyptians, nationals of the Fertile Crescent, and Qataris. There was evidence for higher seroprevalence in older age groups.

**Conclusion:** HSV-2 seroprevalence among MENA men nationals was found to be lower - in the range of few percentage points - than that commonly found in other regions. However, There were no major differences in seroprevalence by nationality. These findings inform our understanding of HSV-2 epidemiology in MENA, and indicate unmet needs for sexual health and control of sexually transmitted infections.

## Unexplained Hemorrhagic fever outbreak in southern Ethiopia

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## Unexplained Haemorrhagic Fever in Rural Ethiopia

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**Abstract:** This case study was written based on events of an outbreak investigation of an unfamiliar disease in Ethiopia during October–December 2012. Ethiopia did not have reports of similar cases in the 50 years prior to this outbreak. In this case study, we recapitulate and analyse this outbreak investigation based on data gathered from the community, health facility, and laboratory systems. It can be used to teach: 1) the outbreak investigation process; 2) selection of appropriate epidemiological design for the investigation process, 3) basic statistical analysis of surveillance data, and 4) principals of disease control. The target audiences for this case study are officials working in public health and public health trainees. It will take at most 3.5 hours to complete this case study. At the end of the case study, participants should be able to apply the principals of outbreak investigation and use surveillance data to respond to an outbreak in their country-specific context.

### How to Use the Case Study

**General instructions:** To conduct this case study in the classroom, the authors propose that the participant's guide be distributed one part at a time. Background material, including the appendices, should be distributed before the case study for review by the participants.

Participants should take turns reading the narrative aloud, paragraph by paragraph. Reading all paragraphs aloud and in turns has two advantages: first, everyone is given an opportunity to participate and get beyond the inhibition of having her/his voice heard in a large room; second, the whole class is given time to understand the issue and think about the answers.

The participants reading the question may try to answer it if s/he can; otherwise, it can be discussed as a group or completed as an exercise as the instructor's notes dictate. Instructor's notes are included in the instructor's guide for each question. Complete all reading and questions before the next part is distributed. Then the next participant continues and so on until the case study is over. Once the conclusion is read, re-visit the learning objectives – this reinforces the learning and provides an opportunity to clarify any remaining issues.

**Audience:** Officials working at the National Surveillance Department, Ministry of Health, Regional Surveillance Office, District Surveillance Office, District Head of Heath Department, and FETP/ Public Health trainees.

Prerequisites: Before using this case study, participants should have received lectures in outbreak investigation, application of epidemiological study designs, and Integrated Disease Surveillance & Response guidelines and have experience or be currently working in a health-related field, or contributing to the government health surveillance functions. Unexplained Haemorrhagic Fever in Rural Ethiopia – Participant's Guide Version 1.0

**Materials needed:** White board or flip cha

## Incidence of human rabies exposure and associated factors at the Gondar Health Center, Ethiopia: a three-year retrospective study

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**Background:** Rabies is one of the oldest known and most feared human diseases. Epidemiological studies provide basic information about the burden of the disease and underline the importance of prevention and control interventions. However, there have been limited studies conducted regarding the incidence of rabies and associated factors in Ethiopia, in general, and in this study area, in particular. Therefore, the aim of this study was to assess the incidence of human rabies exposure and associated factors at the Gondar Health Center, Ethiopia.

**Methods:** A retrospective cross-sectional study was conducted at the Gondar Health Center where post-exposure prophylaxis (PEP) for rabies was available for the whole population in the North Gondar Zone catchment area. Data of human rabies exposure cases between 2011 and 2013 were collected from the rabies PEP registration book using data abstraction sheets. The data was entered and analyzed using SPSS version 16 statistical software.

**Result:** A total of 261 cases of human rabies exposure were reported to the Gondar Health Center from 2011 to 2013. The sex and age specific distribution showed that the majority of these cases were among males (142/226, 62.8%) and children under 15 years of age (87/226, 38.5%). A predominant number of cases were observed in individuals from rural areas (161/220, 73.2%), and during fall and winter seasons (67/222, 30.18%). A significant number of people exposed to rabies (23.2%) came to the health center for PEP two or more weeks after the injury. The incidence of human rabies exposure cases was 4.6, 2.61, and 1.27 per 100, 000 population in 2011, 2012, and 2013, respectively. Being male and living in an urban setting were found to be risk factors for human rabies exposure in 2011.

**Conclusion:** A significant number of human rabies exposure cases were reported to the Gondar Health Center. Being male and living in urban settings were found to be associated with rabies exposure. A community-based follow-up study is recommended to more accurately estimate the incidence of human rabies exposure.

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## Hepatitis C Virus Genotypes in the Middle East and North Africa: Distribution, Diversity, and Patterns

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Objective: Characterizing the distribution, diversity and patterns of hepatitis C virus (HCV) genotypes in the Middle East and North Africa (MENA) by estimating, for each country, the 1) pooled mean proportions of HCV genotypes, 2) genotype diversity, and 3) genotype-specific number of chronically infected individuals.

**Methods:** Source of data was a database of HCV genotype studies in MENA populated using a series of systematic literature searches. Pooled mean proportions were estimated for each genotype and by country using DerSimonian-Laird random-effects meta-analyses. Genotype diversity within countries was assessed using Shannon Diversity Index. Number of chronic infections by genotype and country was calculated using the pooled proportions and country-specific numbers of chronic infection.

**Results:** Analyses were conducted on 338 genotype studies including 82,257 genotyped individuals. Genotype 1 was dominant (≥50%) in Algeria, Iran, Morocco, Oman, Tunisia, and UAE, and was overall ubiquitous across the region. Genotype 2 was common (10-50%) in Algeria, Bahrain, Libya, and Morocco. Genotype 3 was dominant in Afghanistan and Pakistan. Genotype 4 was dominant in Egypt, Iraq, Jordan, Palestine, Qatar, Saudi Arabia, and Syria. Genotypes 5, 6, and 7 had limited or no presence across countries. Genotype diversity varied immensely throughout MENA. Weighted by population size, MENA's chronic infections were highest among genotype 3, followed by genotype 4, genotype 1, genotype 2, genotype 5, and genotype 6.

**Conclusions:** Despite ubiquitous presence for genotype 1, the vast majority of chronic infections were of genotypes 3 or 4, because of the sizable epidemics in Pakistan and Egypt. Three sub-regional patterns were identified: genotype 3 pattern centered in Pakistan, genotype 4 pattern centered in Egypt, and genotype 1 pattern similar to common global pattern. These patterns appeared to reflect cross-border population movements and geographic proximity. These findings inform the DAA treatment programs being expanded in MENA, and provide insights about HCV transmission pathways.

## Challenges to Control Ebola in West Africa: A Review

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Ebola Virus disease (EVD) is a severe, often-fatal, zoonotic viral disease in humans and nonhuman primates (monkeys, gorillas and chimpanzees) that has appeared sporadically since its initial recognition in 1976. The virus is one of two members of a family of RNA viruses called the Filoviridae. There are five identified subtypes of Ebola virus. Four of the five have caused disease in humans: Ebola-Zaire, Ebola-Sudan, Ebola-Ivory Coast and Ebola-Bundibugyo. The fifth, Ebola-Reston, has caused disease in non-human primates, but not in humans. Filovirus epidemics have originated from West Africa and now spreading to other continents. This outbreak has been so challenging to control in West Africa. The main objectives of this paper are to highlight the general characteristics of Ebola virus disease and to review the possible challenges of controlling the disease outbreak in West Africa. The affected countries in West Africa do not have the basic infrastructure to contain the Ebola epidemic. Most primary health workers did not have any prior experience dealing with this virus. Ebola is transmitted through body fluids and immediately attacks the immune system, then progressively attacks the major organs and the lining of blood vessels. Treatment to date has been supportive, not curative and outbreak control strategies have been met with distrust due to fear, stigmatization and misinformation. Traditional burial practices also pose a major risk to close relatives, since they typically involve the cleaning and rubbing of dead bodies. Interagency policies for outbreak detection and rapid response increased understanding of cultural and traditional risk factors within and between nations, delivery of culturally embedded public health education and regional coordination and collaboration, particularly with governments and health ministry throughout Africa were required to control these challenges.

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## Corona viruses detected in bats of Rwanda: diversity at human – wild life interfaces and a call for one health approach

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Bats are documented to be the natural reservoir for some corona, filo, paramyxo and lyssa viruses. Coronaviruses cause infections that are of public health importance, as in the recent past, human pandemics have been caused by SARS- CoV and MERS- CoVs. Using consensus PCR we investigated the presence of corona virus in 503 bats of 17 species in Rwanda from 2010 to 2014. Twenty-seven bats belonging to 8 species were found to have known and new coronaviruses. Known viruses detected included the betacoronaviruses Kenya bat coronaviruses, Eidolon bat coronavirus, Bat coronavirus HKU9 and alphacoronavirus Chaerephon Bat coronavirus, while new coronaviruses included two betacorona viruses that clustered with SARS-CoV and SARS-related CoV, one 2d coronavirus and one alphacoronavirus. These viruses were detected in bats at diverse high-risk human-wildlife interfaces. These results provide support for a multidisciplinary approach to examine emerging infectious diseases in wildlife, and the need for further viral characterization to better understand their spillover potential into humans.

## RSV Seasonality in Oman

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**Background:** In the developing world pneumonia represents a major public health disease burden. Respiratory syncytial virus (RSV) is the main viral cause of severe pneumonia and bronchiolitis in infants and young children contributing considerably to the burden on health services. The global estimate in 2005 indicated that at least 33.8 million episodes of RSV associated acute lower respiratory infection (ALRI) occurred worldwide in children younger than 5 years and most of these deaths occurred in developing countries.

**Introduction:** RSV season varies over time and from location to location. The start and end of RSV season can vary year to year, and can even vary within communities in the same region.2

**Methodology:** RSV disease is not a notifiable disease in Oman and the primary data source for this study is the Central Public Health Laboratory (CPHL) Virology. This study aimed to systematically aggregate and analyze published virological data on the seasonality of RSV in young children and adults in Oman between 2013 and 2015.

**Result:** In temperate climates, as well as Mediterranean and desert climates, the RSV season corresponds to the cold season1, a finding consistent with the pattern found in this review.

Most communities with temperate climates have a well-defined season of 3 to 5 months usually starting in the Northern hemisphere in October or November and continuing until February or March.3 In the southern hemisphere, wintertime epidemics occur from May to September.2 It is common for there to be a biennial change from one season to the next whereby the subsequent season is milder or more severe than the preceding. However, this is not predictable and the differences may be more related to climactic changes. 3

In Oman, the overall RSV average activity of last 3 years (2013-2015) started to increase in week 40 and ending in week 52,53 however RSV continues circulating at variable numbers like other countries . Figure 1

During the 3 years, 16191 samples were tested for respiratory viruses; 3658 (22%) samples were positive for respiratory virus, including 449 (11%) positive for RSV.

**Conclusion:** The season in which RSV epidemics occur typically depends on geographical location and altitude. It is likely that several factors interact in complex ways in the development of epidemics under favorable climatic conditions 2. During the study, RSV infections were seen throughout the last three years, predominating in the ( week 40-53) October to December in Oman. Figure 2

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## Estimating the burden of influenza associated hospitalization and deaths in Oman (2012-2015)

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**Background:** Influenza is a serious vaccine-preventable disease with high incidence, high rate of hospital admissions and mortality in high risk groups. The epidemiology, seasonality and risk factors for seasonal influenza are well defined in most of the temperate countries, but there are few estimates of influenza burden in the WHO Region for the Eastern Mediterranean. In Oman, despite the advancements in influenza surveillance, the clinical burden and seasonality influenza remains not fully understood.

**Objectives:** To estimate the incidence of influenza associated hospitalizations and in-hospital death Oman

Patients and Methods: Influenza-associated hospitalizations and in-hospital deaths in Oman were estimated using hospital discharge records based on ICD-10 codes (J 09-18), results of virological analysis, and population census for the period between 2012 and 2015.

**Results:** Between 2012 and 2015, 19405 SARI case diagnosed with 847 related deaths and average influenza positivity rate of about 17%. The total influenza associated hospitalization ranged between 7.3 (95% CI: 6.4-8.1) per 100000 in 2013 and 27.5 (95% CI: 25.9-29.1) per 100000 in 2015 with an overall rate of 20.6 (95% CI: 19.9-21.3) per 100000. The highest incidence of influenza associated death was in elderly aged ≥65 years and ranged between 11.3(95% CI: 7.5-15.1) in 2015 and 39.5 (95% CI: 27.3-51.8) per 100000 in 20145.

**Conclusion:** Influenza causes a substantial numbers of hospitalizations and deaths in Oman. Hospitalization rates were highest among children and adults ≥65 years showed the highest death rate. Thus, the potential value of using seasonal influenza vaccine in these groups should be considered.

**Keywords:** Influenza-associated hospitalizations, Influenza in-hospital death, SARI and Oman.

## Dengue and Chikungunya in the Middle East and North Africa: A Systematic Review

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**Background:** The epidemiology of Dengue virus (DENV) and Chikungunya virus (CHIKV) in the Middle East and North Africa (MENA) is not well characterized despite increasing recognition of their expanding geographic reach and disease burden in recent years.

**Methods:** Following the PRISMA guidelines, we systematically reviewed available records across the MENA region describing DENV and CHIKV human incidence and prevalence, infections in vectors, outbreaks, and reported cases. The data was summarized through descriptive statistics and maps.

**Results:** For DENV, we identified 105 human prevalence measures in 13 of 24 MENA countries, 81 outbreaks reported from 9 countries from 1941–2015, and reports of Ae. aegypti and/or Ae. albopictus occurrence in 15 countries. The majority of seroprevalence studies were reported from the Red Sea region and Pakistan, with multiple studies indicating >20% DENV seroprevalence in general populations (median 25%, range 0–62%) in these subregions. For CHIKV, we identified 29 human seroprevalence measures, one human incidence study, one study reporting CHIKV infection rates in Aedes, and nine outbreaks and case reports/series reported in the MENA from 1970–2015. Overall, anti-CHIKV antibody or reports of autochthonous transmission were identified from 10 of 23 countries in the MENA region (Djibouti, Egypt, Iraq, Iran, Kuwait, Pakistan, Saudi Arabia, Somalia, Sudan, and Yemen), with seroprevalence measures among general populations (median 1.0%, range 0–43%) and acute febrile illness populations (median 9.8%, range 0–30%). Sudan reported the highest number of studies (n = 11) and the highest seroprevalence among general populations (median 12%, range 0–43%) and undifferentiated acute febrile illness populations (median 18%, range 10–23%). CHIKV outbreaks were reported from Djibouti, Pakistan, Sudan, and Yemen. Multiple DENV and CHIKV studies utilized assays susceptible to serologic cross-reactions and less than 10% of seroprevalence studies utilized viral neutralization testing. There was considerable heterogeneity in study design and outbreak reporting, as well as variability in subregional study coverage, study populations, and laboratory methods used for diagnosis.

**Conclusion:** Published evidence suggests endemic transmission of DENV and CHIKV in at least the Red Sea region and Pakistan. However, indications of seroprevalence despite a low quantity of epidemiologic research from the region suggest that DENV and CHIKV transmission is currently underrecognized.

## Delay in Diagnosis of Pulmonary Tuberculosis in Low-and Middle-Income Settings: Systematic Review and Meta-Analysis

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**Background:** Assessment of delays in seeking care and diagnosis of tuberculosis is essential to evaluate effectiveness of tuberculosis control programs, and identify programmatic impediments. Thus, this review of studies aimed to examine the extent of patient, health system and total delays in diagnosis of pulmonary tuberculosis in low- and middle- income countries.

**Design:** It was done following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses. Electronic databases were searched to retrieve studies published from 2007 to 2015 including Springer link, Pubmed central, Hinari and Google scholar. Searching terms were pulmonary tuberculosis, health care seeking, health care seeking behavior, patient delay, diagnostic delay, health system delay, provider delay and doctor delay. Retrieved studies were systematically reviewed and summarized using comprehensive meta-analysis software.

**Results:** Forty studies involving 18,975 patients qualified for systematic review and 14 of them qualified for meta-analysis. The reported median delays ranged from 30 to 366.5 days for diagnosis delay; 4 to 199 days for patient delay, and 2 to 128.5 days for health system delay. The meta-analysis showed 42% of pulmonary tuberculosis patients delayed seeking care by a month or more; uneducated patients [pooled OR=1.5, 95%CI=1.1-1.9] and those who sought initial care from informal providers [pooled OR=3, 95%CI=2.3-3.9] had higher odds of patient delay.

**Conclusion:** Delay in diagnosis is still a major challenge of tuberculosis control and prevention programs in low- and middle- income settings. Efforts to develop new strategies for better case-finding and improving patients' care seeking behavior need to be intensified.

**Keywords:** patient delay, health system, diagnosis delay, pulmonary tuberculosis

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## Silent Hepatitis E Virus (HEV) Infection: Potential Threat to Blood Banks

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**Abstract:** HEV is a small spherical RNA virus transmitted mainly through fecal-oral route. More than 80% of Qatar's population are expatriates, including many coming from hyperendemic countries; thus, it is important to estimate the seroprevalence and to compare between different nationalities. The results can be useful in alerting blood banks to the importance of HEV screening, and to investigate possible transmission patterns.

Samples from 5854 blood donations provided by Hamad Medical Corporation (HMC) were tested in the period between June 2013 to June 2016. Samples were tested for the presence of anti-HEV IgG and IgM antibodies and viral RNA using real time polymerase chain (RT-PCR) reaction. Descriptive statistics, bivariate analysis and multivariate logistic regression were used. The study received an "Exempt" classification reference number (Protocol #14292/14).

Anti-HEV antibodies seroprevalence was 20.7 %. A statistically significant association was detected between HEV seroprevalence with age and nationality. HEV IgM and RNA were also detected, suggesting the possibility HEV transmission by transfusion.

# Session 1:
# Parasitic and Environmental Zoonoses

## Title: Climate change, biodiversity, ticks and tick-borne diseases: The butterfly effect

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Abstract: We have killed wild animals for obtaining food and decimated forests for many reasons. Nowadays, we are burning fossil fuels as never before and even exploring petroleum in deep waters. The impact of these activities on our planet is now visible to the naked eye and the debate on climate change is warming up in scientific meetings and becoming a priority on the agenda of both scientists and policy decision makers. It may be anticipated that warmer winters as well as extended autumn and spring seasons will continue to drive the expansion of the distribution of some tick species (e.g., Ixodes ricinus) to northern latitudes and to higher altitudes. Nonetheless, further studies are advocated to improve our understanding of the complex interactions between landscape, climate, host communities (biodiversity), tick demography, pathogen diversity, human demography, human behaviour, economics, and politics, also considering all ecological processes (e.g., trophic cascades) and other possible interacting effects (e.g., mutual effects of increased greenhouse gas emissions and increased deforestation rates). The multitude of variables and interacting factors involved, and their complexity and dynamism, make tick-borne transmission systems beyond (current) human comprehension. That is, perhaps, the main reason for our inability to precisely predict new epidemics of vector-borne diseases in general.

* This title and abstract have originally been published at: https://doi.org/10.1016/j.ijppaw.2015.07.001

## Molecular characterization of Echinococcus granulosus s.l. cysts from cattle, camels, goats and pigs in Ethiopia

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Cystic Echinococcosis (CE) caused by Echinococcus granulosus sensu lato (s.l.) is a neglected helminth zoonosis affecting humans and various animal species. Human CE has been reported in almost all coun-tries of sub-Saharan Africa but its prevalence and public health impact are subject to large geographical variations. The reasons for these differences are not well understood; among other factors, occurrence of different species/genotypes of E. granulosus s.l. has been suggested. CE is very common in all livestock species in Ethiopia; human CE is poorly documented in the country. The aim of this study was to assess the fertility and molecularly characterize hydatid cysts collected from cattle, camels, goats and pigs from different parts of the country. From the 137 samples characterized by PCR-RFLP and sequencing, 115 (83.9%) were identified as E. granulosus s.s. (G1, common sheep strain), 6 (4.4%) as Echinococcus ortleppi (G5, cattle strain) and 16 (11.7%) as Echinococcus intermedius (G6/7, camel strain). In cattle, E. granulosus s.s. and E. ortleppi were found; in camels and goats, E. granulosus s.s. and E. intermedius; two cysts found in pigs were identified as E. granulosus s.s. and E. ortleppi, respectively. All cysts recovered from goats and pigs were sterile, while fertility was 34% and 50% in cysts from cattle and camels, respectively. In cattle, 31% of E. granulosus s.s. cysts were fertile, showing the importance of cattle in the transmission of the “sheep strain”. Next to E. granulosus s.s., E. intermedius (camel strain) was the predominant species: 34.4% of the cysts collected from camels and 62.5% from goats were identified as E. intermedius. These animals originated from the drier Central, Eastern and Southern parts of the country. For the first time, we showed the presence of CE in pigs in Ethiopia. The presence of these strains and especially the fact that the zoonotic E. granulosus s.s. and E. intermedius are dominant, make CE an important public health concern in Ethiopia.

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## Survey of zoonotic myiasis in domestic cavies farms in rural areas of Cameroon

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Domestic cavies is gaining interest in many rural areas of Cameroon, especially in the West region of the country due to cavy potential to provide rapid means for income generation and to also to provide manure for crop production. Since livestock production if often associated with occurrence of diseases, a study was initiated on cavy farms to investigate any occurrence of the zoonotic tumbu fly known to occur in other domestic animals. Thus, a total number of 62 cavy farms in villages of Menoua Division were examined for the presence of the larvae of the tumbu fly, Cordylobia anthropophaga. Only suspect animals, with any sign of ectoparasitim (limping, inhability to compete for food, to walk or to run effectively) were caught and examined. 16 out of 62 farms (25.8%) were infested with this parasite. The potential role of infested cavies in the zoonotic transmission of C. anthropophoga myiasis is supported by the finding of this study.

## Seroprevalence and risk factors of Tænia solium cysticercosis in pigs from rural areas of Boucle du Mouhoun region, Burkina Faso

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This study aimed to assess the seroprevalance and identify risk factors of porcine cysticercosis at Boucle du Mouhoun region in Burkina Faso. To reach it, 373 serum samples collected in pigs randomly selected in four villages, were tested using Ag ELISA test in order to detect circulating antigens of Tænia solium. In addition, surveys were carried out among breeders in order to spot factors that can be considered as risk factors. The seroprevalance of the disease was 54.9 ± 5 %. Prevalence was significantly higher ($p<0.05$) in Koumbia (60.7 ± 11%), Sadon Bobo (60 ± 11%), and Toné (58.4 ± 8.5%) in comparison to Kabourou (39.3 ±10 %). It was also higher ($p<0,05$) in males (63.3 ± 8.3 %) than females (50.6 ± 6.2%) and in pigs held by men (81.2 ± 19.1 %) in comparison to the ones by women (53.8 ± 5.1). The identified risk factors were belonging to the village of Koumbia (OR = 2.4 IC 95% : 1.3 - 4.6) ; Sadon Bobo (OR = 2.1 IC 95% : 1.1 - 4.0); Toné (OR = 2.5 IC 95 % : 1.2 - 3.9), male pigs (OR = 1.7 IC 95% :1.1 - 2.7) and being held by men (OR = 3.7 IC 95% :1.2 - 16.4). However, no variation was noticed considering the age and the gender of pigs. The existence of old cases of swine cysticercosis did not influence either

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## Determination of Parasitic Load in Government Cattle Breeding and Dairy Farm, Charsadda, Khyber Pakhtunkhwa-Pakistan

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Abstract | This study was conducted to determine the parasitic diseases in Cattle Breeding and Dairy Farm, Harichand. For this purpose a total of 234 blood samples and 100 fecal samples were collected from different breeds, age and sex of cattle and screened for endo-parasites. Giemsa stained thin blood smears were used for haemo-protozoan while for gastrointestinal parasites direct examination and floatation technique was used. Incidence of haemo-parasitic diseases was recorded as 18 and 28% for Theileria and Anaplasma, respectively while incidence of intestinal parasites were recorded as 12, 8 and 9% for Trichostrongylus, Bonostomum and Monezia bending, respectively and 53% were recorded as mixed infections. Incidence of haemo-parasitic diseases was found significantly higher ($P<0.05$) in exotic and cross breeds cattle. Haemo-parasitic diseases were found significantly higher ($P<0.05$) in female while no significant differences ($P>0.05$) was recorded with respect to age, though occurrence was higher in adult animals. Gastrointestinal parasitism was significantly higher ($P<0.05$) in female and young animals while no significant differences ($P>0.05$) was recorded breed wise. It can be concluded from the results that indigenous breeds of cattle offer significant resistance to onset of haemo-parasitic diseases while exotic and cross bred animals are easy targets for these dreadful diseases. Various therapeutic and managmental measures should be adopted for complete eradication of parasitic diseases in farm.

## A rapid, sensitive and low-cost real-time PCR assay for the detection of Leishmania infantum and Leishmania braziliensis kinetoplast DNA in canine blood samples

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3. *Department of Veterinary Medicine, University of Bari, Valenzano, Bari, Italy*

Leishmaniasis is a major public health problem in Brazil and the diagnosis is a challenge in both human and veterinary medicine. In this study, we describe an improved TaqMan®-based real-time PCR assay (designated as "Leishmania-FAST15") for the detection and quantification of Leishmania infantum and Leishmania braziliensis kinetoplast DNA minicircles in canine blood samples. The analytical sensitivity of this technique is 0.1 fg of DNA, which is equivalent to 0.002 parasite per reaction. This assay uses a small reaction volume (15 µl) and is rapid to perform, with the results being available in less than 34 min. We compared our improved assay with a standard assay using the same primers and probe and agreement between the results obtained with both assays was almost perfect (Kappa value: 0.90, P value < 0.0001). The real-time PCR assay described herein represents a rapid, low-cost molecular tool for the detection and quantification of L. infantum and L. braziliensis DNA in blood samples from dogs. This improved assay might also be suitable for detecting and quantifying Leishmania spp. DNA in other tissues, such as bone marrow and lymph nodes. This assay will be useful not only to veterinary practitioners, but also to public health authorities, as its low cost allows for its use in leishmaniasis control programs.

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## Epidemiology of intestinal helminthiasis among school children with emphasis on Schistosoma mansoni infection in Wolaita zone, Southern Ethiopia

Fiseha Wadilo

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**Background:** Intestinal helminth infections are major parasitic diseases causing public health problems in Ethiopia. Although the epidemiology of these infections are well documented in Ethiopia, new transmission foci for schistosomiasis are being reported in different parts of the country. The objective of this study was to assess the prevalence of Schistosoma mansoni and other intestinal helminth infections among school children and determine the endemicity of schistosomiasis in Wolaita Zone, southern Ethiopia.

**Methods:** Cross-sectional parasitological and malacological surveys were conducted by collecting stool samples for microscopic examination and snails for intermediate host identification. Stool samples were collected from 503 children and processed for microscopic examination using Kato-Katz and formalin-ether concentration methods. Snails collected from aquatic environments in the study area were identified to species level and Biomphalaria pfeifferi snails, the intermediate host of S. mansoni,, were individually exposed to artificial light in order to induce cercariae shedding. Cercariae shed from snails were used to infect laboratory-bred Swiss albino mice in order to identify the schistosome to species level.

**Results:** The overall prevalence of intestinal helminth infections was 72.2% among school children. S. mansoni infection prevalence was 58.6%. The prevalence and intensity of S. mansoni infections varied among schools and sex of children. Swimming was the only factor reported to be significantly associated with S. mansoni infection (AOR = 2.954, 95% CI:1.962-4.449). Other intestinal helminth species identified were hookworms (27.6%), Ascaris lumbricoides (8.7%), E. vermicularis (2.8%), Taenia species (2.6%), T. trichiura (1.2%) and H. nana (0.6%). Only B. pfeifferi snails collected from streams shed schistosome cercariae and 792 adult S. mansoni worms were harvested from mice exposed to cercariae shed from B. pfeifferi on the 6th week post-exposure.

**Conclusion:** The present study found high level of intestinal helminth infections in the study area. The study also confirmed autochthonous transmission and endemicity of S. mansoni as evidenced by both parasitological and malacological findings as well as by further establishing infections in lab-bred mice. Therefore, there is a need to include the area

## Cystic echinococcosis, Echinococcus granulosus; Ethanol-preserved tissues, Formalin-fixed tissues;

Mohamed Ahmed[1, 4], Sara Abdalla[2], Martin Grobusch[3], Imadeldin Aradaib[4]

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**Background:** Formaline-fixed tissues represent the most important specimens for diagnostic surgical pathology and, moreover, have proven to be an invaluable source for retrospective studies, particularly on cancer and infectious diseases. In contrast to classical histo-pathological examinations, molecular-based assays have the advantage of conclusive species determination as well as strain differentiation of the strains of Echinococcus granulosus -complex, which causes serious diseases worldwide.

**Methods:** In the present study, eleven archives specimens of Hydatid cysts were used. Of these specimens, 7 samples were preserved in ethanol and 4 specimens were preserved in formaline. DNAs were extracted from hydatid cyst samples and amplified by nested PCR for detection and genotyping Echinococcus granulosus- complex in formalin-fixed and ethanol-preserved tissues.

**Results:** The first round of PCR amplification produced a 530 bp specific PCR product from only 5 out of 7 (71%) hydatid cysts ethanol-preserved specimen and no amplification was produced from formaline-fixed tissues (0.0%). However, nested PCR amplification increased the sensitivity of the assay and produced a 471 bp PCR product from all ethanol-preserved tissues (100%) and from 3 of the 4 (75%) formaline-fixed tissues. PCR products were purified and submitted for sequencing to determine the genotypes of hydatid cysts used in the study.

**Conclusion:** The described nested PCR assay proved sensitive for simultaneous detection and genotyping of detection of protocol for genotyping Echinococcus granulosus- complex in ethanol-preserved and formalin-fixed tissues.

## Comparison for Detection and genotyping of Hydatid Cysts of Echinococcus granulosus in Ethanol-preserved and formalin-fixed tissues Using PCR Assay

Mohamed Ahmed[1, 4], Sara Abdalla[2], Martin Grobusch[3], Imadeldin Aradaib[4]

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**Conclusion:** The described nested PCR assay proved sensitive for simultaneous detection and genotyping of detection of protocol for genotyping Echinococcus granulosus- complex in ethanol-preserved and formalin-fixed tissues.

## Role of Cattle in the Epidemiology of Echinococcus granulosus sensu lato in Central Sudan

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Cystic echinococcosis (CE), caused by infection with larval stage of Echinococcus granulosus sensu lato (s.l.), is a cosmopolitan zoonotic parasitic disease of humans and a wide range of mammalian species including cattle. Currently, little information is available about the genetic diversity and public health significance of Echinococcus species among livestock in the Sudan, particularly the indigenous cattle. In the present study, fifty (n=50) hydatid cysts were collected from each cattle carcasses at Al-kadarou slaughterhouse, Khartoum North, Sudan. DNA was extracted from protoscoleces and associated germinal layer of eachcyst and subsequently amplified by PCR targeting the mitochondrial NADH dehydrogenase subunit 1 (NADH1) gene. The amplifiedPCR products were furtherand purified and subjected to direct Sangersequencing for phylogenetic tree and network analysis. The resulted phylogenetic tree revealed a presence of Echinococcus canadenesis genotype 6(88.0%, n=44), followed by Echinococcus ortleppi genotype 5 (8.0%, n=4)andEchinococcus granulosus sensu stricto genotype 1(4.0%, n=2). Furthermore, the phylogenetic network analysis revealed clear genetic variation among the different haplotypes/genotypes. This report has provided for the first time an insight of the role of cattle in transmitting the zoonotic echinococosis disease by harboring genotype 1 (G1). In addition to, harboring 88% of circulation of the camel genotype (G6) that suggest cattle may play an important role in the transmission dynamic and the epidemiology of the disease in Central Sudan.

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## Molecular identification and characterization of Cryptosporidium spp. among pediatric and food-handlers subjects in Qatar.

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World Health Organization (WHO) has identified Cryptosporidium spp. as globally the most common diarrhea-causing protozoan. Its transmission occurs mainly through ingestion of water or food contaminated with the feces of an infected human or animal. Infected food handlers are also a major Cryptosporidium contamination risk. A wide diversity of Cryptosporidium spp. and subtypes infect humans and due to the host specificity of each species, the use of molecular techniques and genotyping of subject's stool samples will help in identifying contamination source.

Molecular prevalence was investigated using real-time PCR targeting a 214 base pairs fragment of 18s-rRNA. The analyzed populations consist of hospitalized diarrheic pediatrics and asymptomatic food handlers. The positive samples by RT-PCR were subjected to species identification by PCR-RFLP and GP60 gene sequencing.

The parasite was detected by RT-PCR in 15% of the children and 4% of the food-handlers. Genotyping of Cryptosporidium spp. revealed a predominance of Cryptosporidium parvum. Sequence analysis of the GP60 locus in the present study has identified only C. parvum subtype family IId with mostly the IIdA20G1 subtype among the two populations. This study provides supplementary information for implementing prevention and control strategies to reduce the burden of these pediatric protozoan infections.

## Cryptococcus gattii environmental dispersal and adaptation surveillance in Oregon, USA

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Human and animal infections of the virulent fungus Cryptococcus gatti have been recognized in Oregon since 2006. Transmission is primarily considered via air-borne environmental spores and now thought to be locally acquired due to infection in non-migratory animals and humans with no travel history. Previous published efforts to detect C. gatti from tree swabs and soil samples in Oregon have been unsuccessful.

Cryptococcus gattii, an important pathogen in humans and animals, has a worldwide distribution with the first documented human cases of C. gattii infections in North America occurring in 1999 on Vancouver Island, BC, Canada. Additional Pacific Northwest human and veterinary (domestic and wild) cases were first identified in 2006 - 2008 from Washington and Oregon respectively. Since then, many more U.S. cases have been documented.

Little is known about the environmental and climatic conditions required to allow colonization by C. gattii, but it is considered to be a highly adaptive organism. Environmental niche modeling studies conducted on Vancouver Island, BC, Canada indicated specific Coastal Douglas fir and Coastal Western hemlock (dry) zones were strong indicators of where C. gattii was found in British Columbia. Less is known about the environmental niches of C. gattii in Washington and Oregon, with limited environmental sampling done in each state.

Because of large-scale ecoregions present where human and animal C. gattii infections have been confirmed in WA and OR, ecological niche modeling may be less effective in predicting exposure. Instead, other epidemiologically significant factors affecting exposure risk may be more useful to predict where the fungus may be present. Timber harvesting activity, climatic conditions, and usage patterns of people and animals are examples of these factors. In Oregon, surveillance efforts would be valuable in specific cities and city environs where both human and domestic animal cases of C. gattii infections have occurred. With environmental exposure the primary means of transmission, we were interested in locations where humans and animals shared space in a community as possible sites of exposure to C. gattii. We combined this concept of shared local places with the knowledge of C. gattii colonization of specific tree species.

We chose cities in the Willamette Valley, Oregon where the fungus has been found in both people and animals. Urban parks were sampled due to spatial and temporal overlaps of humans, companion animals and wildlife. Two of sampled parks had positive samples for C. gatti. One park had a positive tree and the other park, 60 miles away, had positive bark mulch samples from a walkway. Genotypic subtypes included C. gattii VGIIa and VGIIc, both considered highly virulent. Precaution in regions where C. gatti is not known to be endemic is recommended due to public health risks of environmental exposure.

### Prevalence of Cattle trypanosomiasis and babesiosis in the Western Highlands of Cameroon

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The prevalence of trypanosomiasis was studied in the Sudano-Guinean highlands of western Cameroon in 107 cattle through parasitological examination and serological analysis. Parasitological examination revealed the presence of trypanosomes in cattle with a prevalence of 16.82%, regardless of cattle breed. The highest prevalences were obtained from cross-breeds (23.33%) and Red Fulani (21.74%), followed by Gudali cattle (6.67%). Conversely, serological analysis highlighted antibodies against T.brucei in 42.17 % of cattle. The highest seroprevalences were identified in White Fulani (60.00%), followed in order by the Gudali (37.14%), the Red Fulani (48.15%) and the crossbreeds (21.05 %). Seroprevalence obtained were significantly higher than the parasitological prevalence. The dilutions performed on the positive sera have proven that regardless cattle breed, the level of antibodies produced was generally low. Infestations in trypanosomes have not significantly affected the neither haematocrit nor blood cell counts. Concerning babesiosis, parasitological search revealed 11.20% of cattle infected, with 6.67, 10.87, 6.67 and 20.00% respectively for the white Fulani, red Fulani, gudali and crossbreeds. Infections with Babesia sp did not affect significantly blood parameters studied. Concerning babesiosis, parasitological search revealed 11.20% of cattle infected, with 6.67, 10.87, 6.67 and 20.00% respectively for the white Fulani, red Fulani, gudali and crossbreeds. Infections with Babesia sp did not affect significantly blood parameters studied

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### Parasitic and serological prevalence of Trypanosomosis and babesiosis in small ruminants in the Sudano Guinean Highlands of Western Cameroon

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An epidemiological survey on trypanosomosis and babesiosis of small ruminants was carried out in the Western Highlands of Cameroon. 114 and 67 blood samples were collected from goats and sheep respectively. The samples were parasitologically analyzed by the Buffy coat and slide techniques. A serological test for antibodies against Trypanosoma brucei gambiense was also carried out by the Card Agglutination Test for Trypanosomiasis (CATT) technique on the plasma of 85 goats and 57 sheep. Parasitological investigations revealed no trypanosome in sheep and goats. On the other hand, the prevalence of babesiosis was 33.33 and 50.75% respectively for goats and sheep. Considering the sex and age in the two species of ruminant, the highest infection rates occurred in animals between 0-18 months (50.48%). In these animals, no significant difference ($P \geq 0.05$) existed between the sexes, while among animals of 19 months and above, males had highest infection rates (62.50%) compared to females (32,65%). Antibodies directed against T. b. gambiense were found in 35.29 and 31.58% of goats and sheep respectively. Serological prevalence were significantly ($P \geq 0.05$) higher than parasitological prevalence (0.0 and 0.0%) in goats and sheep respectively. Different dilutions (1:1, 1:2, 1:4, 1:8, 1:16 and 1:32) on positive plasma revealed that antibody level in the animals is generally too low (titers 1:1 and 1:2), irrespective of the animal species, age and sex. Trypanosome and babesia infections did not significantly ($P \geq 0.05$) affect the packed cell volume (PCV), the blood cell count and the differential leucocytes count.

## Localized cutaneous leishmaniasis is the common clinical form of cutaneous leishmaniasis in Ethiopia

Nigatu Kebede

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**Background:** The current study was conducted to assess the distribution of the three clinical forms of cutaneous leishmaniasis (CL): localized (LCL), disseminated (DCL) and mucocutaneous (MCL) and location preference in patients in Ethiopia.

**Methods:** The study participants were those who came from different regions of Ethiopia seeking medical treatment and referred to Addis Ababa University and /or Armauer Hansen Research Institute Leishmania laboratory. The patients were from 18 CL endemic areas in the five regions of the country. The suspected cases were subjected to detailed clinical examination to identify number of lesions, site in the body, duration of the lesion and type of lesion.Skin scraping samples were taken from 85 of the cases suspected of CL. Parasitological confirmation was completed based on culturing and identification of the Leishmania species and genetic variability within Leishmania aethiopica (L. aethiopica) were done by ITS1-PCR and MLMT-PCR amplifications, respectively.

**Result:** All of the 85 skin scraping samples were able to grow in culture. In this study, the PCR result confirmed that all the cases of CL were due to L. aethiopica. Of the 85 patients 69.4% (n=59) were males and 30.6% (n=26) were females. The result indicated that CL is distributed in all of the five regions in the country. Among the three clinical forms, LCL occurs more frequently than DCL and MCL: 82.4%, 9.4% and 8.2%, respectively, of the CL cases. LCL occurs commonly on the cheek, 48.2% (41) and arms. Both sexes of children age less than 15 years are equally affected. The male youth between the ages of 16-30 are highly prone to infection than females. Lesion duration can go more than one year. Genetic variability was observed among the different clinical forms.

**Conclusion:** CL incidence is increasing and, it affects all ages and both sex with more prevalence in young males. This study provided evidence indicating that the clinical features of the disease caused by L. aethiopica differs with regard to clinical aspects where LCL is more prevalent and the face and arms are the most affected part of the body. Further investigation on the epidemiology of CL, strains of L. aethiopica and the reason for the occurrences of various types of clinical lesions in patients is recommended.

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## Epizootological Study of Trypanosoma vivax in Kenana calves in the Blue Nile State, Sudan

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Trypanosomosis is a worldwide parasitic disease caused by species of flagellated protozoa belonging to the genus Trypanosoma, which affects humans, as well as domestic and wild animals. and it inhibits the blood, body tissues and fluids. The disease has direct impacts on livestock health and productivity, management, human health and settlement.

Trypanosoma vivax, Trypanosoma evansi, Trypanosoma equiperdum, Trypanosoma cruzi, and Trypanosoma theileri are of medical and veterinary importance.

Trypanosomes was reported in Sudan as early as 1904. T. vivax was found to be predominant outside Tsetse infested belt, while T. bruci and T. congolense were confined to Tsetse infested area.

The predominance of T. vivax in cattle had been reported in Southern Darfur, South Kordofan and at different locations of Central States, Khartoum and the Blue Nile State. In Africa most of pathogenic species to man and animals are transmitted cyclically by Tsetse flies and / or mechanically by other haematophagus insects, mainly Tabanids. Other transmitter incriminated include Muscidae and Stomoxys.

Non -Tsetse transmitted Trypansomosis due to T. vivax and T. evansi occurs in various forms in South America, Africa and Asia, and it constitute potential risks for about 500 million buffaloes and twelve million camels.

A survey on trypanosoma species in blood was conducted in the Blue Nile State to determine the prevalence of Trypanosoma vivax infection in Kenana calves, using haematocrit centrifugation technique, wet blood film, thin and thick blood stained smears. The prevalence during the dry season ranged between 6.5 – 2.2% compared with 6.3 – 1.4% during the rainy season.

This indicated that bovine trypanosomes due to T. vivax infection was quite prevalent in calves and it is also season dependent. The increase of infection rate during the rainy season is highly likely due to the increase of biting flies' densities during the rainy season of heavy rain fall levels and floods.

This study recommended that efforts should be implemented to eradicate the vectors. Various integrated strategies should be used to control Trypanosomsis, using sterile insect techniques, insectsides and insect repellents.

As this study highlighting the increasing seasonality of infection rates, and as atypical human infections caused by species that normally are restricted to animals have been reported, mostly transient but some required treatment or even can be fatal, precaution measures and great attention should be drawn to prevent human infection.

## Epidemiology and molecular characterization of Cryptosporidium spp.in humans and cattle in Addis Ababa and its environs, Ethiopia

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Cryptosporidiosis causes significant diarrheal disease in humans and animals worldwide. Cross-sectional and longitudinal studies were used to investigate the molecular epidemiology and identify risk factors of the infection in humans and dairy cattle in Addis Ababa and its surrounding areas during June 2014 to June 2015. Faecal samples from 422 cattle and 300 dairy farm workers and HIV seropositive individuals were examined by the Modified Ziehl-Neelsen, PCR-RFLP and sequencing, data on risk factors of the infection were collected using a pre-tested questionnaire and. the SPSS software was used to analyse all collected data. The overall prevalence of Cryptosporidium in cattle and humans was 18.6% (95% CI: 14.8–22.5) and 9% (95% CI: 5.5–12.3), respectively. Cryptosporidium andersoni (73.3%) and C. parvum (26.7%) were identified in cattle, whereas C. parvum (81.5%) and C. hominis (18.5%) were detected in humans. In cattle, Cryptosporidium infection was significantly associated with absence of calving pen (OR=2.46, 95% CI: 1.08–5.61), absence of calf bedding (OR=10.55, 95% CI: 4.89–22.66), drinking river/stream water (OR=2.9, 95% CI: 1.5–5.5) and group penning of calves (OR=2.7, 95% CI: 1.0–7.0). While in humans, the infection showed significant association with drinking stream/well water (OR=3.3, 95% CI: 1.5–7.4) and contact with cattle and their faeces (OR=3.6, 95% CI: 1.4–9.5). Cryptosporidium infection occurred from week 1 to 3 months of age in the longitudinal study calves with an overall prevalence of 40% (12/30). Pre-weaned calves were merely infected with C. parvum and post-weaned calves were infected by C. andersoni. Phylogenetic analysis showed that the C. parvum human isolates belong to the bovine genotype family. In conclusion, the zoonotic C. parvum is prevalent and widely distributed in cattle and humans in the study area, pre-weaned calves are the potential risk group for human infection requiring special management attention to prevent transmission of the infection to humans and lessen contamination of the environment.

## Leishmania donovani: an in vitro study of antimony-resistant amphotericine B-sensitive isolates.Leishmania donovani: an in vitro study of antimony-resistant amphotericine B-sensitive isolates.

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2. *Department of Clinical Pathology and Immunology, Institute of Endemic Diseases, University of Khartoum, Khartoum, Sudan*

**Objectives:** This study was initiated in an attempt to determine the in vitro sensitivity of Leishmania donovani isolates from Sudanese VL patients with diverse clinical drug responsiveness to standard leishmanicidal drugs.

**Methods:** Eight isolates, six from antimony-resistant and two from clinically responsive patients were included in the study. Parasites were tested as promastigotes and four of them were selected to be tested as amastigotes using a murine macrophage-like cell line. The results indicated that the conventional promastigotes and amastigotes-screening assays did not correlate with the clinical picture of patients. In vivo unresponsiveness does not necessarily mean primary parasite resistance.

**Results:** The results indicated that the conventional promastigotes and amastigotes-screening assays did not correlate with the clinical picture of patients. Increasing concentrations of SSG diminished the incorporation of the [3H]thymidine in a linear fashion compared to the control values in both sensitive and resistant isolates. [3H]thymidine uptake was inhibited in all isolates in a linear fashion with increased concentrations of amphotericin B. In the macrophage assays, the four parasites tested were highly infective to the cells (80–99%) and exhibited moderate to high intracellular replication potentials.

**Conclusions:** Amphotericin B could be a suitable second line drug in patients unresponsive to pentostam and without concomitant diseases, if close hospital monitoring is available. Promastigotes sensitivity testing concentrations are virtually incomparable with the in vivo clinically curable doses and the amastigotes/macrophage test concentrations.

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## Rapid epidemiological risk mapping of patterns of Leishmania donovani infection in Eastern Sudan

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**Objectives:** We performed a rapid epidemiological survey (RES) and spatial analysis in order to i) map the population at risk of VL in eastern Sudan, and ii) produce an environment-based map of the areas at risk for VL in the same area.

**Methods:** Following informal consent 800 randomly selected volunteers from eight villages in Eastern Sudan were enrolled. Eight parasite isolates were cultured, characterized as L. donovani using Heteroduplex analysis (HDA) and RFLP. These parasites were tested for their in vitro sensitivities to pentostam and amphotericin B using both promastigote model and macrophage-like cell line system (J774).

**Results:** The overall leishmanin reactivity (induration ≥5 mm) was 24.5%. Children <15 years had higher leishmanin reactivity (≥5 mm) of 13.2% compared to 11.3% in adults. The DAT results showed that 13% (238/800) titers above the diagnostic cut-off level of 1:3200, while 78% had titers under the cut-off point. Eighty patients with VL and three patients with PKDL were seen in the study population. In vitro tested parasites showed marked linear reduction in H3-thymidine incorporation. In the J 744-macrophage system, the parasite survival index (PSI) was similar for both drugs.

**Conclusion:** RES can provide useful information in a short time (~10-14 days) about disease pattern, population at risk (drug requirement) and target population for future vaccination compagins. The constructed map and interactive map (GIS) can act as a nidus for development a Pan-Sudan/Pan-Africa VL map.

## Determination of risk factors for the human host of leishmaniasis in Morocco

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**Introduction:** In Morocco, three forms of leishmaniasis are known. Zoonotic cutaneous leishmaniasis (ZCL) due to Leishmania major (L. major), anthroponotic cutaneous leishmaniasis (ACL) by Leishmania tropica (L. tropica) and visceral leishmaniasis (VL) due to Leishmanias infantum (L. infantum).

To characterize the human population at high risk for cutaneous and visceral leishmaniasis, an epidemiological case-control study was conducted in Marrakesh-Safi (endemic area of ACL) and Fes-Meknes (endemic area of VL) regions, with a total of 200 cases and 313 controls.

**Study area & Methods:** The total population of Marrakesh-Safi region was estimated to 4520569 inhabitants; with 42.87% are urban inhabitants and 57.13% rural inhabitants. While the population of Fes-Meknes region was estimated to 4236892 inhabitants; with 60.52% are urban inhabitants and 39.48% rural inhabitants (Moroccan High Commission for Planning, 2014).

We have adopted a case-control study. Thus, for each patient (case) and his witness, anonymous questionnaires have been met, where we recorded all the information concerning the civil status, activity, life style and conditions of immediate environment.

**Results:** Identifying the risk factors of leishmaniasis in study areas offers significant information to design and develop effective control measures. Our results show that the presence of animals, individual houses with cracked walls, age and gender were associated with increased risk of leishmaniasis infection. On the other hand, healthy living, education, vaccination and use of insecticide were associated with reduced risk of both visceral and cutaneous leishmaniasis

**Discussion and conclusion:** Our findings have implications for planning and control of leishmaniasis in Morocco. Firstly, individual protective measures such as use insecticide and improve hygiene conditions could easily be adopted for the prevention of leishmaniasis in our study areas; and secondly improving housing conditions such as removing cracks from houses and keep breeding away from the house would help to reduce risk of leishmaniasis in Morocco.

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## Cross-boarder issues in elimination of Onchocerciasis in Africa: The Galabat focus, Eastern Sudan.

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**Background:** The Galabat focus in eastern Sudan close to the Ethiopian border is the largest in Sudan following the recent elimination of Onchocerca volvulus from the Abu Hamed focus in the north. Its historically known as hyper-endemic, with prevalence up to 63%, to a nonblinding disease characterized with severe onchodermatitis. Annual community-based treatment with ivermectin commenced in 2007 and upgraded to semiannual (every 6 month) regime in 2011 with the objective of eliminating the disease. We describe recent assessments to investigate interruption of disease transmission in the focus and consequent cessation of mass treatment.

**Methodology/Principal Finding:** The Galabat focus went through four years of annual treatment followed by five years of semiannual treatment by 2015; with coverage of over 85% of the targeted population in each round. No O. volvulus L3 larvae were found in 9267 black flies collected from 3 sentinel sites throughout the focus by O-150 PCR pool screening (0/2000 flies; 0.41/2000 UL 95% CI). Ov16 assay applied to 4424 children 10 years old from collected in Dec 2014 from 20 communities within the focus also showed no evidence of O. volvulus antibodies (0%; 0.03% UL 95% CI). No skin snip microfilariae were found in 1046 individuals from 10 communities within the focus in 2016. In addition, no evidence of skin snip microfilaria or Ov16 antibodies were seen in communities north of the focus in 2013. These results are well below the 2016 WHO thresholds for interruption of the disease transmission.

**Conclusions/Significance:** We provide evidence that continued and intensified ivermectin treatment alone could interrupt the disease transmission in as little as 15 rounds of documented treatment. Although the Galabat focus has interrupted transmission based on the current WHO guidelines, mass treatment continues bending the status of the disease in the Ethiopian focus across the border. However, the decision has been made to continue mass treatment pending the interruption of transmission in the neighboring focus of Metama in Western Ethiopia. This first example of cross-boarder coordinated strategy in Africa will be discussed.

## USING ONE HEALTH APPROACH TO CONTROL THE CAMEL-DOG-MAN RISK ZOONOTIC CYCLE OF ECHINOCOCCUS GRANULOSUS IN KARAMOJA REGION, UGANDA.

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Cystic echinococcois (CE) a zoonotic disease caused by Echinococcus granulosus is one of the most important helminthic disease worldwide. In this abstract we report the prevalence of this parasite in indigenous camels in Karamoja region.

Three hundred and sixty two (362) camels slaughtered for human consumption were examined at four slaughter slabs in the region between 2014 until 2016.

The overall infection rate was recorded as 44.6%. Considering infection in the liver 43.5% of the animals were infected while 33.4% presented infection in the lungs, 3.1% in the peritoneal cavity and 20% in the spleen.

The infection rate in males (54.2%) was slightly higher than that in females (45.8%). The study also showed that there was a higher susceptibility of multiple organ infections in the female camels (33.6%) as compared to 21.7% in male camels. The prevalence in camels above six years of age was 45.7% while in camels younger than six years was 23.6%.

We observe also here that the pastoralist production system, the stray dog population (109,000) and the extreme lack of hygienic conditions at slaughter slabs had significant impact on the high infection due to Echinococcus granulosus in the area and those pastoralists were at a higher risk of being infected. This paper discusses strategies that could be used to control CE given the enormous challenges associated with the pastoralist production system of Karamoja region in Uganda and how the ONE HEALTH approach could offer solutions to this Public Health problem.

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# Plenary Session 2:
# One Health and Impact on Climate Change

## Characterisation of commensal Escherichia coli isolated from apparently healthy cattle and their attendants in Tanzania

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**Abstract:** While pathogenic types of Escherichia coli are well characterized, relatively little is known about the commensal E. coli flora. In the current study, antimicrobial resistance in commensal E. coli and distribution of ERIC-PCR genotypes among isolates of such bacteria from cattle and cattle attendants on cattle farms in Tanzania were investigated. Seventeen E. coli genomes representing different ERIC-PCR types of commensal E. coli were sequenced in order to determine their possible importance as a reservoir for both antimicrobial resistance genes and virulence factors. Both human and cattle isolates were highly resistant to tetracycline (40.8 % and 33.1 %), sulphamethazole-trimethoprim (49.0 % and 8.8 %) and ampicillin (44.9 % and 21.3 %).

However, higher proportion of resistant E. coli and higher frequency of resistance to more than two antimicrobials was found in isolates from cattle attendants than isolates from cattle. Sixteen out of 66 ERIC-PCR genotypes were shared between the two hosts, and among these ones, seven types contained isolates from cattle and cattle attendants from the same farm, suggesting transfer of strains between hosts. Genome-wide analysis showed that the majority of the sequenced cattle isolates were assigned to phylogroups B1, while human isolates represented phylogroups A, C, D and E. In general, in silico resistome and virulence factor identification did not reveal differences between hosts or phylogroups, except for lpfA and iss found to be cattle and B1 phylogroup specific. The most frequent plasmids replicon genes found in strains from both hosts were of IncF type, which are commonly associated with carriage of antimicrobial and virulence genes. Commensal E. coli from cattle and attendants were found to share same genotypes and to carry antimicrobial resistance and virulence genes associated with both intra and extraintestinal E. coli pathotypes.

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## Occurrence of Oestrus ovis parasitism in a necropsied sheep at a teaching and research farm in the western highland of Cameroon (Central Africa)

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The teaching and research farm (TRF) is a perfect livestock-human interface area for a rapid dissemination of zoonoses. The sheep nasal bot, Oestrus ovis (Diptera: Oestridae), a parasite commonly found in sheep, and occasionally in goats and man, is known to occur in the Mediterranean area. This study reports the occurrence of O. ovis in sub-Saharan Africa, in an area characterized by an increasing and permanent interaction between livestock and human. Following complaints of sudden deaths in sheep flock at the farm, a sheep was examined at necropsy to determine the possible cause of the mysterious deaths often reported. The head was found to be infested with the larvae of O. ovis. Since the area is open to wild life, and animals are not quarantined before introduction into the TRF, the infestation with this parasite would be widespread in small ruminants on the farm. Infestation of human (students, farm personnel and even visitors) would also be widespread but ignored due to the fact that O. ovis diagnosed only at post mortem examination, would not be suspected when ophthalmomyiasis and ear-nose-throat myiasis are observed in humans. This study highlights the interconnectedness of animals, humans, and the environment.

## The Influence of Weather Patterns on Biodiversity and Health in Uganda

Fredrick Kabbale, Martha Kaddumukasa

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Changes in weather patterns and anthropogenic activities are evident in Uganda and are posing a serious threat to the country's natural resources, biodiversity and health, as well as the social and economic development. Changes have been predicted to continue in the form of higher temperatures and inter-annual rainfall variability. Emergence and re-emergence of pests and diseases, and increasing frequency of severe floods will continue presenting social and economic hardships. Loss of plant mass due to reduced rainfall and high temperatures, promoting desertification will disturb the symbiotic relationship between plants and animals including insects. Some species of plants and animals may suffer extinction or change in locations and/or behaviour. Controlled anthropogenic activities, enforcement of existing policies and regulations on sustainable use of ecosystem resources, awareness raising to all stakeholders, strengthening institutional capacity to design and implement adaptation and mitigation strategies and improved monitoring of weather patterns and biodiversity are recommended.

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## SITUATION OF BACTERIA INFECTION IN PORK AFTER SLAUGHTER IN MARKET IN HUE CITY

Hung Pham

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This study was conducted to determine bacteria contamination rate by time. Total of 270 samples were collected randomly in butcher counter at 3 market in Hue city are An Cuu, Dong Ba, Tay Loc. Prevalence of total aerobic bacteria, E. coli, S. aureus and Salmonella spp. on pork in all 3 markets increased over time of slaughter. Total aerobic bacteria after the slaughter of 1 hour, 4 hour and 8 hours. After 1 hours of slaughter: S. aureus infection rates 81,11 CFU/g; Salmonella spp.: 4,44%; E. coli: 94,44%. After 4 hours of slaughter: S. aureus infection rates 85,56%; Salmonella spp. is 5,56%; E. coli is 98,89%. After 8 hours of slaughter: S. aureus infection rates average: 87,78%; Salmonella spp: 6,67%; E. coli: 100%. Prevalence of microorganisms in samples collected in the markets mentioned above are higher than the Health Ministry's regulations on microbiological criteria for fresh meat.

## What motivates students’ participation in One Health Innovations Club Activities?

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**Introduction:** One Health Students Innovations Club (OHSIC) is a strategy used in pre-service training to promote experiential learning and support breaking disciplinary silos among the future One Health workforce. One Health Central and Eastern Africa, a network of 21 schools of Public Health and Veterinary Medicine has been supporting creation and nurturing of OHSIC as part of the One Health workforce development strategy.

**Methods:** We conducted an online survey to understand what motivates students to join and participate in OHSIC activities. The survey covered OHSIC members from Uganda, Rwanda and Tanzania. Emails with a link to the survey were sent to all OHSIC members with email addresses. Reminders to complete the survey were sent through social media, OHSIC leadership, and emails. Data were exported to SPSS-PC for statistical analysis. Wordle™ as a word cloud generator.

**Results:** 122 respondents participated in the survey and 72% were male. Majority (83.2%) were bachelors’ degree students, 6% diploma level, while 9% were post-graduate. Composition in terms of academic discipline was as follows: 38% veterinary medicine, 17% public health, 14% wildlife, 9% nursing, 5% human medicine, 3% zoology and conservation, and 5% others. Motivation to join and participate in OHSIC activities was due to networking opportunities, learning opportunities, multidisciplinary collaboration benefits, support received from faculty, community outreach opportunities, Clubs’ mission and vision, and potential for One Health in addressing challenges.

**Discussion:** OHSIC has been effective in bringing together multidisciplinary teams of students and to build their skills in One Health. Students from non-science based disciplines are not motivated to join and participate in the club activities despite recent epidemics such as Ebola having highlighted the need for involvement of such disciplines in order to successfully manage epidemics. Understanding what motivates student participation in the club’s activities is important in informing the nurturing of the clubs and ensuring their sustainability.

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## Epidemiologyof hepatitis C virus among hemodialysis patients in the Middle East and North Africa: systematic syntheses, meta-analyses, and meta-regressions

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We aimed to investigate hepatitis C virus (HCV) epidemiology among hemodialysis (HD) patients in the Middle East and North Africa (MENA). Our data source was an HCV biological measures database populated through systematic literature searches. Descriptive epidemiologic syntheses, effects meta-analyses and meta-regressions, and genotype analyses were conducted. We analysed 289 studies including 106463 HD patients. HCV incidence ranged between 0-100% as seroconversion risk, and between 0-14.7 per 1000 person-years as incidence rate. The regional pooled mean estimate was 29.2% (95% CI: 25.6-32.8%) for HCV antibody positive prevalence and 63.0% (95% CI: 55.4-70.3%) for viremic rate. Region within MENA, country income group, and year of data collection were associated with HCV prevalence; year of data collection adjusted odds ratio was 0.92 (95% CI: 0.90-0.95). Genotype diversity varied across countries with four genotypes documented regionally: genotype 1 (68.8%), genotype 2 (9.6%), genotype 3 (7.9%), and genotype 4 (13.5%). Our findings showed that one-third of HD patients are HCV antibody positive and one-fifth are chronic carriers and can transmit the infection. However, HCV prevalence is declining. In context of growing HD patient population and increasing HCV treatment availability, it is critical to improve standards of infection control in dialysis and expand treatment coverage.

## CHARACTERIZE THE TEMPORAL EVOLUTION OF HIV INCIDENCE AMONG STABLE COUPLES IN SUB-SAHARAN AFRICA

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**Introduction:** We quantified and characterized the temporal evolution of the contribution of several types of sexual-partnership HIV statuses to total HIV incidence in six representative countries at different HIV epidemic scales in sub-Saharan Africa (SSA).

**Methods:** A pair-based deterministic compartmental mathematical model was constructed to describe the dynamics of HIV transmission in SSA. The model accommodated for movement of individuals between different forms of sexual partnerships and infection statuses. Stable couples (SCs) were divided into sero-concordant negative couples (SCNCs), sero-discordant couples (SDCs), and sero-concordant positive couples. Throughout epidemic phases, historical and future trends (1980 to 2030) of sources of HIV incidence by partnership status were projected based on population-based nationally-representative epidemiologic and demographic input data.

**Results:** As the epidemics emerged and peaked, HIV incidence resulting among SDCs increased from 6%-32% to 19%-44% of total HIV incidence, mostly due to HIV transmissions within the SDCs. As the epidemics started their natural decline and further decline with antiretroviral therapy (ART) scale-up, the contribution of SDCs to total HIV incidence declined in intermediate and high HIV-prevalence countries, but increased in low HIV-prevalence countries. As the epidemics emerged and peaked, HIV incidence resulting among SCNCs from extramarital sex declined from 54%-80% to 35%-73% of total HIV incidence. As the epidemics started their natural decline and further decline with ART scale-up, this proportion increased in intermediate and high HIV-prevalence countries, but declined in low HIV-prevalence countries. Between 9% to 29% of total HIV incidence occurred among individuals not engaged in SCs. This proportion was stable throughout the HIV epidemics, but was higher with higher HIV prevalence.

**Conclusion:** The contribution of different forms of sexual-partnership HIV statuses to total HIV incidence varied with time and was dependent on HIV epidemic phase and scale. Throughout the epidemics, more than two thirds of HIV incidence occurred among individuals engaged in SCs, however, the majority of incidence among couples was due to extramarital sex. These projections highlight that prevention approaches that target both SCs and individuals not engaged in SCs are critical to achieve substantial reductions in HIV incidence.

## HANDLING PRACTICES, QUALITY AND SAFETY OF MILK ALONG THE DAIRY VALUE CHAINS IN FOUR SELECTED SUBCITES OF ADDIS ABABA, ETHIOPIA

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A cross sectional study was conducted from January 2016 to April 2017 in four selected sub cities of Addis Ababa, Ethiopia with the objectives of assessing milk handling practices, determine bacterial contamination and detect selected milk-borne zoonotic pathogens along the dairy value chain. A total of 146 respondents were interviewed to collect the required information from farmers, vendors and restaurants about owner and workers' awareness about pre and post-harvest milk handling practices. About 75.7% of farmers did not clean their hands between milking, 25.7% did not wash cow teats (udder) and 25.7% clean animal houses three times per a week. The majority (62.86%) of farmers were not trained on farm management and milk handling. Forty milk samples (29 raw and 11 boiled) from different sources were analyzed for bacterial load and the result reveals that overall mean total aerobic bacterial counts and coliform counts were 7.17 and 4.85 log10 cfu/ml respectively, and significantly different between sample types (raw and boiled milk), and sample sources (farm and restaurants, and vendor and restaurants) ($P<0.05$). The highest coliform (5.56log10 cfu/ml) and total aerobic bacteria counts (8.99 log10 cfu/ml) were observed at farm and vendor level respectively. A total of 248 milk and swab samples were collected for laboratory detection of E.coli and Escherichia coli O157:H7. The overall isolation rate of E.coli and E.coli O157:H7 were found 123(49.60%) and 17(6.85%) respectively. There were statistically significant difference between sample sources, sample types and districts (p><0.05) except between districts for E.coli O157:H7. All isolates of E. coli O157:H7 were checked for their susceptibility pattern for 14 selected antibiotics. Even though all isolates were susceptible (100%) to kanamycine and nalidixic acid, most of the isolates showed resistance to most drugs. It was concluded that unhygienic practices of milking and post-harvest handling along the dairy value chain possibly contributed to microbial contamination of milk. Detection of E.coli and E.coli O157:H7 in milk is of public health significance due to their zoonotic potential. Public education should be given to all stakeholders in dairy industry on milking and post-harvest handling of milk to limit the likely losses due to rejection of spoiled milk, and milk-borne pathogens resulting from contamination.

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## The Role of ICT in Global One Health

Susan Muriithi

*KEMRI, Nairobi, Kenya*

Global One Health connects Ohio State University to Health Institutions in Kenya, Ethiopia, Tanzania, Brazil, Thailand, China, India and beyond in a coordinated, multidisciplinary approach to improve health, build capacity, and provide learning opportunities for students across the globe.

## Why is Environmental Risk Assessment and Environmental Risk Management lagging behind?

Salome Margaret Molefe, Mangaka Mahlako

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Environmental risk assessment (EnRA) deals with the interactions of agents or hazards, human and ecological resources. It describes human population, ecological resources and agents, analyzes agents and exposure potentials, characterizes the potential for adverse effects, defines uncertainties, generates options to deal with the risks, and communicates information about the risks to humans and ecosystems. EnRA has two components: Human Health Risk Assessment (HHRA) and Ecological Risk Assessment. (EcoRA). EnRA can also be used in Environmental Impact Assessment (EIA) processes.

**The aim:** To explore the current use of EnRA and its component EcoRA within South Africa, evaluate its effectiveness and suggest how to make improvement, answer the question of whether the EnRA use will add significant value to the EIA process, and exploit its strengths and its limitations and briefly consider the role that EnRA plays and could potentially play in the transition to the Green Economy.

**Methods:** Methodology involves: reviews of chemical risk assessment and EIA legislations, methodologies for evaluation of chemical risk assessment of human medicines, veterinary drugs, pesticides and industrial chemicals in South Africa, literature reviews relating to use of environmental risk assessment in EIA processes

**Results:** EnRA is not developed compared to human health risk assessment. It is not well understood how chemicals affect the environment and ecological risk assessment and as such the EnRA was neglected in evaluations of pharmaceuticals, veterinary drugs and pesticides. Ecotoxicological risks of released and disposed chemicals and chemical ingredients used in pharmaceuticals, cosmetics (e.g. plastic microbeads) and their impacts on wildlife species, amphibian, reptile, and non-target species and their impacts on biodiversity and the ecosystem is insufficiently considered in risk assessment. Soil risk assessment of chemical stressors and the influence of molecular structure on the environmental persistence of a chemicals is not well understood. EnRA is not integrated with EIA and the risk assessment usually focuses only on a single chemical substance at the time ignoring the actual complexity of the world and the range of exposures and vulnerabilities.

**Conclusion:** EnRA provides a systematic, transparent and consistent means to analyze potential environmental impacts. The use of EnRA in urban and regional planning and management is fast becoming a standard practice, either as a stand-alone or as a component of to EIA as modern environmental planning and management integrate EnRA, EIA and urban environmental management. EnRA value lies in identifying potential environmental resources for development and allowing decision-makers to select management options with least negative effects. EnRA key products are risk management and communication plan, therefore its positive use in EIA offers a more holistic assessment, it enables integration of environmental, social and economic aspects and it assist to prioritize issues requiring management.

## Review of mHealth Programs for Infectious Disease Management in Punjab - Pakistan

S.M Mursalin

*Lahore, Pakista*

**Introduction:** Infectious and contagious diseases pose a severe burden on the health care system in Pakistan as well as having a negative impact on socio-economic growth and productivity. These are exacerbated by the limited access to quality assured health care services in impoverished urban and rural communities. To address this situation and to ensure real time data collection on important infectious diseases, smart phones based simple and easy to use tools are being used to improve infectious disease surveillance and management

**Aim:** Pak One Health Alliance (NGO) was mandated for the development and launch of a mHealth application for vector borne disease prevention and control. This idea is based on lessons learnt during the worst outbreak of Dengue Haemorrhagic Fever (DHF) in 2011 in Punjab that led to around 300 deaths and affected around 19000 patients.

**Method:** A baseline exercise was thus organized to determine the availability and use of mHealth applications deployed for real time data collection for infectious diseases. This was in turn matched with the International Best Practices. Quantitative cum Qualitative approach was used by evolving a structured questionnaire and semi structured interviews for information collection from the end users, developers, program and policy managers and community. Snowball sampling was used to collect data from relevant stakeholders.

**Results:** The data obtained from 9 mHealth projects indicated that more than 50% users were trained for less than 1 week and only 10% were trained for 4 weeks for using mHealth apps. Since 77% of the surveyed mHealth projects were owned by Govt. of Punjab, therefore, technically designed by Punjab Information Technology Board while implemented by respective health projects.

It was also observed that there was insufficient coordination between the ultimate beneficiaries /users and application developers. This hindered ownership by the end users had created a sense of alienation between designers and implementers. One hospital based application was termed as ‘un-necessary workload on already overburdened the hospital administration.

**Conclusion:** mHealth was appreciated by all respondents. It was recommended to widen the scope of mHealth projects for all categories of health services by engaging all stakeholders.

## Prevalence of bovine subclinical mastitis and associated risk factors in smallholder dairy farms of Mecha district, West Gojjam zone, Ethiopia

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3. *The Ohio State University, College of Veterinary Medicine, Columbus, United States*
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A cross sectional study was conducted in Mecha district, west Gojam, Ethiopia from December 2016 to April 2017 to estimate the prevalence of subclinical mastitis and see associations with potential risk factors. The study was carried out using California Mastitis Test (CMT) at quarter level on a total of 344 (225 local and 119 cross breed) lactating cows. The overall prevalence of subclinical mastitis in the study area was 21.8%, with higher rate in crossbreds (31.1%) than indigenous zebu breeds (16.9%) ($p<0.05$). The result at quarter level shows a total prevalence of 7.65% (104 out of 1360 tested quarters) and there were no statistically significant variation between the front quarter teats (3.75%) and hind quarter teats (3.89%) ($p > 0.05$). Based on this study among expected potential risk factors considered, breed and stage of lactation were found to have statistically significant correlation with subclinical mastitis ($p<0.05$) but age and parity have no statistically significant relation with the occurrence of subclinical mastitis. The result on the assessment of knowledge and practices towards subclinical and clinical mastitis in the study area reveled that almost all (99.98 %, N=89) have no idea on subclinical mastitis though 78.9 % (N= 71) of them heard about and know major clinical signs of clinical mastitis. Majority of the participants (81.1%, N=73) used to wash their hands before and after milking with water but not insignificant number (18.9%, N=17) didn't wash their hands at all or use separate towels while milking the cow. Likewise 87.8% (N= 79) of the participants responded that they didn't clean teats of the animal before or after milking. Hence implementing proper sanitation in dairy farm is essential not only in the prevention of mastitis and financial losses due to low milk productivity but also in the prevention of milk-borne zoonotic diseases, it is strongly recommended to implement regular awareness creation programs regarding dairy farm management system and zoonoses to dairy farm owners in the study area.

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## Identification, selection and weighting of food safety risk factors to be considered for their inclusion in the Canadian Food Inspection Agency's Hatchery Risk Assessment model

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The poultry meat and egg industries represent the most important segments of the food processing industry in Canada, generating more than 4 billion dollars each year. Both the Canadian and world's productions of these commodities has kept increasing over the past 15 years, probably explaining why foodstuff of poultry origin is linked to the majority of human cases of foodborne zoonoses. Combined with the constantly growing demand for poultry meat and egg products, as well as with the Canadian national strategy currently implemented to reduce the use of antimicrobials at the farm and hatchery levels, this situation reinforces the need for implementing strategies to address pathogen contamination and transmission issues along the poultry production chain in order to preserve the health of Canadians. For pathogens such as Salmonella, epidemiological studies have clearly shown that the transmission, either vertical or horizontal, from the parent stocks to the hatching or table eggs, was contributing to the dissemination of these pathogens posing a threat to public health, given their foodborne nature and most often, their antibiotic resistance profile. Controlling pathogens of public health concern in poultry production is a core challenge. In the transmission pathway of many pathogens in poultry, the hatchery represents a critical juncture.

Various factors and measures can contribute to lowering the contamination risk posed by a hatchery, and these elements were used as a basis for the development of the first steps of the new Canadian Food Inspection Agency hatchery risk assessment model. By quantitatively assessing these factors in their relative contribution to the infectious foodborne disease risk represented by each of the 96 federally-registered hatcheries in Canada, this new inspection model will help CFIA to appropriately allocate inspection resources in its risk-based food safety continuous improvement aiming at ensuring the best public health protection.

The objective of the current study was to identify, select and weight the critical food safety-related risk factors that should be included in a hatchery risk assessment model. An initial literature review, along with advices from an expert panel, was used to develop a comprehensive list of all potentially contributing risk factors. A second step involved a refinement process looking at merging risk factors with a similar focus and at redefining and clarifying these factors to avoid duplication and overlap between risk factors. Among the 37 risk factors selected, 6 were pertaining to the global inherent risk attributed to a hatchery facility, 17 were classified as mitigation factors and 14 were falling into the compliance factor category.

On March 22nd 2017, 11 Canadian hatchery experts, participated in a two-round face-to-face Delphi exercise to assess the relative risk of each factor on the human food safety burden attributed to hatcheries. Results showed that there was a broad consensus among the various risk factors and clusters weighted, regardless of the respondent professional profile. As a result, the median values assigned to each risk factor and clusters during the second round will be used in the new Canadian Food Inspection Agency risk assessment model for hatcheries.

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# PREVALENCE AND ANTIMICROBIAL SUSCEPTIBILITY PROFILE OF STAPHYLOCOCCUS AUREUS ISOLATED FROM MUTTON IN MEKELLE CITY, ETHIOPIA

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Staphylococcus aureus is a leading cause of food poisoning resulting from the consumption of contaminated food with staphylococcal enterotoxins. Moreover, development of drug resistant Staphylococcus strains causes considerable therapeutic problems. Hence, the current cross-sectional study was conducted from July 2016 to November 2016 in Mekelle City, Ethiopia to isolate and characterize S. aureus from raw mutton, to estimate its prevalence and to determine its antibiogram against nine selected antibiotic discs. For this, 210 mutton samples were collected from abattoirs (n= 70), butchery shops (n=70 ), and restaurants (n= 70) and analyzed for presence of S. aureus following the standard bacteriological techniques and procedures in Molecular Biotechnology Laboratory of College of Veterinary Medicine, Mekelle University. Descriptive statistics and Chi-square test were used for analyses. Out of the total 210 raw mutton samples 45 (21.4%) were found to be positive for S. aureus. The sample source based prevalence of S. aureus were 9/70 (12.9%), 20/70 (28.5%) and 16/70 (22.9%) from abattoir, retail meat outlets, and restaurants, respectively. There was no significant difference ($p \geq 0.05$) among the different sample sources in the prevalence of S. aureus. All (100%) of the tested S. aureus isolates were found to be susceptible to Gentamycin and Cefoperzone. However, all of the S. aureus isolates (100%) were showed the highest level of resistance to Amoxicillin and Tetracycline. The current study indicated that the existence of photogenic S. aureus in mutton and its multidrug resistant development to many tested drugs in the study area. Therefore, the food safety requirements should be followed strictly in accordance with Hazard Analysis Critical Control Point (HACCP) at various stages of food handling and processing and Gentamycin and Cefoperzone should be properly used as a choice of drugs in the study area when they are available.

## Influenza viruses in backyard poultry, pigs, and people in pig rearing communities in northwestern Bangladesh, 2014-2016

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**Background:** The surveillance and detection of endemic and novel emerging influenza viruses in poultry, pigs and humans is important for human and animal health. The purpose of this study was to estimate the prevalence of influenza virus infection among sick poultry, pigs with influenza like symptoms and people with influenza like illness (ILI) and identify cross-species transmission in pig rearing communities in northwestern Bangladesh.

**Methods:** From June 2014 to August 2016, we performed surveillance in sick poultry, pigs with influenza like symptoms, and humans with ILI in 240 pig raising households from 13 villages in northwestern Bangladesh. Once a week, we visited the households to screen sick poultry that showed clinical signs and symptoms of highly pathogenic avian influenza, pigs with influenza like symptoms and humans with ILI. We collected oropharyngeal and cloacal swabs from sick poultry, nasal swabs from pigs with influenza like symptoms and nasopharyngeal and throat swabs from humans with ILI. We performed real-time RT-PCR on the swab samples to identify influenza virus subtypes.

**Results:** We collected swab samples from 173 sick poultry, 253 pigs with influenza like symptoms, and 146 humans with ILI. The prevalence of influenza A virus infections was highest in poultry (32%, 95% CI: 25-39) followed by people (23%, 95% CI: 17-30), and pigs (4%, CI: 2-7). In sick poultry, the most common subtype identified was H5 (95%, 52/55). In people, the most common subtype was H3 (68%, 23/34); 32% were pandemic H1. Pigs were primarily infected with the pandemic H1 (90%, 9/10). Most influenza A virus infections among people (31/34, 91%) and pigs (9/10, 90%) occurred during June-August. In poultry, most of the influenza A virus infections occurred during February - May.

**Conclusions:** Our study provides evidence that seasonal human influenza A viruses circulating in these communities were also infecting pigs during the same time period. Further characterization of samples from this study will elucidate if these influenza strains have genetic changes that might carry a public health risk. Continued surveillance is recommended because circulation of H5 influenza in poultry, cross species transmission suggests that this is a high risk setting for reassortment of strains and so emergence of novel potentially dangerous strains that could infect humans.

## PROBIOTICS AS ALTERNATIVE POTENTIAL THERAPEUTICS FOR SMALL RUMINANT MASTITIS PATHOGENS: STAPHYLOCOCCUS AUREUS AND ESCHERICHIA COLI, ABA'ALA, AFAR, ETHIOPIA

Yisehak Redda[1], Mohamed Said Abdulle[3], Getachew Amede[2], Nesibu Ababelgu[2], Meselu Ahmed[2]

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Subclinical mastitis is well known to cause huge economic losses in the dairy production. Thus, the current cross sectional and experimental studies were employed from July, 2016 to November, 2016 to isolate and characterize E. coli and S. aureus from mastitic lactating small ruminants and to isolate and evaluate the indigenous beneficial lactic acid bacteria strains as a potential probiotic for the prevention of small ruminant mastitis in Aba'ala and its environs, Afar Region. Clinical examination of the udder, California Mastitis Test, bacteriological characterization of the isolates were performed. Biochemical and BIOLOG isolation and identification and evaluation of antibacterial activities of lactic acid bacteria strains were done to identify the potential probiotic bacteria. Descriptive statistics were used for analyses. The overall prevalence of sub clinical mastitis was found to be 25.3%. The prevalence of sub clinical mastitis was higher in sheep (30.8%) than goats (20.8%). The overall prevalence of the pathogens were found to be 36.8% and 27% for S. aureus and E. coli, respectively. The highest mastitis pathogen wise prevalence was recorded for S. aureus (36.8%). From a total of 19 pure colonies of LAB isolates, only 10 of LAB isolates showed maximum growth of inhibition and further identified.. Two of them were identified to species level (Tetragenococcus halophilus) and three were to genus level (Enterococcus, Lactobacillus and Dsygonomonas). But the remaining five LAB isolates were identified neither at genus nor species level because of their slow growth nature. Isolates 1MX (Enterococcus), 3MM (Lactobacillus), 1M3 (Dsygonomonas), and 3M3 (Tetragenococcus halophilus) were showed inhibition for both E. coli and S. aureus. Whereas isolate 372 (Tetragenococcus halophilus) was only showed inhibition for E. coli. The current finding is a new insight in the use of locally isolated beneficiary probiotics. Therefore, further characterization of the promising lactic acid bacteria should be done and before the use of the promising candidate lactic acid bacteria isolates, the safety of the isolates should be carefully and systematically assessed.

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## Sources of Professional Information for Kenyan Veterinary Surgeons and Veterinary Paraprofessionals

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The need for evidence-based Veterinary Medicine forces Veterinary Surgeons and para-professionals to remain in touch with latest developments in the veterinary sector but the flood of irrelevant data remains a challenge. Overcoming this needs identification of efficient information sources and selective acquisition of scientifically valid information. This study sought insight into the information seeking behaviour of veterinary professionals in Kenya. The objectives were to identify are accessible, reliable, relevant and preferred sources and channels of information used by Veterinary professionals and to understand what influences their preferences. A survey monkey was disseminated to Kenyan Veterinary surgeons and paraprofessionals in Kenya through recognized channels such as email, yahoo groups, and google groups.

Majority of respondents seek extra information/training with different factors motivating them. The highest ranking reason was personal interest hence why the cost of attending most of the trainings is self-sponsored. Conferences are the largest avenue used by Kenyan veterinarians to obtain professional information, followed by peer reviewed journals and online courses. Google and yahoo groups are the biggest avenue through which the Kenyan veterinary professional discovers upcoming conferences. The Kenya Veterinary Journal was reported as the most read journal and the FAO the most consulted website followed by Merck Veterinary Manual online mostly to find out about disease prevention. Keeping updated with professional information is one of the leading reasons why the Kenyan veterinary professional consults their preferred sources. Electronic sources were preferred by majority of respondents. However, the veterinary profession engages quite largely in consultations among colleagues in clinical practise which shows a connection between colleagues in the field.

## The Role of Soluble Adhesion Molecules in Type 2 Diabetes Mellitus

Ola Al-jammal, Maryam abdel-Hady

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## One Health in South Asia and Its Challenges in Implementation through Stakeholder Perspective

Rojan Dahal

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**Abstract:** One Health is a concept which fosters collaborative relationships between human health, animal health and environmental health partners. Diseases are emerging and remerging in South Asia due to poor sanitation, close proximity of people to livestock, deforestation, porous borders, climate change, changes in human behaviour and unhygienic food preparation and consumption practices.

This review was completed in two stages. First, we conducted a review of peer-reviewed literature and grey literature available in Google search engine related to One Health in four countries (Bangladesh, Bhutan, India & Nepal). Second, we used a structured questionnaire completed by the key stakeholders working on One Health for the collection of information related to the challenges in implementing One Health.

Bangladesh and India did considerable work in advancing One Health with limited support from the government agencies. Most of the One Health activities in South Asia are determined by donor preferences.Weak surveillance mechanisms, uncertain cost effectiveness of One Health compared to the existing approach, human resources, and laboratory capacity are some of the factors hindering implementation of the One Health concept.

Implementation of One Health is growing in the South Asia region with limited or no government acceptance. To institutionalise it, there is a need for leadership, government support and funding.

## Global One Health initiative (GOHi) eastern Africa Region: The Ohio State model system

Getnet Yimer, Emia Oppenheim, Ashely Bersani, Tigist Endashaw, Wondwossen Gebreyes

*Global One Health initiative: The Ohio State University, Addis Ababa, Ethiopia*

Cognizant of the huge gap in capability while handling One Health related agenda in Eastern Africa and building on the longstanding fruitful partnership, the Ohio State University established a regional Global One Health initiative (GOHi) based at its central regional office in Addis Ababa, Ethiopia. While its office was established in Fall, 2016, a number of One health capacity building activities had been underway since 2010 launched from the Ohio State office based in Columbus, Ohio. The unique aspects of the GOHi include: 1) building mutually-beneficial partnership both for the African regional as well as U.S. partners; 2) it is centrally-anchored on capacity building across breadth of areas including research capacity, training capacity and outreach capacity; 3) GOHi, unlike many One Health programs addresses not only acute biological hazards (such as zoonotic diseases) but also chronic issues as well as chemical hazards, all at the interface of human, animal and the environment. Using one of its model partnerships, One health Ethiopia, GOHi identified four technical areas that must be addressed in dealing with most One Health issues. These include: 1) surveillance and monitoring; 2) Prevention and control in humans; 3) Prevention and control in animals (or environment) and 4) Education and advocacy to sustain success. Major achievements of the GOHi regional office include:

Efficiently executing the CDC GHSA cooperative agreement involved from training, field coordination, liaising with stakeholders and smoothly running the different projects (Brucellosis, Rabies and Anti-microbial resistance)

Acquiring grant and smoothly conducting a new world-class USAID funded project (WHIP3 TB Clinical trial): from clinical trial capacity building to actual operation

Coordinating and conducting the 6th annual Ohio State Eastern Africa One Health Summer Institute activities: delivery of successive trainings, running projects and workshops;

Convened NIH-Fogarty International Center sponsored the Eastern Africa Regional Antimicrobial resistance Workshop

Support Eastern Africa regional Governments in activities beyond One Health (National Health Research Ethics Committee, Ministerial Advisory Committee, Drug importation Authorization Committees (FMHACA) in Ethiopia; regional rabies prevention engagement workshop in Kenya and an service in PhD external examination Muhimbili University in Tanzania and others;

Conducted One Health leadership and communications training for the top level managers of the Ethiopian Public Health Institute.

# Abstracts Day 2

## November 8, 2017

**Session 3: Innovative Capacity Building, e-Learning and Outreach approaches.**

**Session 4: Antimicrobial Resistance and Drug Related Issues**

**Session 5: Biosecurity, Biodefense, and Disaster Response**

Lead Session 3: **Nicole Kraft**, Clinical Assistant Professor, School of Communication, The Ohio State University

Title: Global One (Tech) Health: How technology guides education, research and outreach

Lead Session 4: **Satoru Suzuki,** PhD Ehime University, Matsuyama, Japan Professor of Microbiology Division of Aquatic Biosciences Center for Marine Environmental Studies (CMES)Laboratory of Marine Molecular Ecology (MME)

Title: Aquatic environments as a reservoir of antibiotic resistance genes (ARGs)

Lead Session 5: **Barbara Kowalcyk,** kowalcyk.1@osu.edu, The Ohio State University, Columbus, OH, | RTI International, Research Triangle Park, United States | Food and Agriculture Organization of the United Nations, Rome, Italy

Title: Ranking food safety risks: a guided approach

Plenary Speaker 5: **Douglas T. Shinsato**, JD, MBA, Board of Regents, University of Hawaii, Hawaii, USA.

Title: Bio-Security, Silos and Solutions

## Plenary Session 3:
## Innovative Capacity Building, e-Learning

### Analysis of knowledge, attitudes and practices of the population in rural areas of Boucle du Mouhoun region (Burkina Faso) regarding Tænia solium life cycle.

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3. *Direction Générale des Services Vétérinaires, Ouagadougou, Burkina Faso*
4. *Centre Muraz, Bobo Dioulasso, Burkina Faso*

The aim of that study was to analyze knowledge, habits and practices of the populations of Boucle du Mouhoun region (Burkina Faso) in relation with the life cycle of Tænia solium. We carried a knowledge attitudes and practices (KAP) survey was carried with 320 people randomly chosen in four villages. More than half of the interviewees (54.4%) were men, 89.4% had not been to school, 82.2% were animists and 43.1 % were pig breeders. The disease is called “Dah” or “Zah” in the area and about the three fifth (60.3%) have already seen a swine carcass with cysts of the parasite. Regarding the method used to recognize the disease on a living animal, only 11.9 % know the langueyage method. Only two people (0.6%) knew that pigs are contaminated when it eat human feaces. In addition, 32.2 % though that they could get sick by eating infected meat. Water from wells and rivers is consumed by respectively 62.8 % and 41.2% of the people and 75.1% of the wells do not have edges. Furthermore, the water from the rivers is drunk without any treatment. In addition, 84.1 % of the homes have latrines but 52.2% of people practice open defecation. Swine meat is eaten by 80.6% of the people and 30.9% eat meat even with cysts. This study shows that the ways of transmission of porcine cysticercosis are not well known and that the habits and practices of the people foster the risk of remaining of cysticercosis/ taeniasis in these villages.

## The effect of negative human behavior on the environment and its role in the spread of the diseases.

Thaer Elyas

*Biology and medical super vision department /veterinary directorate, Baghdad, Iraq*

**Conclusion objective of the research:** The aim of the research is to study the effect of the environment on human and animal health and the impact of each of them on the environmentand the extent of the damage that may be left by the human wrong dealing with the environment .

The study included a range of common diseases transmitted from animal to human and may adversely affect the environment causig health and economic problems.

the research included:

1. Echinococcosis
2. Toxoplasmosis
3. Brucellosis
4. Tuberculosis

The spread of these disease is affected by the health of environment due to thethe the negative or posative treatmentof the human towrd the environment including animals ,plants ,soil, water and air ,all of these are very important factors for the maintenance of human health.

The study included the spread of the diseases in different Iraqi provinces through different circumstanses.

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## Bovine Tuberculosis infection in pastoral cattle and wildlife at livestock-wildlife interface of the Greater Ruaha ecosystem, Tanzania

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This is an interdisciplinary collaborative research to investigate the impact of bovine tuberculosis (BTB) caused by Mycobacterium bovis and environmental change resulting to diminishing of water level of the Great Ruaha River as a result of agriculture, overgrazing and drought. We conducted a cross-sectional study to estimate the current prevalence and herd level risk factors for BTB in pastoral cattle and wildlife inhabiting a livestock-wildlife interface of the Greater Ruaha ecosystem, Tanzania. A survey was conducted to assess the potential herd-level risk factors for BTB. A total of 1347 cattle owned by pastoralists from 102 households were tested for BTB. Overall prevalence of BTB infection in tuberculin tested cattle was 1.6% (21/1347) and 1.2% (2/162) in cattle tissue culture. Prevalence of BTB in tested tissues from opportunistically sampled hunter-killed and live-captured wild animals was 8.1% (12/149). Although the prevalence of BTB was relatively low for individual animals, but the herd-level prevalence was high (28.4%), indicating that infection is widespread in the study area and a significant number of households are at risk. This study has detected the unique strains of M. bovis SB0133 spoligotype from wildlife inhabiting the protected area and also from the pastoral cattle along the edges of the wildlife protected areas hence providing evidence for livestock-wildlife pathogen transmission in the interface. Occurrence of BTB in wildlife in the interface represents a permanent reservoir of infection and a potential threat to public health. In view of the fact that pastoral cattle are the largest producer of the milk and meat in the nation, coupled with lack of knowledge of the disease among the communities and the potential risk factors for disease transmission to people, this study therefore, emphasizes on instilling good control measures towards the eradication of BTB to protect health and well-being of the people.

## Need for efficient Monitoring and Evaluation systems for One Health Research

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Monitoring and Evaluation (M&E) has the potential to be a cornerstone for One Health (OH) research, systems strengthening and evidence-informed implementation. In Africa, recent zoonotic out breaks have stressed the need for effective M&E systems as a tool which helps inform research. A well built M&E system for health research can be described as a set of institutions that create, manage, coordinate, demand, communicate and use knowledge resulting from research to improve the population's health and well being.

Management of Emerging Infectious Diseases (EID) require robust sustainable M&E systems that are put in place to 1) enhance public health capacity for detecting EID in a timely manner and 2) disseminate important public health information for research purposes. M&E systems require streamlining existing communication systems for rapid reporting throughout the different sectors including animal and health sectors, trained personnel and surveillance systems to enable baseline surveillance data collection. This information is crucial in identifying disease events requiring further research.

M&E systems which include; 1) Web-based applications with real-time access to summary reporting; 2) timely feedback of information to sites; 3) longitudinal tracking of programs; 4) use of routinely collected aggregate data for analysis and operations research; 5) geographic information systems relevant for monitoring, evaluating, and informing one health initiatives. Although traditionally used in the context of vertical programs, these approaches can form a foundation on which data relevant to one health systems are layered. The availability of a legal framework, political will, skilled personnels, accessibility and reliability of evidence are other critical issues that influence the level of impact of good M&E systems for health research.

This paper provides guiding principles for effective M&E systems for implementation which include country-led development and ownership, support for national one health programs and policies, interoperability, and employment of an open-source approach to software development.

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## Gastro-intestinal parasites infections in mountain gorillas (Gorilla beringei beringei) of Rwanda Volcanoes National Park: One Health Implications

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Mountain gorillas (Gorilla beringei beringei) are endangered worldwide and are the best tourists' attractions of Rwanda. Gorillas of Volcanoes National Park have close contact mostly with tourists, researchers, park workers and the community around the park. Foraging areas outside the park are crossed by village pathways or are in areas where villagers obtain firewood. The study was conducted in the Volcanoes National Park of Rwanda, which is home to mountain gorillas, between March-June 2015. The study assessed the prevalence of the gastro-intestinal parasites affecting the gorillas and identified parasites that can be of public health importance. 24 faecal samples were randomly collected from two gorilla families at different intervals. The faecal samples were examined for parasites using flotation and sedimentation methods. Of the 24 fecal samples examined, the study revealed 5 nematodes, 1 cestode and 4 protozoa. The nematodes eggs found include Trichostrongyle-type (11/24), Strongylus spp (6/24), Ascaris spp (3/24), Hyostrongylus (2/24) and Probstmayria spp. (1/24). The cestode parasite recovered is Anoplocephala gorillae (5/24). The protozoa include Iodamoeba buetschlii cysts and trophozoites (7/24), Entamoeba coli cysts and trophozoites (4/24), Entamoeba histolytica trophozoite (3/24) and Giardia sp. cyst (1/24). Some of the parasites could not be identified. E. hystolytica and Giardia are of zoonotic nature and could therefore be shared with humans. Most of the nematode types found are also found in humans, it is possible that these parasites were from daily human-gorilla interactions by zoonotic, reservoir or paratenic ways. However, there is a need to make the systematic coproculture to definitely identify some parasites and determine the transmission mode in order to confirm whether or not these are multi-host pathogens that can be shared. A similar research in the surrounding human community and livestock in close contact with gorillas would identify the potential one health actions to be taken.

## The tsetse fly (Glossina) challenge at wildlife-people-livestock interface of Akagera National Park, Rwanda

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The tsetse flies (Glossina) are the only biological vectors of the trypanosomes affecting humans and livestock. The Akagera National Park (ANP) and its surroundings remain the lone home to tsetse flies in Rwanda. The wild game-livestock interface plays an important role in the epidemiology, being the reservoirs of the disease. The study was carried out in Eastern province of Rwanda; at the Game/People/Livestock Interface of the Akagera National Park. The aim was to determine the trypanosomes infection rates and identify the pathogenic trypanosome species in field-captured tsetse flies. Tsetse flies were collected from 3 districts surrounding the park between May and July 2015. Tsetse flies were trapped from different locations and live flies were counted, sex-determined and dissected so as to find the trypanosomes in their predilection sites in the tsetse fly. The mouthparts, salivary glands and mid-guts were microscopically examined for the presence and identification of trypanosomes according to the distinct differential morphology. A total of 257 flies were dissected (179 Glossina pallidipes and 78 Glossina morsitans). The study revealed an overall infection rate of 12.8% of which 4.6% is for the mouthparts, 0.7% for salivary glands and 7.3% for the mid-gut. Of the 33 infection cases, Trypanosoma congolense accounted for 57.5%, Trypanosomabrucei for 6%, Trypanosomavivax for 21.2% and the mixed infections of T.congolense and T. vivax accounting for 15.1%. Both G.pallidipes and G.morsitans are potential vectors but G. pallidipes appears to be the most important due to its high density. The study confirmed the presence of trypanosome infected tsetse flies and livestock infective trypanosomes. However, a more accurate DNA based diagnosis is required to identify the blood meal sources and definitely differentiate the species and the sub-species or detect the new species so as to characterize even the human infective trypanosomes as we found the T. brucei-like species.

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## Assessment of Public Knowledge, Attitude and Practices towards Rabies in the Community of Kombolcha, Southern Wollo, Amhara Reginal State, Ethiopia

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The study was conducted from November 2016 to April 2017 in 12 kebeles of Kombolcha, Southern Wollo Amhara Regional state, Ethiopia. The aims of the study were assessing the knowledge, attitudes and practices (KAP) of Kombolcha's community toward rabies and associated risk factors. A cross-sectional study design and multistage sampling procedures were employed to select households for the study. Kebeles were randomly selected using lottery method from list of kebeles in the study area, followed by selection of households from each kebele by systematic random sampling. Data were collected from 384 households through face to face interview using pretested and well-structured questionnaires. Socio-demographically out of the 384 respondents interviewed, 223 (58.1%) were males and 161 (41.9%) were females. From 384 respondents, 345 (89.8%) had heard about rabies before and the majority of the study participants, 329 (85.7%) had good level of KAP. There were statistically significant associations ($p<0.05$) between KAP scores and age, house hold size, educational status, and occupation. In conclusion, the study revealed that, Kombolcha's community has good knowledge, attitude and practice toward rabies. However, there are some inconsistent on mode of transmission, symptoms, appropriate prevention and treatment measures. Therefore continuous and strategic health programs are expected from health professionals, governmental and non-governmental organizations to control and prevent the disease and secure rabies free zone.

## Socio-economic impact of environmentally persistent pharmaceuticals, personal care products and agrochemicals

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Sustainable use of chemicals, sound management of chemicals and effective use of chemical and environmental safety and security are the core pillars to Sustainable Development Goals (DSGs) and One Health and Environment.

The aim of the paper is to determine how environmentally persistent pharmaceuticals, personal care products and agrochemicals impacts on the top priorities of the state i.e. economic growth and infrastructure development, environmental stability, social development and security.

**Methods:** Interviews and literature reviews were conducted to review the environmental and human health impact of the production, use, consumption, imports and exports, and disposal of pharmaceutical, personal care and agrochemicals.

**Results:** Adverse effects observed on environmental sustainability, human health, water and food security, infrastructure development are defeating national priorities for alleviation of poverty and improving the life-expectancy of the society. Human health impacts include increased rate of non-communicable diseases affecting the productive workforce of the country, increased chronic diseases and infectious diseases impacting on the vulnerable groups, and high rate of antimicrobial resistance where microorganisms are becoming extremely resistant to available existing antibiotics and the availability of available antibiotics becoming dry. Environmental sustainability impacts included loss of natural resources, degradability of land and loss of productivity of arable lands, loss of biodiversity and beneficial microorganisms and insects like pollinators, disruption of natural food webs and predator-prey relationships. Food security and water quality impacts are mainly on agricultural, marine production and freshwater productions with impacts threatening the ecology and economy of the ocean, diminishing the economic value of fisheries and aquaculture and creating a loss of export value and loss of jobs, increasing the vulnerability to infectious diseases and emergence of pest resistance pests, and introduction of invasive alien species competing with native species. All costs of inaction to human health, remediation of lands and restoration of soils, purification of water resources falls upon the state.

**Conclusion:** Because of the cross-cutting nature of ministries in terms of their responsibilities, the state needs to prioritize and mainstream the management of these chemicals into the national development plans, and to develop an anticipatory, proactive and precautious preventative approach that seek to reduce, minimize, and eliminate the threats as well as promote circular economy of these chemicals.

## Human health risk of dietary intake of antibiotic residues in beef in Maroua, Cameroon

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The contamination of food by chemical hazards is a worldwide public health concern and is a leading cause of trade problems internationally.Based on former work describing the prevalent use and misuse of antibiotics in cattle in the Far North Region of Cameroon, we designed a study to evaluate the risk of antibiotic (penicillin G and oxytetracycline) intake via beef consumption amongst population in Maroua (Far North Region of Cameroon). To determine the mean concentration of antibiotic residues in beef, each samples of liver and muscle were collected from 202 cattle selected randomly in all the slaughterhouses of Maroua and Godola and analyzed using Liquid Chromatographic tandem Mass Spectrometry (LC-MS/MS). However beef consumption patterns for different populations were determined using a nutrition survey conducted in 202 households selected using a gridded map and random selection method. Results found revealed that out of 202 cattle 41 (20,30%) showed positive results in one or more of their organs. The average concentration of residues in beef determined was 17.58 µg/kg for penicillin G and 240 µg/kg for oxytetracycline. The estimated daily intakes of penicillin and oxytetracycline through consumption of beef were 2.365 ± 0.233 µg and 32.078 ± 8.081 µg respectively. Based on the estimated intake and comparison with the acceptable daily intake, we assessed the risk in Maroua as acceptable (2.17%) for oxytetracycline and greater (9.6%) for penicillin. The findings of the present study could be alarming for the legislative authorities in food security and safety. This highlights a very serious problem, both for the consumers of Maroua and the herders of the region as for the whole economy of Cameroon. It would therefore be important that measures be taken at several levels by the actors of the sector (public authorities, veterinary auxiliaries, etc.) to guarantee the safety of the food from animal origin.

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## In vitro antimycobacterial activity and cytotoxicity of selected medicinal plants against pathogenic and non-pathogenic mycobacterial strains

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**Objectives:** Tuberculosis (TB) caused by Mycobacterium tuberculosis complex represents a never-ending challenge towards which drug discovery efforts are needed. Several medicinal plants are used traditionally in Ghanaian ethnomedicine to treat tuberculosis. In our ongoing research efforts aimed at drug discovery against tuberculosis, we designed the current study to evaluate in vitro antimycobacterial activity and toxicity of eight medicinal plants against pathogenic and non-pathogenic mycobacterial strains. The study was further extended to investigate the non-pathogenic mycobacterial strain which best predicts natural product activity against the pathogenic Mycobacterium bovis.

**Material and methods:** The microplate alamar blue assay (MABA) was used to study the anti-TB activity while the CellTiter 96® AQueous Assay, which is composed of solutions of a novel tetrazolium compound [3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulfophenyl)-2H-tetrazolium, inner salt; MTS] and an electron coupling reagent (phenazine methosulfate) PMS, was used for cytotoxic studies. Correlation coefficients (R2) were used to compare the relationship between antimycobacterial activity of the eight crude extracts against nonpathogenic strains and the pathogenic Mycobacterium bovis.

**Results:** Minimum inhibitory concentration (MICs) values indicated that all the eight tested medicinal plant species had activity against all the three tested mycobacterial strains. Minimum inhibitory concentration values of 19.5 µg/mL, 156.3 µg/mL and 312.5 µg/mL were observed against non-pathogenic strains M. bovis BCG (ATCC® 35745™) and M. aurum (ATCC® 23366™), and the pathogenic strain, M. bovis (ATCC® 35720™) respectively, from the unripe fruits of Solanum torvum Sw. (Solanaceae). Cytotoxicity of the crude extracts towards human fetal lung fibroblast cell lines (ATCC® CCL-171™) varied, and the unripe fruits from Solanum torvum exhibited the most promising selectivity index. Activity of the crude extracts against M. aurum was the best predictor of natural product activity against the pathogenic Mycobacterium bovis strain, with a correlation coefficient value (R2) of 0.1371.

**Conclusions:** Results obtained from the current study validates, in part, the traditional utilization of the tested medicinal plants against tuberculosis. Solanum torvum unripe fruits have selective efficacy against the studied mycobacteria, including Mycobacterium bovis. The unripe fruits from Solanum torvum are a potential source of safe and efficacious anti-TB crude drugs as well as a source for natural compounds that act as new anti-infection agents, and thus deserve further investigation towards development of a new class of molecules with activity against sensitive and drug resistant strains of M. bovis..

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## Diversity and antibiotic resistance profiles of Escherichia coli strains from migratory bird (Branta leucopis) and Reindeer (Rangifer tarandus) reveals dissemination of multi drug resistant (MDR) E. coli to pristine arctic environment

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The short summer and long winter in Arctic region forces many animals to be migratory. This in turn results in the increased risk that migratory birds (and other animals) can bring pathogens or antibiotic resistant bacteria to the Arctic environment. Migratory birds are exposed through numerous sources, including food and water, in parts of the world where the antibiotics are used by the people whereas Reindeer, a native species of Arctic region is never previously exposed to antibiotics. Therefore, there is a considerable significance in isolating Escherichia coli with public health significance from the feces of these animals so as to do a comparative study. Drug resistant E. coli is becoming more prevalent and is on the rise. Migratory birds have turned out to be potential carriers of numerous E. coli strains, thereby spreading multidrug resistant pathogens across geographical boundaries. Barnacle goose (Branta leucopis) breeds mainly in the Arctic islands of North Atlantic and includes three main populations with separate breeding and wintering ranges. The population of barnacle goose studied here is from Svalbard islands, which breeds in Svalbard with wintering on the Solway Firth on the England/Scotland border. Svalbard reindeer (Rangifer tarandus) is the most isolated subspecies of Rangifer, endemic to Svalbard archipelago in the High Arctic. However, contrary to other Rangifer subspecies, the Svalbard reindeers live individually or in small groups. They have limited seasonal migrations and are not nomadic within seasons. They only travel on an average of less than 0.7 km per day during the whole year. Samples were collected as part of Indian Arctic Expedition 2016. Droppings of B. leucopis and dung of R. tarandus were collected at random from the tundra nearby the International Arctic Research station at Ny-Alesund (79oN), Svalbard, Norway. The samples were analyzed using standard methods and typical E. coli like colonies picked up from Eosin Methylene Blue (EMB) agar were confirmed biochemically by performing IMViC test followed by molecular characterization. Phylogenetic analysis was carried out by multiplex PCR method. The isolates were subjected to antibiotic sensitivity testing by disk diffusion method. In order to check further similarity among the E. coli isolates from the two sources, they were subjected to genotyping using ERIC PCR. While six different phylotypes such as A, B1, B2, D, E and F ere encountered among the E. coli strains from B. leucopis, only 4 of them (A,B2,D and E) were seen among the isolates from R. tarandus. Prevalence of pathogenic phylotypes was high among the E. coli strains from B. leucopis. Another important observation was the difference in the prevalence of antibiotic resistance among the E. coli strains from both the sources. While several of the E. coli strains from B. leucopis were multidrug resistant, none of the isolates from R. tarandus were resistant to any of the 11 different antibiotics against which they were tested. Colistin resistance was particularly high among the isolates from migratory bird, which is indeed a cause for worry.

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## Bovine Tuberculosis and Associated Factors among Adult HIV Positive People in Woldya Town, Northeast Ethiopia

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Bovine tuberculosis is among the seven neglected endemic zoonotic disease in developing countries caused by M.bovis. Currently, M.bovis accounts for only 1% of all human TB in developed countries as compared to 10% in developing world. In Ethiopia the magnitude of bovine tuberculosis in animals at different regions is high. Many studies also show its presence in humans. The risk is high among HIV positive people having contact to domestic cattle and consuming raw or undercooked milk and /or meat. Lack or minimum knowledge and practice about the disease exacerbate the disease transmission to humans. The main objectives of this study were to assess knowledge, practice and associated factors about bovine tuberculosis among adult HIV positive people in woldya town. An Institution based cross-sectional study was conducted from March to December 2014 in woldya town. The data were collected by using interviewer administered questionnaire. A total of 630 HIV positive adults were selected by systematic random sampling. Descriptive statistics and binary logistic regression were employed for the analysis of the data. The study included 630 individuals, but twenty of them were excluded due to different reasons. Among the 610 respondents 67.2% lives in urban area. From the study population 58.2% were females and the mean ages were 36.5 years. The level of knowledge about bovine tuberculosis was found to be 9.3%. A good practice for the prevention of bovine tuberculosis was 50.8%. Women's were less knowledgeable than men, [AOR=0.424 CI (0.223-0.805)]. Individuals who consult veterinarians and public health professionals were more knowledgeable [AOR=9.160 CI (3.890-21.570)]. Training also had positive association for the knowledge of bovine tuberculosis. Food consumption habit influence preventive practice for the transmission of bovine tuberculosis. This study had demonstrated that little knowledge about bovine TB among adult HIV positive individuals. Men, consulting veterinarians and public health professionals and training had positive association with knowledge about bovine tuberculosis. Strengthening One-Health and large scale community based cross-sectional studies are recommended.

## A One-Health Approach to Mountain Gorilla Conservation: Disease Challenges and Opportunities for Research, Training and Business

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The Importance of gorilla conservation and tourism in Uganda can not be underscored. The threat of infectious diseases currently is the main concern to the conservation of this endangered species. The Mountain Gorilla Veterinary Project Incorporated (MGVP, Inc.) is one of few conservation programs in the world to provide health care and treatment to an endangered species in its natural habitat. With teams of experienced personnel, MGVP veterinarians track ailing gorillas, observe and treat them when needed - inside their native habitat. The project staff works in close partnership with the protected area authorities of Rwanda, Uganda, and the Democratic Republic of Congo (DRC), in addition to a variety of organizations dedicated to gorilla conservation. The gorillas remain highly endangered due to threats from war, poaching, habitat destruction and human disease. Their numbers remain critically low, with no fallback breeding population in sanctuaries or zoos.

As part of the one-health approach, the MGVP field vets make routine health check visits to habituated gorilla groups, in addition to visits for reported problems. The routine health check visits give the field vets the opportunity to observe healthy animals and establish normal parameters. Complete post-mortem examinations (necropsies) are performed on all deceased mountain gorillas. These exams are an important aspect of monitoring gorilla health as they help determine the cause of death and represent an important opportunity to collect biological samples. Other wildlife species found dead may also be examined because the results may inform the veterinarians about potentially problematic infectious diseases transmissible to gorillas.

Emergency veterinary care for a life threatening illness or injury in a wild mountain gorilla remains a core function of the MGVP field veterinarians and the park staff. The field vets are notified of mountain gorilla health problems by park staff. The next step is a “monitoring visit” to observe the gorilla or gorillas in question and evaluate the situation. But they intervene with treatment or anaesthesia for examination only in cases of human-induced or life threatening injury or illness. Samples for medical evaluation and research are collected opportunistically when possible. While in the field, the veterinarians collect non-invasive samples, such as faeces, urine, saliva, and hair. While gorillas remain the focus of their work, MGVP staff also contributes to programs designed to assess the health of the other species, both domestic and wild. The MGVP collaborates with park authorities and other non-governmental organizations to provide employee health programs for park staff, porters, field veterinarians, and researchers who work with the Mountain Mountains. This is a voluntary, confidential program.

This presentation will highlight the challenges and opportunities for research and training in a one health approach to the Mountain Gorilla Conservation at the Human – Animal Interface.

# Public Knowledge, Attitude and Practice towards antibiotics use and resistance in human and animals in Jimma town, Ethiopia

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**Background:** Poor community knowledge and practices regarding prudent use of antibiotics as well as resistance contribute to the emergence and spread of antibiotic resistance in human and animal isolates. The objective of this study was to determine the knowledge, attitude as well as practices regarding human and animal antibiotic use and resistance among the general population using a one Health approach.

**Methods:** A population based Cross-sectional survey was conducted using a structured questionnaire among a random sample of 443 households' heads representing the urban and Peri-urban community in Jimma town, Ethiopia. Data were analyzed using descriptive statistics and multivariate logistic regression analysis.

**Results:** Of the total household surveyed, 405 household heads (72.8% men) from the urban (47.9%) and semi-urban (52.1%) areas were included and of these, 63.7% (n=258) had at least one species of livestock at the household. About 96.5% (n=391) of the total household heads were familiar with term antibiotics and of these, 84.9% (n=332) reported taking antibiotics for themselves at least once during the past 12 months prior to the study. Among the livestock owners familiar with antibiotics (95.4%, n=246), 75.2% (n=185) also reported providing antibiotic treatment for their livestock's in the past year. The human use of antibiotics was found to be more prevalent among the respondents in the Peri-urban areas than those in the urban (90.4% vs. 79.4%, P = 0.003, AOR, 95%CI, 2.43(1.31-4.64)) whereas, the animal use of antibiotics is more common among farmers than other livestock keepers. (P = 0.0001, AOR, 95%CI, 32.09 (10.08 to 102.22.) after adjusting for other variables. About 57% of the total household heads were self-medicated and 81.4% of the livestock owners reported using non-prescribed antibiotics for their animals. Self-medication was not significantly associated with socio-demographic, knowledge and attitude of respondents in both humans and livestock cases.

In general, only 40.4% and 21.1% of the total respondent had adequate knowledge level about antibiotic use, action and safety and about antibiotics resistance respectively. Higher education level was associated significantly with better knowledge (P=0.008). Nearly half (44.2%, 179) of the respondents had poor attitude towards antibiotic use and resistance.

**Conclusion and recommendation:** The survey showed a high prevalence of antibiotic use, inadequate knowledge and poor attitude regarding antibiotic use and antimicrobial resistance. Effective public education initiatives targeting the households should provide practical and appropriate means to achieve behavioral change.

**Citation:** unpublished

Antimicrobial Resistance and Drug Related Issues

## PREVALENCE OF BOVINE TUBERCULOSIS AND ASSOCIATED RISK FACTORS IN MECHA DISTRICT, WEST GOJAM ZONE, ETHIOPIA

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Bovine tuberculosis, which is caused by Mycobacterium bovis, is a chronic debilitating disease of animals characterized by the formation of granulomas (tubercles) in tissues and organs. This study aimed to estimate the prevalence of bovine tuberculosis and associated risk factors. The study used a cross sectional study conducted from November 2016 to June 2017 on dairy farms that are found in Mecha district, Northwestern Ethiopia. The study site was selected purposefully and tuberculosis (TB) caudal fold tuberculin test (TCFTT) and TB LAM AG test (TLAT) were used to investigate the diseases. Information from owners was collected using questionnaire, to evaluate the possible potential risk factors. Sample size was determined using single population proportion sample size determination techniques and a total of 385 cattle were tested using TCFTT and 220 using TLAT. In this study, the level prevalence of BTB at individual animal was 1.6% (6/385) by TCFTT, while it was 5.9% (13/220) by TLAT. One point four percent (3/220) animals were positive for both tests. Similarly, herd level prevalence of 3.75% (6/160), 10% (12/120) and 2.5% (3/120) were recorded by using TCFTT, TLAT and both tests, respectively. Based on the current finding, the Kappa test indicated that the two tests agreement was poor (Kappa < 0.4). Herd size and management of the farm showed a significant association for the occurrence of bovine tuberculosis ($p < 0.05$); whereas, age, body condition, and breed of animals ($P < 0.05$) were significant contributing factors for bovine TB occurrence at the cow level while using TCFTT. Among the total 71 respondents 15 (21.1%) knew about bovine tuberculosis (BTB) and 10 (14.1%) knew BTB being a zoonotic disease with a history of at least one human TB patient. In conclusion, the present study shows an overall low level prevalence of BTB in the dairy cattle and farms (herds) of the study area and also low knowledge level of the community regarding BTB. Although the test indicated low level problem, it should not be taken as warranty and requires to design and implement an acceptable control strategy to the disease before reaching its climax and poses great socioeconomic impacts as well as public health hazard in addition to community awareness programs regarding the disease.

## Immigration and Nativism in America: Opened and Closed Doors

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**Question:** Is President Trump's anti-immigrant/nativist rhetoric a new phenomenon in the U.S. or does it draw upon a rich history of opposition to the "other" dating back to the founding of the Republic?

**Answer:** From its beginning the U.S. has vacillated between times of welcoming immigrants and fearing immigrants.

**What is nativism?:** The term "nativism" was coined in the U.S. in the 1840s at the time of vast migrations from Ireland and Germany changing the nation and transforming its port cities. Nativism would include every type and level of fear and antipathy toward foreign peoples and foreign religions.

Since the founding of the U.S. Republic at the end of the 18th century the U.S. has experienced five separate intervals of heightened nativist eruptions each linked to moments of national insecurity. The first nativist outbursts took place in 1798 with Congress passing four bills (Alien and Sedition Acts) targeting opponents to Federalist policies accusing aliens in the U.S. of holding sympathies for Revolutionary France. The second major eruption of nativist reaction occurred in the 1850s with the large-scale flowering of the "Know Nothing" or American Party aiming to halt Catholic immigration from Ireland and Germany. The third nativist episode rose to prominence in the 1880s and 1890s at a time of labor unrest and periodic economic crises. With leadership from the American Protective Association, nativist proponents advocated for restrictions on Asian and Southern European immigration. A fourth nativist reaction broke out during the 1920s at the time of the "Red Scare" and the rise of the 2nd Ku Klux Klan. During this fourth interval, nativists targeted principally Jews and Catholics. The fourth episode of nativism led to the preferential (racially-based) immigration quota system which lasted until the 1960s. The fifth and present phase of nativist reaction erupted with the presidential campaign of Donald J. Trump and seeks to limit overall immigration to the U.S. with special emphasis on halting Muslim immigrants and refugees from entering the U.S. while deporting illegal immigrants from Mexico and Central America.

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## Establishing a New Unique Partnership Between The Ohio State University and China Global One-Health Partners

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2. *The Ohio State University, Global One Health initiative (GOHi), Columbus, United States*
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4. *The Ohio State University, College of Public Health, Columbus, United States*
5. *The Ohio State University, College of Veterinary Medicine, Columbus, United States*

**Background:** Emerging and re-emerging infectious diseases, chronic non-communicable disease, and other environmental hazards such as environmental pollution and those at the interface of animal and human health are leading causes of mortality worldwide with the potential for rapid transmission across many populations. Antimicrobial resistance among tuberculosis (TB), other vector-borne and zoonotic bacterial pathogens such as malaria, and viruses further complicate treatment and surveillance. Majority of emerging infections are known to be zoonotic and are a major threat to our food supply and natural resources and the environment. A global one health multi-disciplinary interactive needs assessment is needed to identify key priority issues for China.

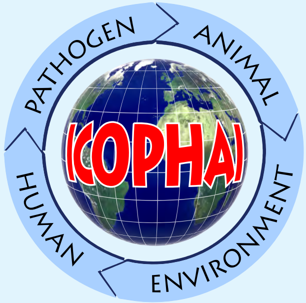
**Method:** We proposed to conduct a needs assessment interactive scientific workshop bringing together The Ohio State University (OSU) faculty and key Chinese academic, research, industry, and government regulatory partners to expand our Global One Health initiative (GOHi). Networking sessions by topic was a specific focus of the meeting to allow researchers with similar interests to meet, discuss, and organize future research collaborations.

**Result:** We used a Focus Forward Format to determine top priorities for short and long-term engagement as well as enhance and/or establish of new partnerships among OSU and Chinese academic, public health, and government institutions resulting in future research collaborations.

Specific theme tracks presented and discussed include: Antimicrobial resistance, antimicrobial stewardship and infection control; Utilization of new technology for diagnosis and management zoonotic diseases; Impact of environmental and occupational hazards on health and wellness; "Farm to table" food safety; Impact of climate on chronic diseases. Participants with expertise in thematic areas were invited from Chinese academic institutions, China's Public Health and Agricultural Ministry, Center for Disease Control, and other key community and industry stakeholders. We had two GOHi Workshops in China. First was in Shanghai, China in October 2016 in collaboration with Fudan University, in Shanghai in October 2016. A second GOHi workshop was held June 2017 in collaboration with Shang Tong University and Jinan Qi Lu Hospital, in Jinan, China.

**Conclusion:** Antimicrobial resistance, antimicrobial stewardship, and tuberculosis were identified as key priority areas. Development of Memorandum of Understanding (MOU) between OSU and participating institutions are underway for future collaborative projects.

# Plenary Session 4: Antimicrobial Resistance and Drug Related Issues



## Aquatic environments as a reservoir of antibiotic resistance genes (ARGs)

Satoru Suzuki

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**Background:** After the G7 summit in 2013, most developed countries are eagerly fighting against antibiotic resistance issues according to the concept of “One Health Approach” proposed by WHO. Heath of humans, animals and environments should be studied by linking each other to dissolve the cross-area and cross-border problem. Reducing excess drug use, public health enlightenment, systematic monitoring and so on are generally valuable to reduce the antibiotic resistance threat. Improvement of wastewater treatment facility has also been tried. On the other hand, real situation of natural environment especially aquatic environment is still a black box as a potential source of ARGs. Risk assessment of environmental ARGs based on quantitative analysis of antibiotic resistant bacteria (ARB) and ARGs is needed to make appropriate strategy for this issue.

**Aquatic microbial community:** Aquatic environments receive ARGs from land. The origins of ARGs from land should be human and animal clinical settings, effluent of municipal wastewater treatment plant and agriculture. Addition to the effluents from land, aquaculture is also potential origin of ARGs. When bacteria are introduced to aquatic environment, bacteria are grazed by protists and infected by virus. These microbial interactions decompose bacteria, but in the meanwhile the ARGs can be horizontally transferred to sensitive bacteria by the transferable DNA elements, such as plasmids and integrative conjugative element (ICE). The DNA elements are suspected to stably persist in environment and environmental bacterial community. It is known that more than 99% of marine bacteria are yet-to-be cultured. Whether the silent majorities are reservoirs of ARGs or not is not clear. It is hypothesized that the yet-to-be cultured bacteria (silent majorities) receive and preserve ARGs derived from ARB.

**Actual status of ARGs in aquatic environments:** I would show examples of ARGs research topics from my lab. First one is from the Philippines case. Sulfonamide resistance genes, sul1, sul2 and sul3, were found in seawater assemblage, but not in freshwater assemblage. Culturable bacteria possessed sul1 and sul2, but not sul3. This suggests that seawater community is a reservoir of all sul genes, and sul possessing culturable bacteria are not abundant in natural freshwater. Culture method selects culturable bacteria having sul1 and sul2. Second new evidence shows that transferable multi-drug resistance plasmid pAQU1 is not easily decomposed under the conditions without selection pressure and with high grazing pressure in seawater. These suggest that the ARGs can persist in marine environment even after the grazing or lysis of ARB. Third topic shows that the bivalves are not enhancing ARGs in coastal sea. Our aquarium experiment using clam (Ruditapes philippinarum) indicated that the clam ingests ARB and digests. As a result, the copy number of an ARG tet(M) in digestive tract of the clam was balanced. Wild mussel (Mytilus galloprovincials) monitoring also indicated that mussel did not accumulate the tet(M) from seawater. The tet(M) copy numbers in seawater and mussels were stable through April to October. This suggests that bivalves might not be a serious risk factor enhancing ARGs in environment.

**Risk management for natural waters:** The marine bacteria possess ARGs, which can be transferred to human enteric/pathogenic bacteria if the case occurs. Water use, seafood and recreation are the possible cases. Freshwater environments should have much higher possibilities. Enteric and pathogenic ARB from animal and humans are able to survive for longer time in freshwater than seawater. Use of freshwater is much frequently, which makes exposure chance high. We should list up reasonable scenarios based on scientific evidences, and develop strategies to mitigate releasing ARGs, to reduce exposure risks.

**Acknowledgments:** Grants from JSPS (A-22241014, A-25257402, A-22254001, B-19405004, 16H01782, 17H04476) supported the ARGs project in my lab, and supporting staffs, collaborators and students for their excellent skills and team works are highly acknowledged.

## Global trends in antimicrobial consumption in food animals

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**Purpose:** Demand for animal protein for human consumption is rising globally at an unprecedented rate. Modern animal production practices are associated with regular use of antimicrobials, potentially increasing selection pressure on bacteria to become resistant. Despite the significant potential consequences for antimicrobial resistance, there has been no quantitative measurement of global antimicrobial consumption by livestock.

**Method:** We address this gap by employing Bayesian statistical models combining maps of livestock densities, economic projections of demand for meat products and current estimates of antimicrobial consumption in high-income countries to map antimicrobial use in food animals for 2010 and 2030.

**Results:** We estimate that the global average annual consumption of antimicrobials per kilogram of animal produced was 45, 148 and 172 milligrams per kilogram for cattle, chicken and pigs, respectively. Starting from this baseline, we estimate that between 2010 and 2030, the global consumption of antimicrobials will increase by 67%, from 63,151 ±1,560 tons to 105,596 ±3,605 tons. Up to a third of the increase in consumption in livestock between 2010 and 2030 will be imputable to shifting production practices in middle-income countries where extensive farming systems currently dominates. For Brazil, Russia, India, China and South Africa, the increase in antimicrobial consumption will be 99%, up to seven times the projected population growth in this group of countries.

**Conclusion:** The rise in antimicrobial consumption in food animals is likely to be driven by the growth in consumer demand for livestock products in middle-income countries and a shift to large-scale farms where antimicrobials are used routinely. Better understanding of the consequences of the uninhibited growth in veterinary antimicrobial consumption is needed to assess its potential effects on animal and human health

**Relevance:** Our findings call for initiatives to preserve antibiotic effectiveness while simultaneously ensuring food security in low- and lower-middle income countries.

**link to publication:**
http://www.pnas.org/content/112/18/5649.short

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## ANTIMICROBIAL RESISTANCE PATTERN OF COMMON BACTERIAL PATHOGENS IN ETHIOPIA: A META-ANALYSIS

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**Introduction:** Antimicrobial resistance is a global problem affecting both developed and developing countries. It is one of the causes of treatment failure and associated with morbidity and mortality. The problem of AMR is worse especially in developing countries where there are trends of inappropriate use of antimicrobials. Although there were few studies conducted on nation wide AMR survey in Ethiopia, this meta analysis systematically reviews published reports on AMR to common bacterial pathogens in Ethiopia during a period of 2009 to 2017 G.C.

**Methods:** PubMed online published and AMR survey reports were analyzed using combination of the following keywords, subjects and title words: ‘antimicrobial resistance’, ‘antibiotic resistance’ and ‘Ethiopia. Only major pathogenic bacterial species isolated from humans and or animals were searched.

**Results:** The available published reports in Ethiopia indicate that most bacterial pathogens (>50%) isolated from humans/humans were resistant to commonly prescribed antimicrobial agents such as ampicillin, amoxicillin, penicillin, erythromycin, tetracycline, chloramphenicol, gentamicin, trimethoprim/sulfamethoxazole. Resistance were also observed against newer drugs such as methicillin, vancomycin, amoxicillin/clavulanic acid, cephalosporins, ciprofloxacin, monobactams, carpepenems, tigecycline and tobramycine. Among the bacterial pathogens, Staphylococcus spp., Streptococcus spp., Enterococcus spp, Enterobacteriaceae, Pseudomonas aeruginosa, Acinetobacter spp., and Mycobacterium tuberculosis were the main clinical isolates and all of them were multidrug resistance.

**Conclusion & Recommendations:** The overall burden of methicillin resistant Staphylococcus aureus is considerably high. The emergence of beta lactamase and Extended-Spectrum Beta-Lactamase (ESBL)-producing Enterobacteriaceae is major concern in hospitalized patients. Carbapenemase-Producing enterobacteriaceae is emerging in a country monbactams and carbapenems prescribed less frequently. MDR and XDR-TB are major concern for TB control program. Based on the AMR data, urgent implementation of Antimicrobial Stewardship program needed with help of concerted actions of antimicrobial stewardship team. Antimicrobial Stewardship program is an interventional strategy for optimal selection, dosage, and duration of antimicrobial treatment that results in the best clinical outcome for the treatment or prevention of infection, with minimal toxicity to the patient and minimal impact on subsequent resistance. In addition, periodic large-scale survey on antimicrobial resistance in Ethiopia have to be conducted to access trends of AMR at different time intervals.

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## Antimycobaterial and antibacterial activities of extracts from Caesalpinia bonduc (L.) Roxb.

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**Aim of study:** The study focused on searching bioactives that can be used to combat pathogenic microbes from leaves, stem wood and stem bark of Caesalpinia bonduc.

**Background:** Many pathogenic microbes have developed resistance to most of the recommended first line and second line drugs. Antimicrobial resistances endanger the control of infectious diseases by increasing morbidity and mortality and impose massive costs on societies in both developed and developing countries. Medicinal plants used for treatment of infectious diseases are potential of bioactives to combat this problem.

**Material and Method:** The plant materials of Caesalpinia bonduc were collected from Kisakasaka mangrove reserve, Zanzibar. Microbes were collected from Department of Microbiology at MUHAS. Methanol, chloroform and n-hexane extracts from stem wood, stem bark and leaves of Caesalpinia bonduc were evaluated for antimicrobials. Antibacterial activity was evaluated against Staphylococcus aureus (ATCC25923), Escherichia coli (ATCC29953) and Pseudomonas aeruginosa (ATCC25922). Antimycobacterial activity was performed against two non-pathogenic mycobacteria species namely Mycobacteria indicus pranii and Mycobacteria madagascariense. Evaluation for antiviral activities, Newcastle diseases virus (NDV) was used for bioassay experiments. The two-fold serial dilution method was used to evaluate MIC for antimicrobial activities. Chromatographic techniques employed in sequential extractions.

**Results:** Extracts with high activity had MIC of 2.5 mg/mL while extracts with low activity had MIC of 5.0 mg/mL.

**Conclusion:** Antimicrobial activity exhibited by extracts indicated that, Caesalpinia bonduc is a potential for bioactive metabolites which can be used as leads for the development of broad spectrum antimicrobial agents.

## An in-vitro analysis of β-lactam combinations with aminoglycosides versus colistin among multi-drug resistant Pseudomonas aeruginosa

Derek N. Bremmer[1], Keelie Thomas[2], Debra Smith[2], Preeti Pancholi[2], Joan-Miquel Balada-Llasat[2]

Joan-Miquel Balada-Llasat, Derek N. Bremmer, Keelie Thomas, Debra Smith, Preeti Pancholi

Department of Pathology, The Ohio State University Wexner Medical Center, Columbus, United States

Extensively-drug resistant (XDR) Pseudomonas aeruginosa (PsA) infections have limited treatment options available. We sought to determine the clinical utility of a real-time checkerboard platform.We tested PsA isolates by the checkerboard method using 9 wells for each drug combination, labeled the serum achievable concentration (SAC) wells. The results were correlated by time-kill assay utilizing the concentrations of drug from the fractional inhibitory concentration well. Aminoglycoside-β-lactam combinations were more likely to achieve synergy and showed inhibition of all P. aeruginosa SAC wells compared to colistin-β-lactam combinations (115/376 (30.6%) vs 12/282 (4.3%); p= 0.0001). A real time checkerboard platform for XDR PsA may have clinical and microbiologic benefit.

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## National Action Plan to Combat AMR in the State of Qatar Using "One health" Approach

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*Ministry Of public Health - Healthcare Quality and Patient safety Department, Doha, Qatar*

Antimicrobial resistance (AMR) is a multi-sectoral problem and it imposes a huge burden on human and animal health as well as the economy worldwide. In the State of Qatar, the increasing number of antimicrobial-resistant infections in the community and healthcare settings is alarming and mandates actions to be taken to monitor and control antibiotics use.

The Ministry of Public Health (MOPH) - HealthCare Quality and Patient Safety Department has developed national integrated multi-sectoral action plan to combat AMR in the State of Qatar. Qatar National Action Plan, using "One Health approach", is aligned with the Global Action Plan on Antimicrobial Resistance, resolution WHA 68.7 and the UNGA declaration and the GCC strategic plan. The action plan is particularly important for improving adherence to stringent infection control measures, applying regulations controlling antimicrobial use in both human and animal sectors, implementing proactive surveillance of resistance, and enhance awareness and education about AMR among healthcare workers, public, veterinarians, and workers in the food sectors.

Our proposed talk will help the audience to understand how the AMR Qatar national action plan provides all the elements and rationale to justify the choice of country Vision, mission , goals , strategic objectives and interventions that aims to draw a road map for preventing and controlling AMR at local, national and regional level.

**Objectives:** Raise awareness and orientation on the problem of AMR as a true multi-sectoral problem and a huge burden on human and animal health as well as the economy on national and regional level.

Share the methodology used to develop thenational action plan to combat AMR in the State of Qatar using one health approach.

Discuss theNational Action Plan to combat AMR in the State of Qatar.

Identify interventions and priorities based on country requirements.

## Identification of potential drivers for antimicrobial resistance and screening for genetic basis of resistance in E. coli strains obtained from people with a recent history of diarrhea and/or fever residing along the Lake Victoria basin of Western Kenya

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*2. University of Ghent, Ghent, Belgium*

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**Background:** Past studies in Kenya have concentrated on antimicrobial resistance (AMR) among clinical strains but little is known regarding community-associated AMR. In this study, we investigated community AMR using E. coli as an indicator species.

**Methods:** A total of 1640 people from the Lake Victoria basin from 389 households with at least one adult who had a recent history of diarrhea and/or fever were recruited. The households were geo-mapped, and a questionnaire used for capturing socio-demographic, sanitation and clinical data. E. coli was isolated from the fecal samples and screened for resistance against a panel of 14 antimicrobials. Selected strains were subjected to whole genome sequencing and screened for genetic basis of resistance, mobile genetic elements and clonal relatedness.

**Results:** Diarrhea was more common in the rural settings than in urban settings and adults were more likely to seek medication for diarrhea than children. Fever was treated empirically for malaria in 53% without clinical testing. Only less than 6% of participants were requested for specimen for culture and susceptibility testing for diarrhea compared to 41% of those who were tested for malaria after developing fever. Those living near rice growing areas were more likely to have been treated for a febrile illness. At least 13% of those recruited prefer not to seek treatment for diarrhea and/or fever even when medication was available or affordable. No association between access to a toilet and the likelihood of a diarrhea was found. At least 27% of adults combined herbs and antibiotics for management of diarrhea and/ or fever but this practice was less common for children between the age of 0-16years. More than 73% obtained antibiotics them from chemists without prescriptions. Those in rural areas were more likely to share their antimicrobials than those in urban areas. At least 16% of adults could identify augmentin, septrin, flagyl, coartem as some the most common antimicrobials without assistance. Only less than 40% of the isolates were susceptible to ampicillin, and streptomycin and tetracyclines. Close to 11.5% of isolates obtained from people with a of ESBL-producers were also resistant to ciprofloxacin and gentamicin. The blaCTXM-15 was the most common ESBL gene and was closely associated with strains belonging to ST131, ST405, ST1642 clones. blaCTXM-15 was borne on incF and/or incl1 plasmids carrying a aa(6')lb-cr-containing class 1 integron. Resistance to clavulanic acid in these strains was mainly mediated by OXA-1 β-lactamase. MSLT analysis revealed that most strains were not clonally related even when they shared similar antimicrobial profiles.

**Conclusions:** This study reveals that antimicrobial resistance is a major problem in community settings. Various socio-demographic and clinical descriptors that may be potential drivers of resistance were also identified. Since most resistances were borne on mobile elements, there is likelihood that the rate of spread of such resistances will increase in both hospital and community settings. Measures to mitigate an expected rise in antimicrobial resistance are therefore needed.

## Use of African indigenous spices supplement as alternative to antibiotic growth promoter in poultry feed

KANA Jean Raphaël, Mube Kuetché Hervé, Ngouana Tadjong Ruben, Komguep Ronald, Yangoue Antoine, Tsafong Francklin, Teguia Alexis

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Due to its side effects, antibiotic feed additives have become a real public health concern and trigger an explosion of interest in the use of alternatives such as plants products (phytobiotics) as supplements in animal rations. Phytobiotics contain active secondary plant metabolites belonging to the classes of isoprene derivatives, flavonoides and glucosinolates which have been suggested to act as antibiotics or as antioxidants. Beneficial effects of these products in farm animal arises from activation of feed intake and secretion of digestive secretions, immune stimulation, anti-bacterial, coccidiostatic, anthelmintic, antiviral or anti-inflammatory activity and antioxidant properties. Afrostyrax lepidophyllus, Tetrapleura tetraptera, Dichostachys glomerata are popular spices in most african countries. They contain sulfur and phenylpropanoid (eugenol) which have the ability to stimulate the function of pancreatic enzymes (lipases, amylases and proteases) and increase the activity of digestive enzymes of gastric mucosa. They are known to improve livestock performances through their anti-oxidative and antimicrobial action, improve palatability, reduce cholesterol level in eggs and meat and maintain gut equilibrium. The present study revealed that, supplementing a kg of broiler diet with 2g of Afrostyrax lepidophisllus, Dichostachys glomerata and Tetrapleura tetraptera decreased feed intake and feed conversion ratio, improved weight gain for about 5%, balanced physiological fluids and blood components, and led to the production of antibiotics residues free chicken carcass as demanded by consumers. Irrespective to the spice types, serum content in creatinine and alanine aminotransferase (ALAT) decreased significantly as compared to the negative control diet. The present findings suggested that common indigenous spices like Afrostyrax lepidophisllus, Dichostachys glomerata and Tetrapleura tetraptera can be used as natural and safe alternative to the antibiotic feed additives that are still commonly and very intensively used in animal husbandry in the tropics where climate conditions are very suitable for pathogens bacteria growth.

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## Antibiotic resistance gene transfer between marine bacteria and E.coli in starved cells and oligotrophic condition

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**Back Ground:** Detection of the same antibiotic resistance genes (ARGs) from marine environment and clinical settings suggests that horizontal gene transfer (HGT) occurs between marine bacteria and human pathogen. Most of HGT studies have been performed on the eutrophic culture condition in laboratory. However marine environment is generally oligotrophic, thus bacterial physical state is different from laboratory condition. The HGT study under the oligotrophic condition is needed for better understanding of HGT in marine environment. In this study, we investigated i) the HGT frequency under oligotrophic condition, ii) HGT potential of starved cell and iii) the expression of HGT elicitation gene.

**Method:** We used marine bacterium Photobacterium damselae as ARG-donor and E.coli as ARG-recipient. Starved cells were prepared by six-day starvation without organic matters in artificial seawater (ASW) for donor and in PBS for recipient E. coli. We here use abbreviations: starved cells, “d” (donor) and “r” (recipient); vigorous cells, “D” (donor) and “R” (recipient). HGT experiment was performed as four combinations of donor and recipient including D×R, D×r, d×R and d×r. The HGT conditions were oligotrophic PBS agar and eutrophic marine agar. We selected for transconjugant by addition of antibiotics and high temperature. In addition, we quantitated the mRNA copy number of traI when the “d” was moved to eutrophic medium.

**Result and Discussion:** When HGT was performed in eutrophic condition, d×R showed 12 fold higher HGT rate than D×R, and the case of d×r showed 5 fold higher than D×r. Starved donors showed high HGT rate than vigorous donors. When HGT was performed in oligotrophic condition, HGT rate decreased, and HGT was observed only in vigorous donors. This suggests that HGT was enhanced when donor cells were exposed to eutrophic condition. The traI expression increased 2 fold ($p < 0.05$) at 5 min, 5 fold ($p < 0.01$) at 1 hr, when “d” was moved to eutrophic medium. This result suggests that starved cell can recover HGT potential immediately after getting nutrient. In conclusion, HGT occurs in eutrophic environment for both starved and vigorous cells. HGT seems to occur in organic matter rich conditions in environments (e.g. aquaculture site and wastewater effluent site) than oligotrophic ocean.

## Increasing Multidrug and Fluoroquinolone Resistance among Salmonella Typhi from Sporadic Outbreaks in Kenya.

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**Background:** Typhoid fever (TF) caused by Salmonella Typhi remains a major public health problem in Kenya. A systematic surveillance in two slum areas in Nairobi, revealed a crude incidence of TF of 247 cases per 100,000 person-years of observation (pyo), with highest rates in children 5–9 years old (596 per 100,000 pyo). Currently over a third of S. Typhi isolates are multidrug-resistant (MDR), and show reduced susceptibility to Fluoroquinolones; the drugs of choice for treatment of MDR cases. The situation is worrying especially for resource-limited settings where the few remaining effective antimicrobials are either unavailable or too expensive to be afforded by the general public.

**Objectives:** To determine the epidemiology and trends in Antimicrobial Resistance patterns among S. Typhi isolated from patients acquiring treatment in four clinics in Nairobi in the last 5 years.

**Methods:** We assessed the susceptibility to commonly available antimicrobials of 225 S. Typhi isolates from 5 years of study (2009-2014) from sporadic outbreaks in clinics around Nairobi.

**Results:** S. Typhi outbreaks were due to a single haplotype H58, which is the main cause of epidemics in South East Asia. Over last 5 years only 17.9% were fully sensitive. The majority (60.5%) were multiply resistant to commonly available drugs - Ampicillin, Chloramphenicol, Tetracycline (Minimum Inhibition Concentration (MIC) > 256µg/ml) and Co-trimoxazole (MIC > 32µg/ml). Nalidixic resistance was observed in 10% in 2009 to 18% in 2014 of isolates while resistance to Ciprofloxacin susceptibility increased from 5% to 10% in 2014.

**Conclusion:** The rate of increase in MDR over the last 5 years is worrying as more S. Typhi have become less susceptible to Fluoroquinolones. Improved hygiene and sanitation and use of World Health Organization-recommended vaccines should be considered for effective management of MDR TF.

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## Extended-spectrum β-lactamases producing Escherichia coli and Klebsiella pneumoniae from humans and minced meat of cattle's in Jimma, Ethiopia

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**Background:** The emergence and increase in the incidence of extended-spectrum β-lactamases (ESBLs) producing organisms remain an important cause of failure of therapy in human and veterinary medicine. So that detecting and reporting of the ESBLs producing organisms have paramount importance in the clinical decision making.

**Objective:** The aim of this study was to assess the prevalence and antibiotics susceptibility patterns of extended-spectrum β- lactamase (ESBLs) - producing E. coli and K. pneumoniae isolates from outpatients in Jimma University Specialized Hospital and from minced meat of cattle's in Jimma town, Southwest Ethiopia.

**Method:** A total of 342 outpatient urine samples and 168 minced meat of cattle's were cultured onto MacConkey agar from March to July, 2016. Double disk synergy (DDS) methods were used for detection of ESBL-producing. A disc of amoxicillin + clavulanic acid (20/10µg) was placed in center of the Mueller-Hinton agar plate, and cefotaxime (30µg), ceftazidime (30µg), and ceftriaxone (30µg) were placed at a distance of 20 mm (center to center) from the amoxicillin+ clavulanic acid disc. Enhanced inhibition zone any of the cephalosporin discs on the side facing amoxicillin+ clavulanic acid was considered as ESBL producer.

**Results:** Extended-spectrum β-lactamase (ESBLs) - producing phenotype was detected in 17 (23%) of 74 human isolates [13 (76.5%) E. coli and 4 (23.5%) K. pneumoniae]. From 35 cattle's isolates of E. coli, ESBLs- production was detected in 7 (20.0%) of the strains. Almost all ESBLs- producing strains isolated from human showed high resistance to cefotaxime (100%), ceftriaxone (100%) and ceftazidime (70.6%), while fewer isolates of ESBLs- producing and non-ESBLs- producing group showed resistance to amikacin (9.5%) and no resistance was detected to imipenem. Among minced meat isolates, the majority of ESBL- producing group showed resistance to cefotaxime (85.7%), ceftriaxone (85.7%) and ceftazidime (71.4%). But, no resistance was detected to amikacin and imipenem.

**Conclusion:** ESBL-producing strain were detected both in humans and minced meat of cattle's isolates. Multi-drug resistance phenotype was common among ESBLs-producers. Therefore, designing and implementation of strategies for prevention and control of ESBLs- producing strains from spread in the community is essential.

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## ANTIMICROBIAL RESISTANCE PATTERNS OF SALMONELLA KENTUCKY ISOLATED FROM ANIMAL SOURCES IN THE NORTHEAST OF AFRICA

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**Background:** Salmonella enterica (S. enterica) is a major zoonotic agent and responsible for a large number of human hospitalization cases and economic losses worldwide. Among the various S. enterica serovars, S. Kentucky has been reported mainly in cattle and poultry and rarely reported as a causative agent of human salmonellosis. In the last years, however, S. Kentucky has emerged as an important foodborne agent in developing countries. Recent findings indicate a dissemination of a highly resistant clone (ST198) putatively linked to the indiscriminate use of antimicrobials as growth promoter in farm animals. This study assessed the antimicrobial resistance patterns of Salmonella Kentucky isolated from animals in Ethiopia and Kenya.

**Material and Methods:** A total of twenty Salmonella Kentucky isolates originated from animal fecal samples in Kenya and Ethiopia and kept at the bacterial bank of The Infectious Diseases and Molecular Epidemiology Laboratory (IDMEL) of The Ohio State University were assessed by Kirby Bauer test using the following antimicrobial disks: ampicillin (A), amoxicillin/clavulanic acid (Ax), ceftiofur (Xnl), ceftriaxone (CRO), cephalothin (Cf), chloramphenicol (C), ciprofloxacin (CIP), gentamicin (G), kanamycin (K), streptomycin (S), sulfisoxazole (Su) and tetracycline (Te).

**Results and Discussion:** The highest resistance rates were observed for gentamicin (95%), ciprofloxacin (90%), and tetracycline (85%). All Salmonella Kentucky isolates were phenotypic susceptible to ceftriaxone and chloraphenicol. The most common resistant phenotype was ASSuTeGCIPCf (40%). Ninety percent (90%) of all S. Kentucky were resistant to 3 or more antimicrobial classes, and therefore considered multidrug resistant (MDR).

**Conclusions:** S. Kentucky isolates from animal fecal specimens in Northeastern Africa showed high resistance rates against most of the tested antimicrobials. These findings are in line with the increasing importance of S. Kentucky to public health in those regions and reveal the need to investigate the factors linked to the emergence of multidrug Salmonella in animals, such as the off-label and indiscriminate use of antimicrobials in animals.

## PLASMID-MEDIATED mcr-1 COLISTIN RESISTANCE GENE IN EXTENDED-SPECTRUM b-LACTAMASE-PRODUCING Eschericia coli IN CHICKEN MEAT

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Despite the high toxicity of polymyxins, colistin (polymyxin E) has become a last-resort antimicrobial to treat human infections caused by multidrug resistant (MDR) Gram-negative bacteria. After firstly detected in China, Enterobacteriaceae harboring the plasmid-mediated colistin resistance gene (mcr-1) has been now found in animals, environment and more sporadically in humans from different parts of the world. Although previous studies have reported the occurrence of the gene mcr-1 in Enterobacteriaceae from animals sources in Brazil, this is the first inestigation to detect extended spectrum β-lactamase (ESBL)-producing E. coli harboring mcr-1 gene in chicken carcasses in Paraiba State, Northeastern Brazil. A total of 21 ESBL-producing Enterobacteriaceae cultured from 50 chicken carcasses were screened by PCR for the presence of the mcr-1 gene. Positive isolates (n=2) were whole genome sequenced (WGS). The mcr-1 gene was confirmed in an O100:H25 E. coli strain ST359 that also harbored resistance genes against β-lactams (blaTEM-1B e blaCTX-M-2), aminoglycoside (aadA1, strA, aph(3')-Iia, strB, aph(6)-Ic, sulphonamides (sul1 and sul2), tetracyclines (tetB) and trimethoprim (dfrA1). The detection of colistin resistant E. coli from such a small sample size indicates the need to further investigate the epidemiology of mcr-1 positive Enterobacteriacea in animal production systems and the role of the use of colistin in the veterinary practice. Colistin-resistant bacteria have been emerged as major public health problem worldwide and the increasing presence of these bacteria in foods could also pose a risk to the Brazilian poultry industry as a major player in the global market.

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## Antimicrobial resistance and molecular characteristics of Staphylococcus aureus isolated from human hospital and dairy farms in Northern Ethiopia

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**Introduction:** Staphylococcus aureus can colonize and cause serious diseases in both human and animals. Continuous evolution of drug resistance in both human and animals make it public health priority pathogen. Molecular techniques have been used successfully to study distribution, drug resistance pattern and determine major lineages of S. aureus.

**Objectives:** to determine the drug resistance pattern and molecular characteristics of S. aureus isolated from hospital (human) and dairy farms in Northern Ethiopia.

**Methods:** we have studied 193 S. aureus isolates obtained from human clinical sources, nares of farm workers and milk of dairy cows from March, 2016 to March, 2017. Antimicrobial susceptibility testing was performed using disc diffusion technique and E-test (for vancomycin and daptomycin) at the Microbiology laboratory of Ayder Referral Hospital, Mekele following CLSI guideline. Molecular characterization that includes; confirmation of S. aureus by nuc detection, MRSA by mecA/mecC detection, determination of toxin genes (pvl, se, tsst-1), spa typing, and SCCmec typing was performed following established protocols at the Infectious diseases molecular epidemiology laboratory, Ohio State University, USA.

**Results:** Out of the 193 S. aureus isolates 123 (63.7%) were from human clinical sources, 22 (11.4%) from nares of dairy farmers and 48 (24.9%) from milk of Dairy cows. Higher resistance was documented for Penicillin (92.7%) followed by Tetracycline (38.3%) and Trimethoprim-sulfamethoxazole (31.6%). All the isolates were susceptible for Vancomycin. Four isolates (2.1%) were MRSA harboring mecA, 2 SCCmec III and 2 SCCmec IV. About 30% of the isolates possessed pvl; However, pvl possession was significantly higher among human clinical isolates than dairy farm isolates (44% vs 5.7%, $P = .000$). Thirty nine percent of the isolates possessed at least one of the 5 classical enterotoxin genes (sea-see). About 10% of the isolates were found positive for tsst-1 where all of them were human isolates. Spa typing revealed 55 spa types plus 11 new types clustered in 12 clonal complexes. The leading spa type

was t042 (16.3%) followed by t355 (12.6%) and t306 (7.4%). Spa types t042, t085 and t306 were found on both human and cow samples indicating cross-transmission.

**Conclusions:** This study reported S. aureus molecular characteristics in the human-animal interface for the first time in Ethiopia. More than 90% of the human and animal S. aureus isolates were resistant to penicillin. This study reported MRSA from Human but not from cow's milk. Possession of pvl was significantly higher among S. aureus isolates associated with human skin and soft tissue infections than milk isolates. t355 was the leading spa type from human clinical sources and t042 from cow milk. This study found spa types t042, t085 and t306 were the adapted strains to both human and animals.

## ANTIMICROBIAL RESISTANCE IN ENTERIC PATHOGENS AND COMMENSALS FROM POULTRY

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Antimicrobial resistance is a threat to human and animal health. There is a widespread, unregulated antibiotic use in Tanzania poultry production, which may impose selective pressure on gastrointestinal commensals and pathogens like E. coli and Salmonella, respectively. This preliminary study is part of an ongoing project investigating the prevalence of antimicrobial resistant Salmonella and E. coli in Tanzanian chicken production. Ten wards were randomly chosen in the Arusha Urban District, with random selection of one farm per ward per production system (extensive, semi-intensive, indigenous intensive and broiler intensive). Per farm, samples were collected from 10 chickens using cloacal swabs and the environment using boot socks. These samples were tested for Salmonella using standard Food and Drug Administration Bacteriological Analytical Manual based culture methods and for E. coli using MacConkey without or with added antimicrobial compounds (tetracycline, ciprofloxacin, ceftazidime, and Imipenem). Preliminary analysis suggests that 270 (81.1%) of samples contain lactose fermenters that are resistant to tetracycline (16µ/ml), 216 (64.9%) to ceftazidime (8µg/ml), 212 (63.7%) to imipenem (4µg/ml) and 190 (57.1%) to ciprofloxacin (4µg/ml). Species identity of cultures is awaiting confirmation so these high prevalences should be interpreted with caution. They do suggest, however, that commensal flora of the chicken gut may be a source of AMR genes. Prevalence of Salmonella in Arusha urban was 3% of which 8 (2%) of 392 local samples and 5 (12.5%) of 40 environmental samples tested positive. Despite the low prevalence of Salmonella at bird level in two wards, in intensive systems (indigenous and broiler), Salmonella was detected in individual chickens when the corresponding environmental samples were positive. Baseline information on the prevalence of Salmonella and is not only paramount in establishing the extent of the problem but can be used as a reference for developing effective risk management strategies to safeguard public health.

## Molecular characterization of extended spectrum beta-lactmaces producing Enterobacteriaceae causing lower urinary tract infection in pediatric population

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**Abstract:** Urinary Tract Infections (UTIs) continue to be the one of the most common cause of infections in pediatric patients in the community. It is important to identify significant trend on anti-microbial resistance that may influence empirical treatment & antibiotic stewardship. This study was designed with an objective of determining the prevalence of resistance mechanisms in ESBL producing Enterobacteriaceae isolated from pediatric patients attending Pediatrics clinic (PEC) Al Saad , Qatar.

The isolates were identified by MALDI-TOF and phenotypic antimicrobial susceptibility testing was performed by BD Phoenix and confirmed by double disk synergetic test (DDST). PCR and multiplex PCR-were performed for molecular characterization of different groups of ESBL. Out of a total of 566 positive urine cultures, E. coli (84 %) was the most predominant uropathogen followed by K. pneumoniae (11%) and 197 (34.8 %) were found to be ESBL producing Enterobacteriaceae isolates. Male to female ratio was 1: 4.7.

Of these positive ESBL isolates, 119 were included in our study with E. coli being the predmajorominant isolate 104 (87.4%), followed by k. pneumonia 13 (11%) then E. cloacae 1(0.8%) and C. koseri 1 (0.8%).TXM was found to be the most gene responsible for 63% of ESBL, followed by TEM 23.5 then a combination of TEM and SHV 9.2% and 4.2% were due to SHV.

In conclusion, to our knowledge, there are no published data on UTI etiological agents and their analogues genotypic characteristics of resistant species of bacteria among children in Qatar. Our findings generate crucial information about the molecular epidemiology of resistant gram-negative bacteria in pediatric population in Qatar.

Accordingly, it will help in understanding the ESBLs dynamic and associated risk factors. More importantly will help in establishing the anti-microbial stewardship program in Qatar and limiting the spread of antibiotic resistant bacteria in the community by implementing the evidence based infection control measures.

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## Detection of the mcr-1 Colistin Resistance Gene and Extended Spectrum Beta-Lactamase (ESBL)-Producing Escherichia coli from Poultry in Qatar

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Antimicrobial resistance (AMR) is a growing public health concern worldwide and is one of the top health challenges facing humanity in the 21st century. AMR among enterobacteriaceae is rapidly increasing especially to third-generation cephalosporins and carbapenems. Further, strains carrying mobilized colistin resistance (mcr) genes 1 & 2 have been isolated from humans, food-producing animals, and environment. Uncontrolled use of antibiotics in animals in large scale could be one of the major contributing factors to generation and spread of antibiotic resistance. No studies have been done to evaluate antimicrobial resistance in animals in Qatar. This study aimed at establishing a primary baseline data for prevalence of antimicrobial resistance among food animals in Qatar. 172 fecal samples were obtained from two broiler farms and one live bird market in Qatar and 90 commensal Escherichia coli (E. coli) bacteria were isolated and subjected to antimicrobial susceptibility testing using Etest method. 90% (81/90) of the isolates were resistant to at least one of 16 clinically relevant antibiotics. 15.5% (14/90) of the isolates were colistin resistant, 2.2% (2/90) were extended spectrum β lactamase (ESBL) producers and similar percentage were multi-drug resistant (MDR) to four antibiotic classes. ESBL-producing E. coli and colistin resistant isolates were confirmed using double disc susceptibility testing and PCR, respectively. In Summary, Our results indicates high antimicrobial resistance in food producing animals in Qatar, including ESBL and colistin resistance. Such AMR bacteria could be easily transmitted to humans through consumption of undercooked food or noncompliance with hygiene practices, which mandates prompt development and implementation of stewardship program to control and monitor the use of antimicrobial agents in community and agriculture.

# DETECTION OF OF BLAKPC-2 AND fosA GENES IN Enterobacteriaceae ISOLATED FROM URBAN RIVER IN PARAÍBA, BRAZIL.

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The increased prevalence of extended-spectrum β-lactamase (ESBL)-producing Enterobacteriaceae in the environment has been activities related to the overuse of antimicrobial agents. Environmental reservoirs of ESBL-producing bacteria is a major issue in public health and currently, the blaKPC-2 gene is no longer limited to K. pneumoniae species but has been identified in a wide range of Gram-negative bacteria, and in regard to CTX-M β-lactamases, isolates carrying CTX-M-8 and other genes have been found worldwide. This study reports the occurrence of an Enterobacter cloacae harboring blaKPC-2 gene isolated from an urban river (Jaguaribe River) in the metropolitan area of João Pessoa city, northeastern Brazil. The isolated was recovered in a study to monitor the occurrence of multidrug-resistant (MDR) Gram-negative bacteria, the water samples were collected from different locations along the river and filtered using a sterile filter membrane (0.45µm) pore size. The membranes were placed in 20 ml of BHI broth, vortexed for 10 sec. and aliquots (100µl) from each samples were streaked onto McConkey agar (McA) in paralel with McA suplemented with ceftriaxone (16µg/ml); and also with meropenem (1 µg/ml) plus 70µg/ml ZnSO4) in order to detect carbapenemase producing samples (KPC, Metalo) and incubated at 370C/18-24h. The samples were also inoculated in Chomagar ESBL and Chomagar KPC (PROBAC). Isolates grown on the selective plates with ceftriaxone were screened for ESBL by the standardized disk approximation test and when grown on selective plates supplemented with meropenem screened for carbapenemase using the Carba NP test (Biomerieux). The identifications was made by routine biochemical test and confirmed using MALDI-TOF (Bruker). Analysis and the antimicrobial resistance patterns were determined by disc diffusion method using antimicrobials belonging to four different classes: beta-lactams (carbapenems and cephalosporins); quinolones; aminoglycosides; fosfomicyn and sulfamethoxazole-trimethoprim, according EUCAST. The carbapenemase-encoding genes were screened by PCR and selected strains were analysed by Whole Genome Sequence (WGS) using a MiSeq platform (Illumina Inc., San Diego, CA). An Enterobacter cloacae strain ST 1 was shown to harbor both blaKPC-2 and fosA genes, as well as several other resistance genes, such asaminoglycoside-modifying enzymes [aadA1, aac(6')-Ib, aph(3')-V], b-lactamase [blaCTX-M-8, blaCMH-3, blaTEM-1A, blaOXA-9] and quinolones [qnrE, qnrB19, aac(6')Ib-cr] encoding genes. The detection of blaKPC-2 and fosA genes in a single isolate suggest that some commensal Gram negative strains found in the environmental might can be highly resistant to antimicrobials and pose a risk to public health. In addition, our findings underscore the distribution of resistant bacteria and highlight a new possible reservoir of blakpc-2 harboring Enterobacteriaceae strains, as well as, several other resistance genes from environmental source. In summary, this is the first report on the occurrence of blakpc-2 and fosA in enterobacteria cultured from an urban river in northeastern Brazil. Surveillance of antimicrobial resistance in microbes from the environmental in urban regions needs to be established as a priority in order to, establish strategies to control high-risk multiresistant bacteria into the environment.

## Evaluating the efficacy of flukicides against Fasciola gigantica and paramphistomes using faecal egg count reduction tests in naturally infected cattle in Arumeru and Iringa Districts, Tanzania

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Fasciolosis caused by the liver fluke Fasciola gigantica and paramphistomiosis are both widespread in cattle in Tanzania and the use of flukicides is encouraged by Government livestock extension officers. However, reduced efficacy of oxyclozanide against Fasciola gigantica and paramphistomes, and albendazole against F. gigantica has been reported in some regions. This study was conducted to assess the efficacy of five different flukicides against F. gigantica and paramphistomes in naturally infected cattle in Arumeru and Iringa Districts.

In each district cattle having concurrent infection of F. gigantica and paramphistomes were allocated into six experimental groups. On day 0, five groups were treated with one of five flukicides (albendazole, nitroxynil, oxyclozanide, closantel and triclabendazole) while a control group was left untreated. Faecal samples were collected from each animal on the day of treatment and again at 7, 14 and 28 days post-treatment, processed to recover and identify eggs using the Flukefinder® method. Faecal egg count reduction (FECR) tests were used to assess the efficacy of the flukicides against F. gigantica and paramphistomes.

The FECR results for nitroxynil, oxyclozanide, closantel and triclabendazole indicate that these flukicides are effective in both districts against patent F. gigantica infection, with faecal egg counts reduced by 100% by day 14 post-treatment. However reduced efficacy of albendazole against F. gigantica was observed with faecal egg count being reduced by just 49% in Arumeru District and 89% in Iringa District by day 14 post-treatment. The reduction in efficacy was greater in Arumeru, where cattle are treated regularly with anthelmintics, than in Iringa where cattle are rarely treated. Oxyclozanide was the only flukicide found to be effective against paramphistomes, with FECR of 99%.

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## Multidrug-resistant Salmonella enterica serovar Typhimurium ST313 isolated from humans and poultry in Burkina Faso

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Multidrug-resistant Salmonella is an important cause of morbidity and mortality in developing countries. Here we characterized multidrug-resistant Salmonella enterica serovar Typhimurium isolates from two patient and two poultry feces samples in Burkina Faso using whole genome sequencing (WGS). These strains were tested for susceptibility to 12 different antimicrobial agents using the disk diffusion method on Mueller-Hinton agar (Oxoid) at 37°C for 24 h to confirm these antimicrobials susceptibility profile. The ResFinder Web server were use to find the antibiotic resistance genes from WGS data. For comparative genomics, publicly available complete and draft genomes of different Salmonella Typhimurium laboratory-adapted strains were downloaded from GenBank. Multilocus sequence type ST313 was detected from all four S. Typhimurium isolates. The S. Typhimurium isolates described in this study were multiresistant to five commonly used antibiotics (ampicillin, chloramphenicol, streptomycin, sulfonamide and trimethoprim). The use of ResFinder web server on the whole genome of the strains showed a resistance to aminoglycoside associated with carriage of the following resistances genes: strA, strB and aadA1; resistance to β-lactams was associated with carriage of a blaTEM-1B genes; resistance to phenicol was associated with carriage of catA1 gene, resistance to sulfonamide was associated with carriage of sul1 and sul2 genes, resistance to tetracycline was associated with carriage of tet B gene, and resistance to trimetoprim was associated to dfrA1 gene for all the isolates. Our finding of multi-drug resistant S. Typhimurium ST313 in poultry feces calls for further studies to clarify the potential reservoirs of this emerging pathogen.

## Phenotypic and genotypic characterization of Staphylococcus aureus isolates recovered from bovine milk in central highlands of Ethiopia

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Antimicrobial resistance is becoming an extremely serious global problem. The goal of this study was to determine the prevalence and phenotypic and genotypic characteristics of Staphylococcus aureus isolated from milk and milk product samples in Ethiopia and also to determine the presence of methicillin resistant Staphylococcus aureus (MRSA). A total of 577 milk and milk product samples were collected from central Ethiopia and Staphylococcus spp. were isolated using the method described in FDA Bacteriological Analytical Manual (BAM). Resistance of S. aureus isolates to 12 antimicrobials was determined by using the Kirby-Bauer disk diffusion method. PCR detection of mecA and nuc gene was also conducted. To determine the clonal relatedness of S. aureus isolates, DNA fingerprinting of selected isolates was performed by PFGE. Of the 577 milk and milk product samples investigated, S. aureus isolates were recovered from 120 (21%) of the sample. In addition, coagulase negative Staphylococcus species were also isolated from 361/577 (63%) of the samples. The highest frequency of resistance was observed for penicillin (83%) and the lowest was noted for amoxicillin/clavulanic acid (3%) and gentamicin (3%). Fourteen (14) isolates (13%) recovered from raw milk were found to be susceptible to all the tested antimicrobials while 57% of the isolates were resistant to more than one of the antimicrobials. All the isolates were susceptible to vancomycin and none were found to be methicillin resistant S. aureus based on mecA gene carriage. PFGE analysis of 39 S. aureus isolates identified three separate clonal clusters and also several sporadic isolates. S. aureus isolates in this study were found to be resistant to multiple antimicrobials. This warrants a larger representative study to fully understand the extent of the problem and design better strategies for regulation of antimicrobial use in both the medical and veterinary sectors in central Ethiopia.

## Antimicrobial suscebtibility and molecular characterization of extended spectrum beta lactamase producing enterobacteriaceae from pediatric unit in Qatar

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Urinary Tract Infections (UTIs) continue to be the one of the most common cause of infections in pediatric patients in the community. It is important to identify significant trend on anti-microbial resistance that may influence empirical treatment & antibiotic stewardship. This study was designed with an objective of determining the prevalence of resistance mechanisms in ESBL producing Enterobacteriaceae isolated from pediatric patients attending Pediatrics clinic (PEC) Al Saad, Qatar.

The isolates were identified by MALDI-TOF and phenotypic antimicrobial susceptibility testing was performed by BD Phoenix and confirmed by double disk synergetic test (DDST). PCR and multiplex PCR-were performed for molecular characterization of different groups of ESBL. Out of a total of 566 positive urine cultures, E. coli (84 %) was the most predominant uropathogen followed by K. pneumoniae (11%) and 197(34.8 %) were found to be ESBL producing Enterobacteriaceae isolates. Male to female ratio was 1: 4.7.

Of these positive ESBL isolates, 117 were included in our study with E. coli being the predmajorominant isolate 102 (87.1%), followed by k. pneumonia 13 (11%) then E. cloacae 1(0.85%) and C. koseri 1 (0.85%). CTXM was found to be the most gene responsible for 55.5 % of ESBL, followed by a combination of genes 35% Then TEM 2.6 % and SHV 0 .9%. In conclusion, to our knowledge, there are no published data on UTI etiological agents and their analogues genotypic characteristics of resistant species of bacteria among children in Qatar. Our findings generate crucial information about the molecular epidemiology of resistant gram-negative bacteria in pediatric population in Qatar. Accordingly, it will help in understanding the ESBLs dynamic and associated risk factors. More importantly will help in establishing the anti-microbial stewardship program in Qatar and limiting the spread of antibiotic resistant bacteria in the community by implementing the evidence based infection control measures.

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## Research Review and Meta-analysis on Antimicrobial Resistance of Bovine Mastitis Bacteria in Ethiopia

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**Background and Objectives:** Antimicrobial resistance (AMR) problems emerging at the human – animal interface represent a pressing global health and livelihood threat. This is particularly true in developing countries like Ethiopia lacking strong appropriate drug use regulation mechanisms. AMR is a common problem in bovine mastitis (BM) pathogens including multiple bacteria having zoonotic transmission potential. Research knowledge on epidemiology and potential impacts of drug resistance problems originating at the human – livestock interface is fragmented in Ethiopia. This work explored research evidence on epidemiology of in vitro AMR challenges associated with BM bacterial pathogens in variable contextual settings of Ethiopia.

**Methodology:** Web search, critical review and meta-analysis of original Ethiopian research on in vitro AMR patterns of common BM bacteria, was conducted between February and July 2017. A total of 18 original research reports were retrieved using Google Scholar, PubMed, ResearchGate, AJOL and other databases. These included 670 in vitro trials wherein 1,188 isolates representing 16 specific BM bacteria were tested against 16 different antibiotics. Occurrence pattern (% trials) and magnitude (% isolates) of AMR against different antibiotics was estimated and contrasted relative to total and specific BM bacteria tested.

**Results:** Generally, AMR was observed in 477 (71.2 %) in vitro trials. Resistance occurred in 50 to 100 % of specific BM bacteria trials (Figure 1; a) mostly against multiple (2 to 9) antibiotics (96.7%) and occasionally (2.2 %) a single antibiotic. Likewise, AMR was noted in 38.1% to 100 % of specific antibiotic trials (Figure 1; b).

Average total AMR % was lower in Gentamycin and higher against Penicillin and Amino-Penicillin's (Figure 2; a). Average Erythromycin (p=0.035), Clindamycin (p=0.027) and Vancomycin (p=0.029) resistance was higher in gram negative BM bacteria (Figure 2; b). Average Cloroamphinicole (p=0.025) AMR % was higher in A. pyogenes, gram negative bacilli (other than E. coli) and Bacillus spp., but lower in coagulase negative Staphylococci and St. uberis. Clindamycin (p=0.049) AMR % was lower in Streptococcus, Micrococcus and Bacillus spp. compared to other BM bacteria (Figure 3).

Average Trimethoprim/Sulpha drug (p=0.000), Penicillin G (p=0.031) and Gentamycin (p=0.017) resistance was higher in south-eastern, southern, central and northern Ethiopia, respectively (Figure 4; a). Average Gentamycin (p=0.000), Clindamycin (p=0.009) and Cephalosporin (p=0.050) AMR % increased from 2003/8 to 2011/16 (Figure 4; b). Meanwhile, average Tetracycline (p=0.037), Trimethoprim/Sulpha drug (p=0.000), Pencilline (p=0.019), Amoxacillin (p=0.049), Chloramphenicol (p=0.015), Erythromycin (p=0.000) and Clindamycine (p=0.030) AMR % varied in different farm types. Higher AMR % was usually noted in large commercial dairy farms than small holder (SH) dairy and/or extensive farms (Figure 5).

**Conclusion:** In vitro resistance against multiple 1st line antibiotics was a common feature of bacteria isolated from BM cases in Ethiopia. Potential threats of in vivo treatment failure in corresponding livestock and zoonotic infections demand serious evaluation. In many cases, BM bacteria AMR problems showed higher frequency in large commercial dairy farms and a temporally escalating tendency. These probably reflect effects of increasing veterinary antibiotic misuse practices emphasizing need for systematic regulatory consideration.

Biosecurity, Biodefense and Disaster Response

## Comparative Genotypic Analysis of Major Virulence Factors of Salmonella Strains Isolated Along the Beef Chain in Mexico

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**Background:** Nontyphoidal Salmonella enterica (NTS) is a common contaminant in food animals including beef cattle and a leading cause of foodborne illnesses worldwide. Various NTS serovars may be present in apparently healthy animals. This could result in contamination during the slaughter process, resulting in human exposure. This study is aimed at comparing the genomes of 59 NTS serovars isolated from non-clinical beef cattle sources to identify genetic differences related to variations in virulence, host adaptability and overall pathogenicity.

**Methodology/Principal Finding:** We sequenced the genomes of 59 NTS isolates from beef cattle feces (n=34), carcass swabs (n=3), primal cut swabs (n=2), and ground beef (n=20). WGS data of these genomes were used to conduct comparative genomics and strain typing. The predicted serovars were Montevideo (n=29), Give (n=8), Muenster (n=6), Newport (n=4), Derby (n=4), Reading (n=2), Senftenberg (n=2), Roodepoort (n=2), London (n=1), and Bergen (n=1). Isolates from the same serovar clustered together in well supported clades, except for Newport strains. Likewise, samples from feces, carcasses and cuts were highly clonal. None of the isolates carried spvRABCD, pefABCD, rcK or mig-5, which are typically present in highly virulent strains. Pathogenicity islands (SPIs) were generally conserved, with minor variations in SPIs 1 and 3.

**Conclusions/Significance**: This study shows major NTS serovars circulating in apparently healthy beef cattle of the studied region harbor genes encoding several factors associated with colonization and persistence. These isolates have a conserved repertoire of virulence genes and occasionally reach carcasses and cuts, posing a food safety risk to consumers.

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## Antimicrobial and Molecular Epidemiology of Extended-Spectrum Beta-lactamases Producing Enterobacteriaceae from Intensive Care Units, at Hamad Medical Corporation in Qatar.

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**Background:** Emergence of extended spectrum beta lactamase (ESBL)-producing isolates has important clinical and therapeutic impli- cations. A high prevalence of ESBL-producing Enterobacteriaceae has been reported in literature from various clinical samples. Aim(s)/Objective(s): The present study was undertaken to evaluate the prevalence of ESBL-producing Enterobacteriaceae, as well as the molecular characterization and the antimicrobial susceptibilities in patients admitted in Intensive Care Units (ICUs) at Hamad Medical Corporations (HMC), Doha, Qatar from November 2012 to October 2013.

**Method(s):** A total of 629 Enterobacteriaceae isolates were included in the study. Identification and susceptibility was done by Phoenix (Becton Dickinson) and the ESBL-producers were confirmed by double disk potentiation as recommended by CLSI. Molecular analysis for the ESBL-producers was performed using polymerase chain reaction (PCR).

**Results:** 109 isolates (17.3%) were confirmed as ESBL-producers and all were sensitive to meropenem in routine susceptibility assay. Most of ESBL producers (99.1%) were resistant to amoxicillin/clavulanic acid and ceftriaxone and 93.6% to cefepime. Among ESBL producing genes, prevalence of blaCTX-M (66.1%) was highest, followed by blaSHV (53.2%) and blaTEM (40.4%).

**Discussion and/or Conclusion(s):** Present study shows high preva- lence of ESBL-producing Enterobacteriaceae within the ICU facilities at HMC, Qatar and emphasizes the need for judicious use of antibiotics and implementation of strict infection control measures.

## Risk factors for rotavirus infection in smallholder pigs in Western Kenya

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We analyzed data that were previously collected for molecular characterization of rotavirus (RV) groups A and C in pigs from Teso and Busia subcounties in Kenya to determine risk factors for its infection. The data included records from 239 randomly selected piglets aged between 1 and 6 months raised in free range and backyard production systems. RV infection was confirmed by screening of fresh faecal samples by using reverse transcription polymerase chain reaction (RT-PCR); selected positive samples were subsequently sequenced and used for phylogenetic analysis. In this analysis, RV infection status was used as outcome variable, while the metadata collected at the time of sampling were used as predictors. A Bayesian hierarchical model which used integrated nested Laplace approximation (INLA) method was then fitted to the data. The model accounted for the spatial effect by using stochastic partial differential equations (SPDEs). Of the 239 samples screened, 206 were available for the analysis. Descriptive analyses showed that 27.7 % (57/206) of the samples were positive for rotaviruses groups A and C, 18.5 % were positive for group A rotaviruses, 5.3 % were positive for group C rotaviruses, while 3.9 % had co-infections from both groups of rotaviruses. The spatial effect was insignificant, and a simple (non-spatial) model showed that piglets (≤4 months) and those pigs kept in free range systems had higher risk of exposure to rotavirus infection as compared to older pigs (>4 months) and those tethered or housed, respectively. Intervention measures that will target these high-risk groups of pigs will be beneficial to farmers.

## Antimicrobial resistance profile of foodborne Cronobacter sakazakii and Salmonella in Lebanon

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Antimicrobial resistance (AR) is a complex problem that poses a significant risk to public health globally. If uncontrolled, AR can limit the efficacy of clinically important antibiotics against common infectious diseases. Many developed countries have established guidelines and monitoring systems to track and control the use of antibiotics and the proliferation of AR bacterial pathogens. However, in developing countries, AR might be exacerbated by several critical problems, including 1) the lack of stewardship and awareness of proper applications of antimicrobials in human medicine and food production, 2) a debilitated infrastructure that facilitates the spread of antibiotics to natural resources (e.g. surface and ground water), and 3) scant data on AR, especially in non-clinical settings. In the case of Lebanon, the latter is clearly evident when considering food production from farm to fork. This implies that the contribution of foodborne AR bacterial pathogens (ARFB) to the overall disease burden in Lebanon remains precariously unclear. Furthermore, since the Lebanese economy relies greatly on tourism and the foodservice sector, ARFB might negatively impact the Lebanese economy and affect public health in other countries. Spurred by the gap in data, we initiated a concentrated effort to profile AR in foodborne bacterial pathogens in Lebanon. While our long-term objective is to establish a base-line for ARFB in Lebanon, we started by targeting two foodborne bacterial pathogens, Cronobacter sakazakii and Salmonella, that were known to have occurred in popular Lebanese food products (sesame seed paste). For this purpose, we isolated 54 C. sakazakii and 31 Salmonella spp. from various foods and cognate production environment using selective media. The identity of the isolates was confirmed using API® strips and genus and species specific PCR. All isolates were then tested for AR using the disk diffusion method. Our results showed that the C. sakazakii isolates exhibited resistance to chloramphenicol (96.3% of the isolates), ciprofloxacin (63%), trimethoprim sulfamethoxazole (44.5%), gentamicin (100%), cephalexin (96.3%), cefotaxime (68.5%), cefepime (100%), and ampicillin (70%). The Salmonella isolates were resistant to chloramphenicol (74.2% of the isolates), ciprofloxacin (45.2%), trimethoprim sulfamethoxazole (6.5%), gentamicin (68%), erythromycin (90.5%), tetracycline (22.6%), cephalexin (64.5%), cefotaxime (22.5 %), cefepime (100%), and ampicillin (26%). In survival studies, our results showed that AR

did not adversely impact the fitness of isolates in the food matrix of origin. Taken together, our results clearly highlight that the pathogens that occur in Lebanese foods can exhibit resistance to diverse and important antibiotics. Additionally, the occurrence of multidrug-resistant (MDR) was notable. Our results emphasize the need to establish a monitoring system that can track the prevalence and emergence of antimicrobial resistant bacterial pathogens in Lebanese food.

# Plenary Session 5:
# Biosecurity, Biodefense and Disaster Response

## Ranking food safety risks: a guided approach

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Efforts to improve food safety to protect public health from microbial and chemical foodborne hazards remain a significant challenge globally. Food safety is complex discipline encompassing a wide range of potential foods and hazards and a multitude of production and processing systems, and must, in addition, adapt to constant changes in food consumption patterns. With limited human and financial resources, it is impossible to efficiently address all food safety threats. Therefore, it is becoming increasingly important to prioritize food safety efforts so that resources can be allocated to most efficiently minimize foodborne illness risks. However, risk management decisions are often undertaken in an ad hoc and subjective manner. Without an objective, structured, and scientific approach to analyzing food safety issues, policy decisions can be difficult to effectively justify and communicate.

Food safety risk ranking is the systematic analysis and ordering of foodborne hazards and/or foods in terms of the likelihood and severity of adverse impacts on human health in a target population. Risk ranking provides national food safety authorities with the scientific basis to make informed regulatory decisions, enhance disease surveillance, determine how food inspections are allocated, oversee inspection and enforcement food safety efforts, inform the public of food safety threats, and continue to improve the safety of the foods produced and consumed in the country. There are a number of methods for ranking food safety risks but these vary widely in terms of methodology, data needs and required expertise. As a result, developing and implementing a country specific risk ranking approach remains a challenge for many. This presentation will provide direction on how to start ranking the public health risk posed by foodborne hazards. While the focus of this presentation will be on public health risks it does not preclude the risk-ranking approach being applied to other endpoints.

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## Bio-Security, Silos and Solutions

Doug Shinsato

Anthill Ventures, Kamuela, United States

Germ warfare is not an invention of modern civilization. There are records from thousands of years ago that describe how warring tribes contaminated their enemy's water supply with animal carcasses.

The Mongols learned that a disease stricken carcass—thrown in a water supply or catapulted over tower walls--was even more effective.

Today, we use the term "biological warfare". Over the past two centuries, warring armies have inflicted bubonic plague, hepatitis, and parasitic pathogens on their opponents. Over the past century, 500 million people have died of infectious disease. Do not be fooled into thinking that military planners—and bio-terrorists—are not aware of this.

Pathogens—especially emerging ones—pose a great danger to all 9 billion people on our planet—not only the herders and farmers who raise animals in remote parts of the world.

Too often, we become aware of a new pathogen after the virus or bacteria has "broken out" and threatens to become a pandemic.

Today, we have the technology to provide us with early warning tools. The problem is that many of the technologies are stuck in silos. The solution is simple: integrate, integrate, integrate. The problem is that this is not an easy solution.

Much of the research and many of the monitoring tools come from universities, which are organized along departmental lines—silos. Most of the technologies that can help pathogens early in their life cycle are packaged and sold separately—in silos.

Look at what is available:

- Cheap and improved sensors and actuators

- Low cost micro-processors

- High bandwidth cellular communication

- Cloud-based ICT systems

-Big data analytics

And much of the date required for precision farming and herd monitoring can be collected through Unmanned Aerial Vehicles—drones. There are a number of regulatory and commercial issues that needto be resolved, but let's return to pathogens.

In our world of technology-based terrorism, have you thought about the use of drones to infect large populations or their drinking water with pathogens carried by a swarm of drones?

During this plenary session, I will discuss the promise--and the dangers-- of integrating the silos of medical device diagnostics, patient medical data protection, bio-hazardous material chain of custody and pathogen monitoring.

## Do Retreatment Tuberculosis Patients Need Special Treatment Response Follow-up beyond the Standard Regimen? A Finding of Five-Year Retrospective Study in a Pastoralist Setting, Ethiopia

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**Background:** Treatment outcomes serve as proxy measures of the quality of tuberculosis treatment provided by the health care system. Hence, assessment of treatment outcomes is essential to evaluate the effectiveness of the Directly Observed Therapy-Short course program in controlling the disease, and reducing treatment failure, death and default. However, TB treatment outcomes and the underlying factors related to poor treatment outcomes, to our knowledge, have not been studied in Ethiopian Somali region where 85% of its population is pastoralist.

**Methods:** A retrospective review of five years (September 2009 to August 2014) data was conducted to evaluate the treatment outcome of 1378 randomly selected tuberculosis patients treated in Kharamara, Dege-habour and Gode hospitals. We extracted data on socio-demographics, HIV Sero-status, tuberculosis type, treatment outcome and year using a prepared checklist. Tuberculosis treatment outcomes were categorized into successful (cured/completed) and unsuccessful (died/failed/default) according to the national tuberculosis guideline. Data was entered using EpiData 3.1 and analyzed using SPSS 20. Chi-square test ($\chi 2$) and logistic regression model were used to reveal the predictors of unsuccessful tuberculosis treatment outcome and a P-value of $\leq 0.05$ was considered as a cutoff point for statistical significance.

**Result:** Out of the 1378 tuberculosis patients, majorities were male (59.1%), pulmonary smear negative (49.2%) and new cases (90.6%), and HIV co-infection rate was 4.6%. The median age (inter quartile range) was 26 (18 - 40) years. Overall, tuberculosis treatment success rate was 86.8%, 95%CI (84.9% - 88.5%), across the five years, however, 4.8%, 7.6% and 0.7% of patients died, default treatment and failed to cure respectively. Treatment success rate fluctuated across the years and ranged from 76.9% to 94% [$p<0.001$]. The odds of death/failure was considerably higher among retreatment tuberculosis patients [AOR =2.4; 95%CI =1.4 – 3.9] compared to new counterparts, and pulmonary smear positivity was higher among retreatment (53.8%)

patients compared to new (22.8%) counterparts [AOR= 2.3; 95% CI= 1.6-3.5]. Tuberculosis treatment success rate had no significant difference between age groups, genders, tuberculosis types and HIV status (P>0.05).

**Conclusion:** This study revealed that the overall tuberculosis treatment success rate has realized the global target for 2011 - 2015. However, it does not guarantee its continuity as the trend showed that adverse treatment outcomes might sporadically occur. Therefore, continual effort to effectively execute DOTS should be strengthen and special follow-up mechanism should be in place to monitor the treatment response of retreatment tuberculosis cases and to take early actions accordingly.

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## Study on Seroprevalence of Bovine Brucellosis and Its Zoonotic Importacne in Yabello District of Borana Zone of Oromia Region, Ethiopia

Hailelule Aleme Yizengaw, Taddesse Debele Beshah

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A cross-sectional study was conducted to determine the prevalence of bovine brucellosis and its zoonotic significance in Southern Ethiopia of Borana Zone (Yabello district) from December, 2015 to March, 2016. Blood samples were collected from randomly selected 424 cattle and 95 human beings. Questionnaire was administered to assess the risk factors associated with the prevalence and zoonotic importance of bovine brucellosis. Rose Bengal Plate Test (RBPT) was utilized as a screening test for Brucella agglutinins at Yabello Regional Veterinary Laboratory while Complement Fixation Test (CFT) was used to confirm the reactors by RBPT at the National Veterinary Institute, Debre-Zeit. A total of 424 blood samples were collected from cattle in study area where 100, 300 and 24 samples from Ranch, Pastoral and agro pastoral PA, and Yabello town, respectively. The overall seroprevalence was 12 (2.83%) and 5(1.18%) by using RBPT and CFT, respectively. All seropositive result found in this study was from female cattle serum which collected from Pastoral and agro pastoral settings. From the studied risk factors, age category, herd size, abortion history, physiological, status PA and parity were associated to seropositivity of bovine brucellosis (P value < 0.05). A total of 95 human blood samples were collected from 9 animal health worker, 10 butchers, 11 abattoir workers and 65 cattle owners, over all prevalence of 17 (17.90%) and 10(10.53%) was observed using agglutination test and CFT, respectively. All seropositive serum samples were from cattle owners 10(15.39%). Being female 2.513 times more likely to be infected with brucella organisms than male (OR = 2.513, CI = 0.684, 9.979). However, except age category (X2 = 7.99, P = 0.045) the association of risk factors (age, sex, risk groups and cattle owners with their respective herd) were not statistically significant (P > 0.05). Current study showed that bovine brucellosis was prevalent in the study area for both cattle and human beings. It had also potential to cause enormous economic as well as public health impacts. Generally, to control the disease test and slaughter with reimbursement and calf vaccination is better option in cattle where as effective diagnosis and treatment of patients with brucellosis is recommended for the control of the disease in human.

Pathogenesis, vaccine development and new Metagenomic Technologies

## The role of domestic cavies (Cavia porcellus) in the transmission of Staphylococcus aureus and salmonella spp in the western highland of Cameroon.

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Living and/ or working in Staphylococcus aureus infected farms, close contact with or eating meat from Salmonella infected animals are general conditions for transmission of S. aureus and or Salmonella from animal to human and vice versa. In rural areas, domestic cavies mostly share their living area with humans (kitchen, bedroom, court yard), which could result in the transmission of these bacteria from cavy to human or from human to cavy. The objective of this study was twofold: 1) to investigate the cause of mortalities in domestic cavies in rural areas, and 2) to investigate the occurrence of pathogenic bacteria of animals and human in domestic cavies in order to draw attention on the possible role of cavies in the transmission of these bacteria to humans. Two clinically sick and agonizing cavies brought from two different farms to our laboratory were examined for bacterial and gastrointestinal parasitic infection at necropsy, soon after their death. Coprological examination using the flotation technique did not show any sign of parasitic infection. Culture from internal organs, as well as feces using selective media revealed the presence of S. aureus and Salmonella spp infection, as evidenced by the heavy growth of bacteria on the selective growth media. These bacterial infections in the two dying cavies suggest that the bacteria are associated with cavy mortalities reported by farmers. Due to interaction between cavies and human in the kitchen, we suggest that these animals can play a role in the transmission of staphylococcosis and salmonellosis in humans in rural areas with such a cavy breeding system.

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## ISOLATION OF ESCHERICHIA COLI FROM POULTRY LIVER AND ITS ANTIBIOGRAM PROFILE

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**Abstract:** Escherichia coli is a Gram-negative facultative anaerobic bacteria which cause serious threat to poultry industry by causing high morbidity and mortality. The aim of the present study was to determine the prevalence of E. coli in recent years (2014-2016) and antibiogram profile of E. coli isolates. Liver samples from different poultry farms were collected and processed for the confirmation of E. coli colonies. Antibiogram profile was also estimated for E. coli isolates by placing antibiotics disc and measuring zone of inhibition. Overall prevalence of E. coli was recorded as 35.1% while year wise prevalence was 29.2, 29.88 and 41.05% for year 2014, 2015 and 2016, respectively. Antibiogram profile of E. coli isolates showed that Gentamicin was highly sensitive in year 2014 and 2015 while ampicillin was least sensitive in these years while Colistin with 60% sensitivity was recorded highly sensitive in 2016 and Oxytetracyclin was highly resistant. Antibiogram profile of E. coli isolates showed that resistance developed to some antibacterial with passage of time while sensitivity of some antibacterial increased. Development of resistance might be due to the vigorous use of these for control of diseases in poultry and also due to use of antibacterials as feed additives. Due to growing resistance to antibiotics it is highly recommended to decrease the unethical use of antibiotics to minimize the development of resistance strain of microbes in future.

## Rapid Assessment Of Bio-Risk Management; Knowledge & Practice in Tertiary Care Hospital Laboratories In Lahore, Pakistan.

Syed Mursalin, Asad Zaheer

Dr. Syed Mohammad Mursalin CEO Pak One Health Alliance, Islamabad, Pakistan

**Introduction:** Laboratory services are essential to identify and confirm the agents involved in important public health events, including those which may cause public health emergencies of national/ international concerns. Ideally laboratory services should rely on adequate sample collection, sample examination and transport systems. Strong laboratory biorisk management measures and laboratory quality systems should ensure that laboratories release results in a safe, secure, timely and reliable manner. These range from applying standard operating procedures to functional specimen transport system, combined with strong laboratory biorisk management and quality systems. Mainly to ensure that laboratories document results in a safe, secure, timely and reliable manner.

**Aim:** Given the recent international and national emphasis on improvement Biorisk and Biosafety management (BRM) specially under Global Health Security Initiative, Pak One Health Alliance (an NGO) in coordination with Ministry of Health Services and University of Health Sciences decided to perform a ‘Rapid Assessment of Biorisk Management and Safety Measures in 30- leading tertiary care hospitals of second largest city of the country- Lahore city.

**Methods:** This study was a comprehensive quantitative and qualitative assessment organized in the wake of standard principles of Biorisk Management and safety A multi-prong approach was adopted to finalize the results. This snap-shot focused on in-depth review of nine major critical Bio-risk areas including; a) An overall status of Biorisk Management b) Status Biorisk Assessment during last 5 Years c) Status of Hand Hygiene d) Status of Physical Security e) Chemical Safety Measures f) Biological Security Mesaures g) Data Security Arrangments h) Waste Management i) Training in Biorisk Management

**Conclusion:** Based on this assessment the participating hospitals were ranked according to the existing international standards of Bio Risk safety and Security. A set of recommendations and need based Bio Risk Management Program was suggested for the adoption by the Provincial Health Department and participating hospitals. Pak One Health Alliance is working with partners to organize similar studies in other major cities of the country to promote the case of One Health in general and Bio Risk Management in particular.

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## Promoting “One Health” approach implementation governance and response capacity approaches against emerging zoonotic threats and outbreaks in Africa

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**Introduction:** Increasing urbanization, globalization and climate changes have been linked to natural and man-made development and needs resulting on increased communities natural and man-made health threats and crises threats and disasters vulnerabilities. The degree, nature and extent national, community and household preparedness and response programs and activities defined the robustness and effectiveness of local, national to regional preparedness and timely decision-making policy, resources mobilization and stakeholder’s partnerships and response actions from policy makers to health planners and implementers. Methods: The paper-based close-ended questionnaire and focal group discussions was used to assess existing “One Health” approach governance and response capacity implementation approaches in strengthening community and national preparedness and emergency response and resilience in exploring translation bottlenecks and opportunities against emerging natural and man-made threats and epidemics disasters in Africa. Results: A response rate of 97% was recorded of the 134 respondents that participated and performed 4 focal group discussions during the conference. 26% of respondent disagreed whereas 74% agreed to the leading role of data-driven One Health governance and programs in Africa. 64% had a common perception that One health data governance is all about policies whereas 36% agreed that it is about collaborative and engaged all in one health data accountability and transparency, compliance and quality control activities. 96% of respondents agreed that adopting and integrating a robust One Health’ data governance model is crucial to gain access to quality, trustworthy data they can use to make proactive and efficient health decisions policy and programs effectiveness and outcomes. Our results showed that inadequacies in effective knowledge and access of and uses of data and information gaps in local community and national levels to strengthen “One health” approach educational and campaigns programs, preparedness and timely response activities. We also documented that inefficient of public health laboratory, veterinary and environmental skills and knowledge resource capacity to identify, understand and map potential risks/threats coupled with lack or weak community early alarm and surveillance systems in threats or disaster occurrence remain of concern. Promoting strategic programs and activities such as “One Health” approach value public awareness campaigns, mitigation strategies and recovery measures against man-made and natural disasters included biological, chemical and ecological, events, flooding and globalization is crucial. We advocate on the urgency in strengthening a comprehensive evidence-based “One Health” approach surveillance in public health threats and disasters preparedness and response priorities and programs including environmental and climate changes mitigation and adaptation strategies that support more healthier and prosperous lives. Conclusion: Promoting “One Health” implementation governance and response capacity approaches at local, national and regional is crucial in in revamping public health resilience and actions including integrated field and laboratory surveillance-response system in community-based preparedness and resilient response programs against emerging zoonotic threats and outbreaks across Africa.

## POTENTIAL PUBLIC HEALTH RISKS FROM BRUCELLA SPP. ALONG THE INFORMAL DAIRY VALUE CHAIN IN DODOMA MUNICIPALITY AND CHAMWINO DISTRICT, TANZANIA

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Brucellosis is a serious zoonotic illness caused by Brucella spp. It is endemic to Sub Saharan Africa and to many other developing nations; and poses dire implications to animal health, livelihoods, economies, and insidiously, to public health; to largely variable extents.

**OBJECTIVES:** A cross-sectional study was carried out in Dodoma Municipal and Chamwino districts of Dodoma region in central Tanzania in March-April, 2016, to determine; (i) the prevalence of brucellosis amongst cattle; (ii) presence of Brucella spp. in milk and sour milk sold along the informal dairy value chain; and (iii) to determine the socio-demographic factors associated with brucellosis in animals and in retail milk and sour milk.

**METHODS:** Blood samples were collected from a total of 422 cattle of all breeds and sexes; excluding animals younger than 4 months. Serum was collected aseptically and stored appropriately till tested. Milk samples were collected from the lactating animals (n=176), and from retailers selling milk (n=16) and sour milk (n=6). Rose Bengal Plate Test (RBPT) was administered to serum as a screening test, and Competitive Enzyme Linked Immunosorbent Assay (c-ELISA) for confirmation. The milk and sour milk samples were subjected to conventional single Polymerase Chain Reaction (PCR) targeting the BCSP-31kDA protein gene. All farmers and retailers had questionnaires administered with the aim of finding out their knowledge levels, attitudes and practices associated with brucellosis.

**RESULTS:** The sero-prevalence of brucellosis in the study area was 0.47% and 0.95% using RBPT and c-ELISA respectively, with good agreement using kappa statistic at $\kappa=0.66$. All serology positive cases originated from the rural areas of Chamwino district. PCR indicated that 8.52% of lactating animals shed

Brucella spp. pathogens into their milk with the prevalence being higher in rural areas (10.8%) than urban areas (6.9%). Of the milk samples from retailers, 12.5% were positive for Brucella spp. with 24.3% of the respondents reporting consumption of raw milk products. Herd size was found to be associated with brucellosis in the herd (p=0.038; 95% CI). Animal breed (p=0.000) and herd size (p=0.014) were also found to be significantly associated with the shedding of Brucella spp. in milk from lactating cows at individual and herd level respectively. Residence in rural Chamwino was significantly associated with low brucellosis knowledge levels (p=0.033), which may affect infection levels in both cattle and humans either directly or indirectly.

**CONCLUSIONS:** The study showed that brucellosis is prevalent in cattle which may expose other animals in the herds as well as their human handlers to infection. Brucella spp. pathogens were also detected in raw milk sold along the informal dairy value chain in Dodoma Municipal and Chamwino District, thereby indicating a risk to milk consumers thus inadvertently jeopardising public health. Both these scenarios call for interventions such as, vaccination of animals, screening of fresh and sour milk along the informal dairy value chain for Brucella spp. and public health sensitization campaigns targeting farmers, retailers and milk consumers on brucellosis transmission and prevention strategies, with concentrated focus on large herd owners as well as cattle keepers and dairy consumers living in rural areas.

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## Tick-Borne Diseases-Possible Threat to Humans-Dog Interspecie Bond

Mohammad Ilyas Khan

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**Abstract:** Dog (Canine lupus familiaris) is one of the most neglected specie in the research institutes in Pakistan. Humans are at great risk of zoonotic diseases due to close association with dogs and humans-dog interspecies bond is at danger due to these diseases. The aim of the study was to determine the haemo-parasitic diseases of dogs, its effect on hematological profile and to correlate it with general health status of dogs. Total of 121 blood samples were collected from district Peshawar and Charsadda from public and private sectors including armed forces. Microscopic results showed 34 and 19% prevalence of anaplasmosis and canine babesiosis, respectively. Prevalence of haemo-parasitic diseases in dogs were studied with respect to different risk factors i.e. season, location, breed, owner, sex and age. Statistically significant ($P<0.05$) relation

was recorded with respect to season, breed, ownership and age while no significant ($P>0.05$) relation was observed with respect to location and sex. Anemia was striking feature in hematological parameters with significant ($P<0.01$) decrease in red blood cells, hemoglobin and hematocrit values and can be classified as normocytic hypochromic with significant decrease ($P<0.01$) in Mean corpuscular hemoglobin concentration (MCHC). Ticks are important vector for the transmission of the haemo-parasites and ticks infestation is favored by hot and humid environment, the reason for higher prevalence of haemo-parasites in the summer season. Awareness among the community should be initiated through media talks, print and electronic media for periodical screening of their dogs for haemo-parasitic diseases and along with that control strategies should be designed.

## Antibiotic resistant airborne bacteria and their multidrug resistance pattern at University teaching referral Hospital in South Ethiopia

Fiseha Wadilo

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**Background:** Hospitals provide a reservoir of microorganisms, many of which are multi-resistant to antibiotics. Emergence of multi-drug resistant strains in a hospital environment, particularly in developing countries is an increasing problem to infection treatment. This study aims at assessing antibiotic resistant airborne bacterial isolates.

**Methods:** A cross-sectional study was conducted at Wolaita Sodo university teaching and referral Hospital. Indoor air samples were collected by using passive air sampling method. Sample processing and antimicrobial susceptibility testing were done following standard bacteriological techniques. The data was analyzed using SPSS version 20.

**Results:** Medically important bacterial pathogens, Coagulase negative staphylococci (29.6%), Staphylococcus aureus (26.3%), Enterococci species, Enterococcus faecalis and Enterococcus faecium (16.5%), Acinetobacter species (9.5%), Escherichia coli (5.8%) and Pseudomonas aeruginosa (5.3%) were isolated. Antibiotic resistance rate ranging from 7.5 to 87.5% was detected for all isolates. Acinetobacter species showed a high rate of resistance for trimethoprim-sulfamethoxazole, gentamicin (78.2%) and ciprofloxacin (82.6%), 28 (38.9%) of S. aureus isolates were meticillin resistant, and 7.5% Enterococci isolates of were vancomycin resistant. 75.3% of all bacterial pathogen were multi-drug resistant. Among them, 74.6% were gram positive and 84% were gram negative. Multi-drug resistance were observed among 84.6% of P. aeruginosa, of 82.5% Enterococcii, E. coli 78.6%, S. aureus 76.6%, and Coagulase negative staphylococci of 73.6%.

**Conclusions:** Indoor environment of the hospital was contaminated with airborne microbiotas, which are common cause of post-surgical site infection in the study area. Bacterial isolates were highly resistant to commonly used antibiotics with high multi-drug resistance percentage. So air quality of hospital environment, in restricted settings deserves attention, and requires long-term surveillance to protect both patients and healthcare workers.

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## High Mortality from Blood Stream Infection in Addis Ababa, Ethiopia, Is Due to Antimicrobial Resistance

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**Background:** Managing blood stream infection in Africa is hampered by lack of bacteriological support needed for antimicrobial stewardship, and background data needed for empirical treatment. A combined pro- and retrospective approach was used to overcome thresholds in clinical research in Africa.

**Methods:** Outcome and characteristics including age, HIV infection, pancytopenia and bacteriological results were studied in 292 adult patients with two or more SIRS criteria using univariate and confirming multivariate logistic regression models. Expected randomly distributed resistance covariation was compared with observed co-resistance among gram-negative enteric bacteria in 92 paediatric blood culture isolates that had been harvested in the same hospital during the same period of time.

**Results:** Mortality was fivefold increased among patients with positive blood culture results [50.0% vs. 9.8%; OR 11.24 (4.38–25.88), $p < 0.0001$], and for this group of patients mortality was significantly associated with antimicrobial resistance [OR 23.28 (3.3–164.4), $p = 0.002$]. All 11 patients with Enterobacteriaceae resistant to 3rd. generation cephalosporins died. Eighty-nine patients had pancytopenia grade 3–4. Among patients with negative blood culture results, mortality was significantly associated with pancytopenia [OR 3.12 (1.32–7.39), $p = 0.01$]. HIV positivity was not associated with increased mortality. Antimicrobial resistance that concerned gram-negative enteric bacteria, regardless of species, was characterized by co-resistance between third generation cephalosporins, gentamicin, chloramphenicol, and co-trimoxazole.

**Conclusion:** Mortality was strongly associated with growth of bacteria resistant to empirical treatment, and these patients were dead or dying when bacteriological reports arrived. Because of co-resistance, alternative efficient antibiotics would not have been available in Ethiopia for 8/11Enterobacteriaceae-infected patients with isolates resistant to third generation cephalosporins. Strong and significant resistance covariation between 3rd. generation cephalosporins, chloramphenicol, gentamicin, and co-trimoxazole was identified. Pronounced pancytopenia was common and associated with increased mortality. HIV positive patients had no excess mortality.

## How South Africa respond to environmental risks of concern with acute and long-term chronic risks

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Environmental risk refers to the combination of the probability and consequences of adverse environmental outcomes for event or activity which is induced by natural cause or human activities. Chemicals can enter air, water and soil when they are produced, used or disposed. Their impacts is determined by the amount of chemical that is released, the type of the concentration, and where it is found. Some chemicals can be harmful if released to the environment even when there is not an immediate visible impact and some can work their way into the food chain and accumulate and/or persist in the environment for many years.

The aim is to investigate sudden and accumulative risks induced by chemicals and their long term effects in soil, water, air, biodiversity and human health.

**Methods:** Interviews and literature reviews conducted to review environmental risk sources and their impact on receptors including entities such as humans, ecosystem and socioeconomic infrastructure that will suffer from risk consequences.

**Results:** Sources of sudden acute risks included the acute poisoning and leakages, fires and explosions from production, transportation, utilization, and storage of flammable and explosive materials or toxic chemical hazardous materials and treatment of wastes. Long-term and chronic risks and accidental environmental risks are due to industrial layout, mainly because many chemical production enterprises are located in densely populated areas, either on or near important water sources, rivers, lakes, wetlands and ecological protection areas. Sources included long existing polluting media such as emissions yielding chronic air pollution, ozone layer depletion and increased UV radiation; contamination of soil and water pollution at contaminated sites like eutrophication due to runoff of agrochemicals, livestock manure; mechanical failures (i.e. equipment failures such as wear, corrosion, ageing, or extended use), and human failure due to violation of the law, non-compliance of operations, operational error, inadequate management and weak capacity.

**Conclusion:** Natural resource contamination is correlated with the degree of industrialization and intensity of chemical usage. Acute responses to environmental accidents is weak and lacks effective emergency response plan. Long-term and chronic environmental risks have been neglected, and the social and economic impact of adverse environmental and human health is devastating with high costs of inaction for human and occupational health, purification of water resources, clean-ups and remediation falling upon the public sector and individuals.

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## Assessment of KAP, economic and public health burden of Anthrax in selected outbreak hit areas of Jimma zone

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Anthrax is zoonotic disease and typically a disease of domestic and wild herbivores causing tremendous economic loss due to its high fatality rate. One time survey was conducted to assess economic and public health burden and communities' knowledge, attitudes and practices on Anthrax in outbreak hit districts of Jimma Zone, Ethiopia from August, 2015 to May, 2016. A structured questionnaire was used where households were selected based on anthrax outbreak history and subsequent were identified using snowball sampling. About 193 respondents were included in the study. Appropriate statistical, economic and DALYs models were used for analysis. From the respondents about 17.3% mentioned that they eat the meat of diseased animal, and do not burn the body of the dead animal and slaughtered moribund animals and partitions its meat among their neighbors. About 22.2% of the respondents didn't know anthrax is zoonotic and 18.6% of them have no clue that vaccination is preventive. An estimated 25 human cases from which 6 died were reported and all of them were by eating meat of diseased animals or becoming in contact during slaughtering. An estimated monetary loss attributed to Anthrax outbreak was about 30,569,893ETB (($1,421,855.49). Public health burden of about 133.55 DALYs was estimated. The cumulative incidence was 36.69% in cattle, 16.162% in sheep, 2.632% in goats and 41.935% in Equines. The case fatality was highest in cattle (94.224%) lowest (37.5%) in sheep. A gap has been identified that the communities' knowledge and practice towards anthrax was/is poor. The outbreak had caused a significant economic and public health burden. Public education and putting in place proactive vaccination strategy and identification of endemic foci could help prevent nest anthrax outbreaks and its losses.

## Epidemiological survey on diarrheal diseases in the arid region of Morocco: case of Marrakesh city.Epidemiological survey on diarrheal diseases in the arid region of Morocco: case of Marrakesh city

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**Introduction:** Diarrheal diseases are one of the major public health problems. In developing countries, diarrhea is among the leading causes of childhood morbidity and mortality. These infections occur most frequently under circumstances of poor environmental sanitation and hygiene, inadequate water supplies, and poverty. Wastewater is an important vehicle of biological agents responsible for millions of estimated cases of diarrheal disease. Therefore the reuse of wastewater without any treatment in agriculture constitutes a risk to the natural resources and also to the populations that are in permanent contact or consuming the agricultural products irrigated with these waters. In Morocco, Various epidemiological surveys have been carried out in parts of the kingdom, including the Marrakech region, showing the prevalence of certain diseases, such as ascariasis, hookworm, anguillulose and trichocephalosis.

**Materials and methods:** The present study aimed to evaluate the risk of intestinal parasitosis from the use of wastewater in agriculture through an epidemiological survey carried out in the region of Marrakech, Morocco. The subjects are of different sexes, ages, and often consuming the products of the region that are irrigated by the untreated wastewater discharged from the sewage treatment plant of Marrakech city. We have also taken the samples of wastewater. The parasitological analyzes were carried out according to the standard diphasic method Bailenger method modified by Ayres & Mara (1996), recommended by WHO.

**Results and Discussion:** As results, a large number of infectious agents were identified, with a high risk of diarrheal diseases for the local population. According to WHO, these diseases are the second leading cause of death in children, so, preventive measures are needed, with emphasis on health education and adequate treatment of wastewater.

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## Screening of antivenom activity of Lavandula sto echas and Aristolochia longa plant extracts against Buthus occitanus venom

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The scorpion envenomation is a major public health problem in Morocco. It is a real concern for citizens and for the health personnel. The main cause of this scourge is the presence of a rich and diverse scorpion fauna characterized by the presence of dangerous scorpion species.

In Morocco, scorpion envenomation is the leading cause of intoxication with a rate 30%–50% of all the poisoning cases reported to the Moroccan Poison Control Center (PCCM). The major causative species belongs to Androctonus and Buthus genus, of these, Buthus occitanus causes severe envenomation (Ismail, 1995).

In this context this study aims to assess on the one hand the Buthus occitanus venom effects. On the other hand, the possible neutralizing effects of some species of medicinal plants extract: Aristolochia longa, Lavandula stoechas.

The venom is extracted by the electrical method. In order to determine the LD50 of the B. occitanus scorpion venom we injected increasing doses of the venom subcutaneously to Swiss mice. We evaluated the histological alteration of the vital organs (heart, kidneys, liver and lungs) and changes in biochemical parameters (ALT, AST, LDH, CPK, and Creatinine) after subcutaneous injection of the venom in the mouse. After calculating the LD99 of scorpion venom, the venom-neutralizing ability of plants extract was determined using in vivo methods. The alleviation in the mean survival time of the animals was used to infer the antivenom property of the extracts after challenging with LD99 of scorpion venom.

The LD50 of B. occitanus scorpion venom was found to be 0.53 mg/kg by subcutaneous injection route. Venom produced focal fragmentation of myocardial fibers, while lungs showed rupture of the alveolar structure. Concomitantly, there was a significant rise in the serum enzymes levels. The study of venom-neutralizing ability of plants extract showed that the ethanolic extract of A. longa (24.5 mg/kg) significantly increases mean survival time and the protection fold, but could not protect animals when used in the higher dose 30 mg/kg. However, the other extract tested: Lavandula stoechas showed no antivenom activity.

The present study provides strong evidence that support the use of Aristolochia longa as anti-scorpion venom in traditional medicine in Morocco with a low dose.

## Biosecurity – The cornerstone for preventing spread of highly infectious agents

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The social concerns for food safety, the growing demand for organic farms and the problematic of antimicrobial resistance make biosecurity the cornerstone for preventing spread of highly infectious agents. In addition, imports of live animals and animal by-products, international human travel, illegal traffic of potentially hazardous materials and fears of bioterrorism (e.g. anthrax) or agroterrorism (e.g. foot and mouth disease) require the constant application of biosecurity measures at several levels, including on-farm level. To prevent, minimize and control cross-contamination between animals, environment and humans, biosecurity protocols are implemented. The main challenge with biosecurity is maintaining compliance.

Several reasons are given to explain the lack of compliance of biosecurity measures. The lack of knowledge or understanding is the traditional reason explaining why compliance is low. Based on videosurveillance, we were able to detail what is misunderstood by listing frequently observed biosecurity errors at the entrance and exit of barns. Forty four different biosecurity errors were observed. The nature and frequency of the errors suggest a lack of understanding of biosecurity principles. In addition, determinants of compliance were identified: length and time of visit, presence of the grower or any other farm personnel accompanying visitors, entrance design, number of barns, number of biosecurity measures required, type of boots, gender and being a family member of the grower. Three personality traits were also associated with compliance: responsibility, action-oriented and complexity, as well as years of experience and education.

There is more than one solution to develop an effective on-farm biosecurity program and to address the potential lack of biosecurity compliance. Several elements are necessary. Of primary importance are the farm and barn designs (or adjustments for existing facilities) in order to facilitate implementation of the measures included in the program. Equally important are the communication efforts aimed at informing all personnel and visitors about biosecurity. It is particularly important to have in place a training program explaining why biosecurity is important, which measures are needed, and how to best implement them. Finally, maintaining a biosecurity program active requires feedback mechanisms keeping farm personnel and visitors aware of the importance of preserving the integrity of the biosecurity program.

# Abstracts Day 3

## November 9, 2017

## Session 6: Pathogenesis, Vaccine Development and metagenomic Technologies

## Session 7: Food-borne and Water-borne Diseases

Lead Session 6: **Barney S. Graham,** M.D., Ph.D. Vaccine Research Center, Viral Pathogenesis Laboratory and Translational Science Core, The National Institutes of Health, USA

Title: Anti-Viral Vaccine Development: Preparing for the Next Pandemic

Lead Session 7: **Manon Racicot** DVM, PhD; Adjunct Professor, University of Montreal, St. Hyacinth, Canada.

Title: Food Safety from Farm to Fork: A Behavioral Perspective

# Session 6:

# Pathogenesis, Vaccine Development and metagenomic Technologies

## ANTI-VIRAL VACCINE DEVELOPMENT: PREPARING FOR THE NEXT PANDEMIC

Barney S. Graham

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Infectious diseases pose the greatest threat to public health than any other process. Sir William Osler noted that “Humanity has but three great enemies: fever, famine, and war; of these by far the greatest, by far the most terrible, is fever.” This remains true despite advances in sanitation, antimicrobials, and vaccines. Sustained by increasing global commerce and travel, disruption of ecologies from conflict or economic development, and many people living with immune deficiencies, we are faced with a continuous microbial challenge. Most emerging infectious diseases are caused by viruses and are either zoonotic or vector-borne. AIDS began as a zoonotic transmission that circulated in humans for decades before evolving to the current pandemic. The HIV pandemic along with subsequent threats from avian influenza, SARS, MERS, Ebola, and Zika illustrate the disruptive impact of infectious diseases on economies and social stability, and have helped clarify the importance of taking a more global view towards building research capacity and infrastructure. Working towards the U.N. Sustainable Development Goals will help achieve the “One Health” agenda and allow us to reach the level of surveillance and advanced preparation necessary to reduce the public health burden of emerging viral diseases.

The talk will review lessons learned from the response to pandemic threats over the last 3 decades, and discuss currently available technology options for designing and delivering vaccines against viral diseases that may become future global public health concerns, with an emphasis on respiratory viruses including MERS CoV. There are 23 virus families associated with human infection from which the next pandemic threat could arise. Within each relevant virus family a database of information with accompanying reagents, assays, and animal models could be developed for prototypic viruses based on properties of tropism, transmission routes, and other distinguishing features of pathogenesis. Candidate vaccine approaches could be designed based on virus structure, transmission dynamics, entry requirements, tropism, and replication strategy. Rapid isolation of human mAbs, structure-based antigen design, next-generation sequencing, nanoparticle technology, and chemical synthesis are key tools for rapid vaccine development, but advanced preparation will be critical for rapid vaccine deployment during future pandemics.

## POINT-OF-CARE LIONEX AND LIPOARABINOMANNAN (LAM) ANTIGEN TESTS FOR RAPID TUBERCULOSIS DETECTION IN CATTLE USING NON-INVASIVE SAMPLES

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Bovine tuberculosis (BTB) is mainly caused by Mycobacterium bovis. BTB has devastating consequences on animal and human health. Currently, testing BTB in cattle requires a significant investment of time, equipment, and labor to determine the disease status of an animal. Effective surveillance protocols are often non-existent in high BTB burden countries, which further hamper control measures. This has created a drive to find novel and cheaper methods for rapid BTB testing. The Lionex Animal Tuberculosis (TB) Rapid Test® (Lionex-test) is a novel TB test that uses serum or plasma to detect three unique mycobacterial antigens. The Alere Determine TB lipoarabinomannan (LAM) antigen (LAM-test) is a World Health Organization supported point-of-care test that uses urine to detect active TB disease in humans. Here we determined the efficacy of the Lionex-test and LAM-test in milk and urine samples, respectively, from dairy cattle, and compare their results to accepted gold standards. Using milk samples (n=25) from M. bovis suspected infected cattle from a recent BTB outbreak in Michigan, the Lionex-test was positive in 23/25 milk samples and was negative 34/37 for the controls. Using urine samples (n=21) from the same cattle, the LAM-test detected M. bovis antigen in 6/21 samples tested and was negative 12/13 for the controls. These results were compared to culture/PCR and histology/necropsy using Cohen's kappa statistic and Pearson's p-values. The Lionex-test vs. histology/necropsy and Lionex-test vs. culture/PCR presented the most promising results with k= 0.2851 (p= 0.0107) and k= 0.3478 (p= 0.0547) respectively. To account for the low sample size of negative controls for culture/PCR, a theoretical kappa was also calculated. This produced a k = 0.8335 which is more consistent with the results. Meanwhile LAM-test vs. culture/PCR and LAM-test vs. histology/necropsy were k= 0.0132 (p= 0.9304) and k= 0.0984 (p= 0.5482), respectively. These findings suggest that performing the Lionex-test in milk samples could be an effective and new screening method for BTB in the field.

# IN VITRO ANTIBIOGRAM OF BACTERIA ASSOCIATED WITH EARLY CHICKS MORTALITY IN POULTRY CHICKS

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**ABSTRACT:** The present study was conducted for the isolation of bacterial agents and in vitro antibiogram of the isolates from the yolk and visceral organs of up to one week old broiler and layer chicks. Samples from the yolk and visceral organs were aseptically collected and cultured on various selective and differential media. The isolated organisms were identified and subjected to commonly used antibiotics for determination of antibiogram. 330 samples from yolk and visceral organs were taken from those chicks which were not medicated with antibiotics, as per history provided by the poultry farmers. Among these, 223(68%) showed bacterial growth. Various bacteria isolated were Escherichia coli (47.93%), proteus (5.87%), mixed infection (3.59%), streptococci (2.89%), klebsiella (1.79%), salmonella (0.5%), staphylococci (0.5%), pseudomonas (0.5%), pasteurella (0.5%) and yarseinia (0.5%). The antibiotics found most effective were ciprofloxacin (60.5%), Norfloxacin (45.3%), Enrofloxacin (36.81%), Gentamicin (33.21%), Chloramphenicol (33.21%), Cephradin (25.1%), Augmentine (24.7%), Kanammycin (17.5%) and Ampicillin (12.1%).

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# Evaluation of the agreement between comparative intra-dermal tuberculin and gamma interferon tests for the diagnosis of bovine tuberculosis in Ethiopia

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The control of bovine tuberculosis is difficult in developing countries because of the high cost of a sustainable testing program and the lack of a diagnostic assay with high sensitivity and specificity to detect animals at all stages of infection. A cross- sectional study was conducted to evaluate the test agreement between comparative intra-dermal tuberculin test (CIDT) and Interferon gamma (INF-γ) tests for diagnosis of bovine tuberculosis (BTB) at Holeta, Ethiopia from December, 2012 to May, 2013. In this study, a total of 114 cattle were tested both by CIDT and INF-γ tests. The agreement between INF-γ (PPDB-PPDA) and CIDT tests was fair (k=0.288). On the other hand, a moderate agreement (k= 0.44) was observed between INF-γ test (PPDB-PPDA) and INF-γ test (ESAT6/ CFP10 - Nil). The differences between reaction sizes at the bovine PPD injection site and the avian PPD injection site was significant (t test; $P<0.001$). INF-γ response was stronger to ESAT6-CFP10 protein cocktails compared to its response to PPD (B-A). Logistic regression analysis showed a significant association of animal age group with the responses of CIDT and INFγ tests. In conclusion, the fair agreement between the CIDT and INF-γ tests could indicate that the two tests are not completely overlapping and thus in addition to detecting a similar stage of the disease they do also detects the different stages of the disease. Hence, it is `advisable to use the two tests in combination.

## Characterization of diverse novel porcine astroviruses in East African smallholder piglets

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Astroviruses (AstV) is widely distributed and is associated with gastroenteritis in human and animals. Its prevalence among pigs with or without diarrhea is reported to be high; however, our knowledge of the diversity and epidemiology of AstV in East Africa is limited. The current study was conducted genetically characterize astroviruses in asymptomatic smallholder piglets in western Kenya and eastern Uganda using viral metagenomic approach. Twenty four (24) samples were randomly selected from a total of 446 piglets aged below 6 months that was initially collected to study rotaviruses distribution and diversity in the same region. Sequence-independent amplification and high throughput sequencing were applied to the metagenomics analysis of viruses in sample selected. Thirteen (13) out of the 24 samples analyzed had contigs with high identity to mamastroviruses. Phlyogenetic analysis of the detected mamastroviruses revealed genetic heterogeneity with four distinct genetic lineages OF porcine astrovirus (PoAstV) detected (PoAstV2, PoAstV3 PoAstV4 and PoAstV5). Nine fecal samples were having contigs that were not assigned to any genetic lineage of Known AstV in the GenBank. In-depth characterization of 5 strains with complete (or nearly) genome revealed diverse nucleotide sequence identities (49–96 %) with known PoAstV strains, indicating novel types or genotypes of PoAstV. This study concluded that genetic diversity among PoAstV strains reported here may presents a challenge for disease prevention, development of accurate diagnostic tools and even vaccine development. These findings provide new insights into the molecular epidemiology and prevalence of astroviruses in East African Swine population. Further research and investigation into the pathogenesis of AstV would benefit both veterinary and human medicine

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## Tumer Necrosis factor -308 gene polymorphism and risk of Plasmodium Falcifarum malaria infection among poeple living in Denbia wereda, Northwest Ethiopia

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**Abstract Background:** Plasmodium falciparum is the most dangerous species of plasmodium parasites in terms of lethality and morbidity. In different studies, polymorphisms in the tumor necrosis factor alpha (TNF-α) gene have been associated with increased susceptibility to mild malaria infection and severe malaria. The aim of this study was to determine the frequency of TNF-α-308 G > A gene polymorphism in P. falciparum malaria infected patients that live in Denbia woreda, North Gondar, North West Ethiopia and to assess the effect of TNF-α-308 gene polymorphism and different demographic factors on the risk of malaria infection. Methods and Results: Two hundred blood samples were collected from November to December, 2014 from clinically confirmed P. falciparum malaria patients (n=100) and from P. falciparum sero-negative individuals (n=100) that live in the study area. TNF-α-308 G > A polymorphism was detected using PCR- RFLP techniques. The mean age of P. falciparum malaria patient study subjects was 23.2 ± 8.36 years old. Age (P=0.000) and occupation (P=0.046) were associated risk factors for malaria infection at 95% CI. The allele frequency in malaria patient study subjects was 0.92 for TNF-α-308G (TNF-1) and 0.08 for TNF-α-308A (TNF-2). The distribution of TNF-α-308 genotypes in cases (P=0.065) and controls (P=0.677) were consistent with the Hardy-Weinberg equilibrium. Conclusion: There was no statistically significant association between TNF-α-308 genotypes and malaria infection (P=0.616). Further studies with large number of sample size and assessment in different malaria endemic areas of the country are warranted for generalization. Key words: Cytokine, Endothelial receptors, Sequestration, Single Nucleotide Polymorphism, TNF-α-308 gene variants

## Seroprevalence of Camel Brucellosis in Mogadishu, Somalia

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**BACKGROUND:** Camels play an important socio-economic role within the livestock dependent Somali communities with an estimated population over 6 million heads. Limited scientific information about foodborne pathogens contaminating camel milk together with the prevailing tradition of raw camel milk consumption are the main encouraging points to the present study.

**OBJECTIVES:** To investigate Brucella antibodies in camel serum as well as to evaluate the knowledge-attitude-practice (KAP) among camel owners in Mogadishu city of Somalia.

**METHODS:** A cross-sectional study was carried-out from December 2015 to March 2016 on sera of 180 randomly selected camels using Rose Bengal Plate Test (RBPT), Modified RBPT (mRBPT), Serum Agglutination Test (SAT) and Competitive Enzyme Linked Immunosorbent Assay (cELISA). A structured questionnaire was administered to sixteen herders whose camels were investigated in this study.

**RESULTS AND DISCUSSION:** The overall seroprevalence rate of brucellosis in the current study was 4.4% and 31.3% at individual and herd levels respectively. The level of agreement between mRBPT, SAT and cELISA was found to be perfect using Kappa statistic (0.841) with high sensitivity of (85.7%) of all tests except standard RBPT which have a sensitivity of (42.9%) and Kappa value of (0.589) when compared to the cELISA. Interestingly, 77% of the interviewed camel farmers send camels with verified reproductive problems to slaughterhouses. This is a good management practice that might have contributed to the low prevalence reported in the present study. However, lack of awareness among the herders and their close contact to animals as well as consumption of raw camel milk reported in this study, can play an important role of distribution of this zoonotic disease between Somali people and his animals, particularly camels.

**CONCLUSIONS:** The present study indicates that Brucella infection exists in the camels reared in Mogadishu, Somalia. This directs the need for a coordinated national epidemiological surveillance in camel and other ruminants and isolation of the causative agent and identification of Brucella biotypes of the country. Thus, enabling the selection of the best option of brucellosis control strategy for the country to reduce the socio-economic consequences of the disease and initiating public health education.

**ACKNOWLEDGEMENT:** Abrar University for funding this research.

## COMPARISON OF CELL SURFACE MARKER AND CYTOKINE EXPRESSION ACROSS STAGES OF LYMPH NODE GRANULOMA IN BCG VACCINATED AND NON-VACCINATED CALVES OF BCG VACCINE EFFICACY TRIAL

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Development of necrotic granulomas in response to Mycobacterium bovis infection in cattle is pathognomonic for bovine tuberculosis (bTB). There is a direct relationship between diseases severity and granuloma score, one of the parameter used to measure vaccine efficacy. Our hypothesis is that early vaccination of calves with BCG is effective in reducing the number and severity of microscopic lesions and also help in developing protective immunity. The objective of this study was, therefore, to compare the cell surface and cytokine differential expression across different stages of granuloma in (Bacillus Calmette–Guerin) BCG vaccinated and non-vaccinated calves. Histopathology and immunohistochemistry (IHC) staining was done on a total of 45 lymph node tissue block, from which a total of 122 (29 stage-I, 27 stage-II, 30 stage-III and 36 stage-IV) granulomas were considered for analysis. Polyclonal rabbit anti-human CD3 and anti-iNOS and monoclonal mouse anti-human CD68, anti-bovine IFN-γ, anti-bovine TNF-α antibodies were used. BCG vaccination was found to significantly reduce microscopic granuloma score within bTB affected lymph nodes. IHC staining for cell surface markers revealed proportion of CD68+ (macrophages) and CD3+ (T-lymphocytes) to be significantly reduced in lymph node granulomas of BCG-vaccinated animals, when compared to non-vaccinated animals (Mann Whitney Test, $P<0.05$). Similarly, iNOS was highly expressed in granulomas from BCG-vaccinated animals compared to non-vaccinated animals for all stages, being statistically significant in stages I and IV ($P<0.05$). Furthermore, IHC staining for IFN-γ and TNF-α demonstrated significantly increased expression within the lymph node granulomas of BCG-vaccinated cattle compared to non-vaccinated group ($P<0.05$). Findings shown in this study suggest that the use of BCG vaccine can reduce the number and diseases severity and induce protective cellular immune response in neonate calves.

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## Genetic diversity, Virulence and antimicrobial susceptibility pattern of Staphylococcus aureus colonizing Abattoir workers in Western Kenya.

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**Background:** HIV-infected outpatient's clinics, cattle and abattoirs provide an environment that promotes acquisition and spread of Staphylococcus aureus increasing risk of colonization and infection in the communities.

**Methods:** Eighty nine HIV + VE and 649 VE - Abattoir workers nasal swabs were tested for S. aureus followed by antimicrobial susceptibility testing, virulence genes were screened and multi-locus sequence typing conducted.

**Results:** Staphylococcus aureus were isolated from 16.6 %(126 isolates) of the 738 samples, 23 isolates from HIV + VE Abattoir workers and 103 from HIV - VE Abattoir workers . Gentamycin, Linezolid and Clindamycin and Ciprofloxacin were the most effective antibiotic 92.7% isolates susceptible,97.7%, of this isolates were resistance to penicillin-G , 65.1 % to Trimethoprim and 25.6 % to Tetracycline respectively , six isolates were multi-drug resistance to >4 antibiotics.

Seventeen different sequence types were identified, ST 152 being the most prevalent (35.0%), followed by ST 8 (13%) and was highly associated with HIV + VE Abattoir workers -Trimethoprim/sulfamethoxazole resistance $P > 0.0001$. Fifty five Panton Valentine Leukocidin gene were detected, majority from ST 152 strains (67.3%) , tst gene were detected in 15 strains of ST 72strains (60%), 5 new Sequence types and a novel clonal complex was identified.

# Zingiber officinale Roscoe and Echinops Kebericho Mesfin showed antiplasmodial activities against Plasmodium berghei in dose - dependent manner in Ethiopia.

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**Background:** The emergence and spread of Plasmodium falciparum resistance to the commonly available antimalarial drugs necessitated the search for new drugs from natural products. Zingiber officinal Roscoe and Echinops Kebericho Mesfin are traditional herbal medicines widely used for the treatment of malaria in Ethiopia. Objective: The aim of the study was to assess the toxicity profiles and in vivo antiplasmodial activities of 70 % methanol crude extracts of both plant materials against Plasmodium berghei. P. berghei was used to infect healthy male Swiss Albino mice of age 4-5 weeks and weight 25-36 g.

**Methods:** The extracts were administered orally at different doses 5000, 2500 and 1250 mg/kg for acute toxicity study of E. kebericho Mesfin and 1000, 500 and 250 mg/kg for four days suppressive studies of both plant materials. Parameters like parasitemia, body weight, packed cell volume (PCV) and survival time were determined.

**Results:** In vivo antiplasmodial activity studies of the crude extracts showed substantial parasitaemia suppression at dose levels of 500 and 1000 mg/kg in dose-dependent manner compared with the negative control. The highest chemo- suppressions of the 1000 mg/kg of E. kebericho and Z. officinale extracts were found to be 49.53 ± 1.90% and 32.83 ± 1.03%, respectively. The study further revealed that the survival times of P. berghei infected mice were also a dose - dependent; however, the extracts failed to prevent weight loss. The extracts also prevented loss in PCV in infected mice in a dose dependent manner. At the dose level of 5000 mg/kg, E. kebericho Mesfin showed no toxic effects; revealing that the LD50 of the methanolic crude extract of the plant could go beyond the dose level.

**Conclusions:** The extracts of the two herbal plants have shown antiplasmodial activities against P. berghei in a dose - dependent manner and further studies to identify the active ingredient(s) responsible for these activities are warranted. Results indicated that both plants have promising dose-dependent antiplasmodial activities against P. berghei, indicating that the result confirmed literature findings and the traditional use.

## Sero-prevalence of Brucella abortus and antibiotic residues in raw milk in Bukombe district Tanzania

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A cross sectional study was carried out in January 2017 with the aim of estimating the sero-prevalence of Brucella abortus, assess the risk factors for infection and establish the presence and levels of antibiotic residues in raw cow milk in Bukombe district Tanzania. A total of 221 blood samples from purposively selected lactating cows in 17 villages were collected and analysed for antibodies of B. abortus using Rose Bengal Plate Test and c-ELISA. Also 221 raw cow milk samples were collected from the same cows and analysed for antimicrobial residues using Delvo SP® test and subsequent quantification of Tetracyclines in milk samples using HPLC. A total of 54 cattle owners were interviewed on animal management practices, uses of antimicrobials in cattle and a tendency of drinking raw milk. Milk samples of sero-positive animals were analyzed by polymerase chain reaction to detect bcsp31 gene of B. abortus using B4/B5 primer sets. It was found that the animal management practices were poor and there was no diseases control programmes like vaccinations. All the respondents admitted to use tetracyclines, penicillin and tylosin antibiotics as prophylactics and treatment of diseases of cattle and farmers themselves used to buy and treat their animals without prescription from veterinarians. All of them did not know anything on drug withdrawal period and the effects caused by antibiotic residues in humans. The sero-prevalence of brucellosis was 1.4% and cattle herd sero-prevalence was 3.8%. Presence of bcsp31 gene was confirmed in one milk which suggested that B. abortus was species infecting cattle in the district. The prevalence of antimicrobial residues in raw milk was 11.6%. Tetracyclines were identified in 9/10 analysed raw milk samples and the levels were 6.1 (±5.8) ug/l which is below the MRL of 100 µg/l. It is concluded that B. abortus infection in cattle exists in Bukombe district which is may be a significant cause of burucellosis in humans. Lack of awareness and negligence of drug withdraw period post cattle treatment could be the factors for antimicrobial residues in milk in Bukombe district.

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## Estimating the Burden of Viral Gastroenteritis and Effectiveness of Rotavirus Vaccine in Young Children in Qatar

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**Objective:** Acute gastroenteritis remains a major cause of morbidity and mortality of young children worldwide. It accounts for approximately 1.34 million deaths annually in children younger than 5 years, or roughly 15% of all child fatalities. Viruses remain by far the major cause of acute gastroenteritis in children, both in developed and developing nations. They are most often transmitted via the fecal-oral route and some enteric viruses, notably noroviruses, are highly infectious and may be easily spread in aerosols. The aim of this study is to determine the etiology of diseases in children hospitalized with gastroenteritis to the Pediatric Emergency Center in Doha, Qatar.

**Methods:** A total of 320 fecal samples were collected from Pediatric Emergency Center, Hamad Medical Corporation (HMC) during the period between June 2016 and February 2017. The ages of the subjects ranged between 4 months to 12 years, with a median of 20 months. Samples were screened for 6 viral infections (group A rotavirus (RV), astrovirus, adenovirus, norovirus, sapovirus, and parechovirus), 4 bacterial infections (Enteropathogenic E. coli, Clostridium difficile, Campylobacter and Shigella) and parasitic pathogens using The FilmArray Gastrointestinal (GI) Panel kit. Viral RNA was extracted from 60 stool samples and were characterized by conventional RT-PCR assays and nucleotide sequencing for their phylogenetic grouping.

**Results:** Out of 320 tested samples, 268 were positive to at least one pathogen. RV, were mostly detected in 55.4% of samples, norovirus in 33%, adenovirus in 19%, sapovirus (15%), astrovirus in 9%. Mixed infections represented about 63% of all AGE cases. The mean and median ages of children with RV gastroenteritis were significantly higher than those of children with other viruses ($p = 0.0002$), followed by higher median ages being found in norovirus-infected children. Diarrhea and vomiting were more frequent among children with coinfection ($p < 0.005$), and the severity score was significantly higher for children infected with RV group A or norovirus ($p < 0.002$). The majority (56%) of the viral AGE occurred in children between the age group 5 months to 12 months. The prevalence of AGE infections were observed significantly higher in the month of September ($p=0.005$). About 39% of subjects had the vaccine but still got infected and the ratio of RV-vaccinated

for each RV1-vaccinated subject was 19%. No parasitic infections were diagnosed from the admitted patients. More-frequent dehydration observed among children with mixed infections compared with coinfection (P=0.01). Among the 60 stool samples extracted, 26 (43%) positive for group A RV, 23 (88%) were identified as P genotype and 7 (2.6%) had G and P combinations. Of 19 (31.6%) norovirus-positive specimens, 1 (0.5%) was identified as genogroups GI and 17 (89%) as GII.

## CHARACTERIZATION OF MULTIDRUG RESISTANT SALMONELLA KENTUCKY FROM ANIMAL SOURCES IN ETHIOPIA AND KENYA USING WHOLE GENOME SEQUENCING

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**Background:** Foodborne infection caused by Salmonella enterica represents a major public health burden worldwide and animals play a key role as important reservoirs of different Salmonella serovars. S. enterica serovar Kentucky has emerged as one of main serovars associated with foodborne diseases in humans in Africa. In addition, there is a high incidence of human clinical cases associated with multidrug resistant (MDR) S. Kentucky, posing a serious threat to public health. This study assessed the existence of strains multidrug resistant (MDR) S. Kentucky using whole genome sequencing (WGS).

**Material and Methods:** A total of twenty Salmonella Kentucky isolates originated from animal fecal samples in Kenya and Ethiopia and kept at the bacterial bank of The Infectious Diseases and Molecular Epidemiology Laboratory (IDMEL) Ohio State were submitted to whole genome sequencing using the Illumina Miseq next-generation sequencing platform.

**Results and Discussion:** Based on the WGS analysis 90% of all S. Kentucky were characterized as multidrug resistant (MDR). The gene blaTEM-1B which confers resistance against β-lactams was found in 85% of the isolates. The genes aac(3)-Id, aadA7, strA, and strB associated with resistance against aminoglycosides were identified in 60% of the isolates. A high numebr of isolates (85%) also harbored genes confering resistance against tetracycline (tet(A)) and sulfonamide (sul1). Only 2 (10%) S. Kentucky didn't harbor any known resistance genes.

**Conclusions:** This study confirmed a high rate of antimicrobial resistance among S. Kentucky isolates originated from animal fecal samples in Kenya and Ethiopia and identified the major antimicrobial resistance mechanisms by means of whole genome sequencing (WGS). The results presented herein reinforce the need to understand the drivers involved in the emergence of antimicrobial resistance in animal production in order to prevent human infections by MDR Salmonella. In this sense, in parallel to the high capacity to identify antimicrobial resistance mechanisms, WGS has also a great potential to generate valuable information on the epidemiology of MDR Salmonella in developing regions.

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## Detection and Phylogenetic Genotyping of Epstein Barr Virus (EBV) Among Blood Donors in Qatar

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**Background:** The Epstein Barr virus (EBV) is a causative agent of infectious mononucleosis. EBV is highly prevalent lymphotropic herpesvirus and had been linked to several malignancies. Transmission is generally by oral secretions, but can be through blood transfusions and transplantations. This study aimed to determine the seroprevalence, viremia rates, and circulating genotypes of EBV in healthy blood donors in Qatar.

**Methods:** Blood samples from 673 blood donors of different nationalities residing in Qatar (mainly Qatar, Egypt, Syria, Jordan, Pakistan, and India) were collected and tested for anti-EBV capsid (VCA; IgG & IgM), nuclear (EBNA; IgG), and early (EA-D; IgG) antigens. Avidity testing was determined when active infection was suspected. DNA was extracted from the buffy coat and subjected to EBV-DNA quantification using qRT-PCR. Genotyping was performed using nested-PCR targeting EBV-EBNA2 gene, and phylogeny by sequence analysis of the LMP-1 gene.

**Results:** 97.9% (673/659) of the samples were seropositive as indicated by the presence VCA-IgG while and 52.6 % (354/673) had detectible EBV-DNA. EBV seroprevalence and viremia rates increased significantly with age. Genotyping of 51 randomly selected samples showed predominance of Genotype 1 (72.5%, 37/51) as compared to genotype 2 (3.5%), and mixed infections were detected in 4% of the samples. Sub-genotyping for these samples revealed that the Mediterranean strain was predominant (65.3%), followed by B95.8 prototype and North Carolina strains (12.2% each), and China1 strain (6%).

**Conclusion:** As a first study to evaluate EBV infection in highly diverse population in Qatar, where expatriates represent more than 85% of the population, our results indicated high seroprevalence and viremia rate of EBV in different nationalities, with genotype 1 and Mediterranean strain being predominant. Clinical significance of these finding have not been investigated and shall be evaluated in future studies.

## No genomic determinant could explain persistence of some Listeria monocytogenes isolates in slaughterhouse and cutting facility environments.

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The ability of L. monocytogenes to colonize and persist in food processing plants increases food contamination risks. Persistent contamination occurs when a sporadic strain becomes a resident of specific niches in manufacturing environments. The ability to distinguish between resident and sporadic strains would support risk based management of Listeria concern in industry. The aim of this work was to assess relationships among L. monocytogenes isolates based on the occurrence of single nucleotide polymorphisms (SNPs) in resident and sporadic strains isolated from a cutting facility environment collected during three visits, over a period of two months. A total of 29 strains were recovered: 23 strains belonged to strains that were present at each visit and were considered persistent contamination since all of the sampling was done after cleaning and sanitation. An additional six different PFGE types isolates were sporadically isolated during the sampling.

The 29 isolates were sequenced and comparatively analyzed using WGS-based tools. Sequencing was performed on the Illumina Miseq technology. High quality SNPs were identified and analyzed with SNVphyl. Logistic regression was used to compare the relatedness between SNPs occurrence and period of sampling. The affected functions were identified in these isolates as well. Results showed that there were no significant SNPs differences in the clonally-related isolates during our sampling period, this suggest that genome rearrangements are not common in L. monocytogenes strains in such a short period of time in these industrial conditions. The phylogeny tree confirmed the clonally-related resident isolates defined by PFGE. This result meant there was clearly an unresolved contamination in the plan due to either the ability of L. monocytogenes to form biofilm which confer resistance to disinfectants or a mechanical protection for the bacteria in the case of hard-to-clean areas. These results provide important information to food manufacturers on the adaptation of cleaning and sanitation methods for persistent strains to avoid the recurrent food contamination.

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## Molecular and Genomics Based Approaches to Assess Public Health Risks Associated with Bushmeat Consumption in Tanzania

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Bushmeat, the meat and organs derived from wildlife species, is the common source of animal protein for human consumption in many parts of Africa, including Tanzania. Given the documented evidence of the presence of dangerous zoonotic pathogens amongst wildlife harvested for bushmeat in Tanzania, our study was designed to assess the biological risk and potential for impact on human health from fresh and processed bushmeat. A comprehensive stratified random sampling approach was used to map the prevalence and the distribution of anthrax, Brucella and Coxiella during rainy and dry seasons in villages and surrounding markets in three targeted ecosystems (Serengeti, Ruaha-Rungwa, and Selous). Preliminary results of real time PCR analysis of more than 1800 samples collected from more than 140 villages across the three ecosystems identified signatures of Bacillus anthracis (1.2%), Brucella (0.80%), and Coxiella (0.57%) in bushmeat harvested and sold in this region. The data also reveal a higher abundance of anthrax in fresh versus dry samples. Microbiome sequencing analyses of the V3-V5 region of the 16S rRNA gene was performed on a subset of 30 fresh and processed bushmeat samples recovered from the Serengeti ecosystem, and provide further evidence for the presence of nucleic acid signatures of genera representing these three select pathogens as well as other dangerous pathogens. Additional studies were performed to determine the species of origin of the bushmeat samples with PCR-based amplification and molecular characterization of the cytochrome B and cytochrome C oxidase I genes sequences, and our preliminary results suggest that the species of origin a large fraction (~ 50%) of bushmeat samples is misrepresented when sold in the markets. Taken together, the results of our investigations provide evidence of the presence of DNA signatures of especially dangerous zoonotic pathogens in bushmeat sold or prepared for consumption in Tanzania. In the long-term, our research will provide a rational basis for defining and mitigating the public health risks associated with the harvesting, trade, and consumption of bushmeat.

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## Silencing of IL-21 on HT29 and HCT116 Cells and Determining its Possible role in the Proliferation of Colorectal Cancer Associated with Schistosoma Mansoni Infection

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**Background:** Interleukin (IL)-21 is a cytokine produced by activated CD4 T-cells and natural killer T (NKT) cells. It is recognized for its anti-tumour effects and association with the development of autoimmune and inflammatory diseases. However, the role of IL-21 in the progression of pathogen-induced T-helper type 2 (Th2) responses, such as Schistosoma mansoni (S. mansoni) infection in colorectal tumourigenesis, remains unclear. Objective: The objective of this study was to determine the role of IL-21 in the proliferation of HT29 and HCT116 colorectal cancer cells after IL-21 is silenced. The proliferative effect of specific gene silencing may then correlate with colorectal cancer and S. mansoni infection. Results: The detection of IL-21 by ELISA and Western Blotting revealed that colorectal cancer patients infected with S. mansoni produced a high level of IL-21 in the serum compared to the serum of patients diagnosed with colorectal cancer only and the serum of patients infected with S. mansoni only. Moreover, the silencing of IL-21 in HT29 and HCT116 cells caused a significant reduction in the proliferation of cancer cells as determined by a Lactate Dehydrogenase (LDH) release assay. Conclusion: This study provides useful information indicating that IL-21 may be a potential target for the regulation, staging and surveillance of colorectal cancer caused by S. mansoni infection.

## Eukaryote-like serine/threonine kinase (StkP)- and phosphatase (PhpP)-mediated modulation of the S. pneumoniae virulence

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S. pneumoniae is the main cause of community acquired pneumonia and meningitis in children and the elderly. Disease occurs around the world but it is more common in developing countries. Travelers may be at higher risk if spending time in crowded settings or in close contact with children in countries where pneumococcal conjugate vaccine is not routinely used. Pneumococcal Ser/Thr kinase (StkP) and its cognate phosphatase (PhpP) play a crucial role in bacterial cytokinesis. Unlike homologs of PhpP in other gram-positive pathogens, the precise role of PhpP in pneumococcal virulence is presently unknown since most available studies on these proteins are carried out using unencapsulated pneumococcal strains. Here, we demonstrate that the encapsulated pneumococcal strain D39-derived ΔPhpP and ΔStkP mutants grow differentially in the presence of different non-glucose carbohydrate sources. Microscopic analysis and RNA-seq-based Global transcriptome analysis including virulence genes-specific transcript abundance displayed significantly down- and up-regulation of the capsule in D39ΔPhpP and D39ΔStkP mutants respectively. This reciprocal regulation was not observed with several other genes indicating that kinase and phosphatase activity of StkP and PhpP act both cognately with as well as independent of each other. Along with these results, the attenuation of virulence in the ΔPhpP mutant as compared to the wild-type strain corroborated with several downregulated virulence-related genes. Despite the upregulation of capsule related genes and increased capsule production, the mutants lacking StkP displayed significantly decreased virulence or delayed onset of infection in mice. The wild-type phpP- as well as stkP-gene complemented respective mutant strains displayed restoration of these lost functions. Our results thus revealed that both PhpP, as well as StkP, play a crucial role in the modulation of pneumococcal metabolic fitness and virulence.

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## Frequency of anti-nuclear antibody and anti dsDNA antibodies in subjects of oral addictive habits

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**Background:** People with addictive habits are prone to both infectious and non-infectious diseases. Conflicting results have been reported about propensity of these individuals for development of autoimmune diseases. Therefore, a study was planned to determine the frequency of anti-nuclear antibody (ANA) and anti-dsDNA (dsDNA) antibody in the serum of habitual smokers, paan (areca nut) chewers and other oral addictive habits as compared to subjects without such addictive habits. Methods: Blood samples from 90 subjects (45 with addictive habits and 45 without any addiction) were taken by random sampling after getting written informed consent. Enzyme linked immunosorbent assay (ELISA) was used to test the sera for ANA and anti dsDNA. Results: One subject in the addictive group had ANA and dsDNA antibodies, whereas in the control group, two subjects had anti dsDNA while none of them had ANA. No significant association of these antibodies was observed between the two groups. Conclusions: Addictive habits do not predispose the subjects to develop autoimmune diseases.

**Conclusions:** Trimethoprim/sulfamethoxazole, is an important antibiotic used for treating and preventing Opportunistic infection among HIV + Ve population, it has broad spectrum of activity against Pneumocystis jiroveci, toxoplasmosis, and bacterial infections making it lifesaving antibiotic. The presence of Panton Valentine Leukocidin combined with Trimethoprim/ sulfamethoxazole in HIV/AIDS patients may complicate treatment of suspected necrotizing pneumonia in immunocompromised individuals in this population and community at large.Genetic diversity, Virulence and antimicrobial susceptibility pattern of Staphylococcus aureus colonizing Abattoir workers in Western Kenya.

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## Prevalence of Autoantibodies in Healthy Adults in Pakistani Population

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**Abstract Introduction:** Autoimmune phenomenon is attributed to a number of diseases which were once considered idiopathic. In humans, production of auto antibodies (a-Abs) against self-antigens is quite frequent but earlier their presence was associated with autoimmune diseases, however a-Abs have been documented in non-autoimmune disorders i.e. complicated pregnancy, cancer, stroke etc. In Pakistan, limited data is available on frequency of a-Abs, therefore this study was designed to determine serum level of antinuclear antibody (ANA), Rheumatoid factor (RF) and anti dsDNA antibodies in apparently healthy population. Materials and methods: After written informed consent, blood sample of 256 subjects was obtained by random sampling. Participants of established autoimmune diseases were excluded. Enzyme linked immunosorbent assay (ELISA) was used to determine ANA, RF and anti-dsDNA antibody. Categorical variables were compared by using $\chi 2$ test. A p value <0.05 was considered statistically significant. Results: Rheumatoid factor was the most frequent a-Ab (18%), followed by anti dsDNA (7.4%), while ANA was the lowest (0.4%) antibody detected. Only RF had a statistically significant association with gender (p=0.047). No association of these antibodies with age was detected. Conclusion: Rheumatoid factor auto antibody was more prevalent as compared to ANA and dsDNA antibody in healthy adults.

## Targeting Bacterial Histone Deacetylase-Like Enzymes for Antibiotic Adjuvants Discovery

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The emerging threat of untreatable bacterial infections to public health is prompting a global action to combat antibiotic resistance. There is a dire need for novel antibiotics and antibiotic adjuvants that can reduce the burden and threat of emerging antibiotic resistance. Neisseria gonorrhoeae is a strict human pathogen that causes the sexually transmitted infection termed gonorrhea. Importantly, > 100 million cases of gonorrhea occur worldwide each year and the gonococcus is noted for its capacity to develop resistance to antibiotics used in therapy. In 2013 the Center for Disease Control declared antibiotic resistant N. gonorrhoeae as urgent threat to public health. Recently, the World Health Organization placed N. gonorrhoeae on the high priority pathogen list for developing new antibiotics. I identified a gene that encodes a histone deacetylase-like enzyme (GC-HDAC) that shares high 3D-homology to human HDAC2 and HDAC8 . I employed computational modeling to predict GC-HDAC-like protein structure-function and found that it has an active catalytic pocket containing the highly conserved zinc-binding constellation, suggesting an HDAC-like activity. Indeed, HDAC inhibitors TSA and valproic acid can inhibit the growth of live gonococci. GC-HDAC gene is constrictively expressed during growth phases as well as during infection. Gonococci mutant lacking GC-HDAC enzyme showed moderate growth defect in vitro and in vivo. Furthermore, proteomic studies revealed that GC-HDAC enzyme affect bacterial growth by deacetylating membrane proteins, transcription and growth elongation factors. These findings suggest that this HDAC-like enzyme is a potential drug target for antibiotic adjuvant discovery.

Bacterial HDAC-like enzymes are ancient and found in many bacterial species. An extensive bioinformatics blast search for an HDAC-like homolog in clinically relevant bacteria showed that this gene is absent in most gut microbiota species including Lactobacillus, Bifidobacteria, Bacteroides, Clostridium and many E. coli strains. In contrast, an HDAC-like homolog is predicted to be produced by many pathogens that cause healthcare-associated infections, namely MRSA (methicillin-resistant Staphylococcus aureus), Acinetobacter baumannii, Klebsiella pneumoniae and Pseudomonas aeruginosa. These pathogens usually carry and spread multidrug resistance in healthcare settings as well as in community acquired infections. Due to the emergence of antibiotic resistance in N. gonorrhoeae and the potential for untreatable gonorrhea, developing novel class of antibiotic adjuvants that selectively target bacterial HDAC-like enzymes and less active against human HDACs is highly desirable. Therefore, GC-HDAC enzyme which is absent in most gut microbiota, is a highly druggable target that can be utilized for novel adjuvant antibiotic discovery.

Food-borne and Water-borne Diseases

# Session 7:

# Food-borne and Water-borne Diseases

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## Food Safety from Farm to Fork: a Behavioral perspective

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Campylobacter is one of the most common causes of foodborne diseases around the world. Even if the burden (in terms of Disability Adjusted Life Year (DALY)) associated to a single Campylobacter case is low (average DALY per case at 0.041; Havelaar et al., 2012), the number of cases per year is significantly high. The estimated annual number of cases of domestically acquired campylobacteriosis in Canada is 213,749 (Thomas et al., 2013). Based on Butler et al., 2015, 62.3% of these cases are attributed to the foodborne route. Campylobacter in food represents 30% of the total burden associated with microbial hazards in Canada. When looking at the source attribution at the commodity level, 60 to 70% of Campylobacter cases are attributed to poultry products (Davidson et al., 2011; Batz et al., 2012). There is a need to enhance efforts throughout the poultry production chain to reduce the incidence in the human population. Reducing the contamination rates early in the poultry production chain would have a major impact on the entire industry.

Several studies have identified risk factors at the farm level for Campylobacter. The lack of a hygiene barrier in broiler barn entrance increases the chances of Campylobacter contamination by more than 3 times (Hald et al., 2000). Van de Giessen and colleagues (1996) reported that chances of Campylobacter contamination are reduced by 5 times when people wash their hands, change farm boots and use footbath. However, these simple preventive measures are unfortunately not followed. Our team evaluated hygienic behavior compliance on poultry farms using hidden cameras (Racicot et al., 2011). We noticed that when the barn entrance design is difficult to comply with, there are 13 times fewer chances to comply with the hygiene barrier. The type of hygiene barrier has also a significant impact on compliance. Furthermore, boot and handwashing compliance are only at 53% and 36%, respectively (Racicot et al., 2013). These failures to prevent the contamination by Campylobacter at the farm level pose a significant risk for the entire poultry production chain, and ultimately to consumers. The impact of these behavioral failures was evaluated in an experimental study where we used a phage and genetically modified bacteria (detectable by bioluminescence) to assess the level of floor and boot contamination. Results show that when performing the right behavior, contamination is prevented (Huard et al., 2017).

Most food safety issues from farm to fork are related to human behaviors. Understanding the connection between environment, behavior and personal factors affecting safety is the basis of a system-based approach to food safety. All personnel involved in the production chain needs to be educated and trained using a simple, visual and risk-based approach. To significantly reduce the number of Campylobacter infections in the poultry and human population, there is a need to set goals, measure performance against those and pair them with consequences, either positively or negatively. All these system components are the foundation of a food safety culture (Yiannas, 2009).

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## Phenotypic and Genotypic Characterization of Temporally Related Non-Typhoidal Salmonella Isolated from Humans and Food Animals in Central Ethiopia

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**Abstract:** Salmonella is one of the most commonly isolated pathogens and is consistently among the top cause of foodborne bacterial illnesses. The primary sources of human non-typhoidal Salmonella (NTS) infection are food producing animals such as cattle, poultry and swine. The objective of the current study was to characterize and compare temporally and spatially related Salmonella isolates from humans and food animals and to determine their phenotypic and genotypic relatedness. Isolation and identification of Salmonella species was conducted according to WHO Global Foodborne Infections Network laboratory protocol. Salmonella serotyping was conducted using slide and microplate agglutination techniques. Antibiotic susceptibility testing was performed using disk diffusion method according to Clinical and Laboratory Standards Institute guidelines. Genotyping of Salmonella isolates was conducted by pulsed field gel electrophoresis (PFGE) and multilocus sequence typing (MLST). The dominant serovars frequently isolated from food animals and humans were S.Typhimurium, S. Virchow, S. Kentucky and S. Saintpaul. Frequency of resistance to tetracycline, ampicillin and cephalothin in Salmonella isolates from humans was relatively low compared to that seen in animals and the level of MDR was significantly higher in

Salmonella isolates obtained from slaughtered cattle, dairy cattle and poultry compared to those obtained from humans ($p < 0.05$). All S. Kentucky isolated from animals and humans were MDR with shared resistance phenotype (AmpAmcCfCipGmTeSuSNa). MLST analysis demonstrated 3 novel alleles and 5 novel sequence types. Despite wide diversity, PFGE analysis revealed clonal or closely related genotypes of S. Virchow, S. Typhimurium, S. Kentucky, S. Braendurp and S. Miami circulating among humans and animals. Of particular concern is isolation of clonally related MDR S. Kentucky from dairy, slaughtered cattle, poultry and humans; MDR S. Virchow from dairy cattle, slaughtered cattle and humans. Detection of clonally related Salmonella isolates from humans and animals, the high MDR status of isolates from animals, and close proximity of farms and human residential area presents major public health problem. Therefore, integrated surveillance of Salmonella serovars in humans and animals and implementation of appropriate pathogen control strategy along critical points in food animal production from farm to bench is recommended.

## Antimicrobial Resistant Listeria Monocytogenes and Source of Contamination in Retail Meat in Eastern Ethiopia.

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Identification of antibiotic resistant L. monocytogenes in Retail Meat of Eastern Ethiopia was conducted; to determine presences and level of L. monocytogenes in retail meat, to assess the potential risk factors to contamination of raw meat by L. monocytogenes, to determine sensitivities of L. monocytogenes isolates to different antimicrobial agents. A total of 318 raw meat were collected using a cross-sectional study from September 2013 to December 2013. A descriptive survey was also used to answer questions concerning the status of food hygiene and sanitation practice. For the isolation and identification of Listeria species in the food samples, the techniques recommended by the International Standards Organization (ISO 11290-1) and the French Association for Standardization was employed (AFNOR, 1993; ISO, 2004).The dominant Listeria species isolated in the present study was L. grayi (20.12%). L. monocytogenes was the third most frequently detected Listeria species (7.86%). Among the study sites included in the study, a frequency of L. monocytogenes was high in meat samples from Dire Dawa (14.00%). The results of antibiotic susceptibility test were revealed that above 50% of the isolates were resistant. On the other hand, some isolates were susceptible to Erythromycin (32.00%), oxacillin (28.00%), tetracycline (40.00), cephalosporin (28.00%), ampicillin (28.00%) and penicillin G (16.00 %). All of the meat samples plate count was below 30 colonies for the quantitative analysis of L. monocytogenes. The result of coliform count was demonstrate that the level of coliform contamination were at an average level of 34.53 MPN with standard deviations of 136.83. From total of 168 abattoirs and butcher house workers interviewed, 72.73% of them practice hand washing before starting of work. The entire respondent in all sites wash their hand after visiting the toilet and 54.17% of them used detergent. Regarding training background of workers, 76.78% did not take any training regarding meat hygiene and 80.95% respondents have no regular health check. In conclusion, L. monocytogenes was widely distributed in retail meat in eastern Ethiopia. And many of the strain were develop antibiotic resistance. Mainly the unhygienic status of abattoirs, butcher and abattoir workers were the source of contamination.

## Systemic Patterns and Predictive Trends of Multidrug Resistant Salmonella typhi Isolated from Sudan

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**Background:** Enteric fever has persistence of great impact in Sudanese public health especially during rainy season when the causative agent Salmonella enterica serovar Typhi possesses pan endemic patterns in most regions of Sudan.

**Objectives:** The aim of this study is to evaluate the recent state of antibiotics susceptibility of Salmonella typhi with special concern to multidrug resistance strains and predict the emergence of new resistant patterns and outbreaks.

**Methods:** Salmonella typhi were isolated and identified according to World Health Organization and International Standardization Organization guidelines. Antibiotics susceptibilities tested using Clinical Laboratories Standards Institute recommendations. The predictions of resistance emergence were done using logistic regression, forecasting linear equations and in silico simulations models for predicting patterns of outbreaks in Sudan.

**Results:** A total of 124antibiotics resistant Salmonella typhi strains categorized in 12 average groups were isolated, different patterns of resistance statistically calculated by ($y = ax - b$). Minimum bactericidal concentration's predication of resistance was given the exponential trend ($y = n\ ex$) and the predictive coefficient $R^2 > 0 <1$ are approximately alike. It was assumed that resistant bacteria occurred with a constant rate of antibiotics doses during the whole experimental period. Thus, the number of sensitive bacteria decreases at the same rate as resistant occur following term to the modified predictive model which solved computationally.

**Conclusion:** This study assesses the prediction of multi-drug resistance among S. typhi isolates by applying low cost materials and simple statistical methods suitable for the most commonly used antibiotics as empirical therapy. Therefore, bacterial surveillance systems should be implemented to provide data on the aetiology and prevailing antimicrobial drug resistance patterns of community-acquired agents causing outbreaks

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## Seroprevalence of Toxoplasma gondii infection among HIV-positive and HIV-negative Subjects in the Khartoum State, Sudan

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**Introduction:** Toxoplasma gondii infection has become a major public health concern in recent years due to the ravaging HIV/AIDS pandemic. Information about human toxoplasmosis and detailed demographic data of groups at risk are missing in the Sudan. Most of the available reports on human toxoplasmosis in the Sudan are in pregnant women. However, nowadays toxoplasmosis in man becomes a serious infection with the emerging of several causes of immunosuppression, particularly HIV/AIDS.

**Objectives:** In order to increase the awareness in the recent public health importance of Toxoplasmosis, the present study was planned to assess the seroprevalence of the disease in HIV-positive and HIV-negative people in the Khartoum State, Sudan.

**Methods:** Patients enrolled in the HIV/AIDS treatment and follow up programme at Bashayer University hospital during September 2014 - February 2015 were freely asked to participate in this study as study group. The control group was consisting of apparently healthy people (workers and visitors) present in the same hospital at the same time. After a verbal consent, a short interview containing history of HIV infection, AIDS treatment, health status, sex, age and social status (marriage) as well as history of abortion for women. Then blood for serum was collected for laboratory work including LAT and IgM ELISA tests.

**Results:** The overall seroprevalence of T. gondii infection was 43.9%. Twenty-two percent were seropositive for IgM and 31.7% were seropositive for the screening test (LAT). The prevalence rate in HIV-positive and HIV-negative people was found to be 42.0% and 46.9 % respectively. Most of the samples (62.5%) reacted positive for both LAT and ELISA-IgM were HIV-Positive. The highest levels of antibody titrations (1:32 and 1:64) were reported in the HIV-positive group, while the rate (IgM Index) of anti-T. gondii IgM was found to be higher in the control group (HIV-Negative), but without statistically significant differences (p=0.710) between the two groups. HIV-seropositive was significantly (p=0.044) associated with higher seroprevalence of T. gondii

(40.0% vs. 18.8%) using Latex Agglutination Test (LAT). However, anti-T. gondii IgM was significantly (p=0.007) more prevalent in HIV-negative people than the immunocompromised group (37.5% vs. 12.0%). The risk factors were analyzed, discussed and published elsewhere.

**Conclusion:** the present study demonstrates the importance of screening and treatment of T. gondii during HIV consultation. Specific measures must be taken by the HIV-patients and their health-care providers to decrease the risk of accruing infection or reactivate a latent one.

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## MICROBIOLOGICAL AND PHYSICO-CHEMICAL QUALITY OF DRINKING WATER IN NORTH GONDAR ZONE: A CROSS SECTIONAL STUDY

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**Statement of objective:** Assessing the microbiological and physico-chemical quality of drinking water sources is important to protect public health. Therefore, this study was aimed to assess the microbiological and physico-chemical quality of drinking water sources in North Gondar Zone, Northwest Ethiopia.

**Methods:** A cross-sectional study was conducted from April-May 2014 in seven districts in North Gondar zone. The physico-chemical and microbiological quality of 71 drinking water samples were determined following the standard procedure. Turbidity, pH, and temperature were measured using turbidity meter, pH meter and thermometer respectively. Arsenic, Cr6+, NO2, NO3 and residual chlorine were determined by the colorimetric methods and rapid kits using DPM apparatus (Kyoritsu chemical-check Lab., Corp. Japan). Coliforms and Vibrio parahemolyticus were tested by rapid microbiological test strips (Sankori coliform and SankoriVibrio parahaemolyticus) following appropriate standard procedure. Consumers assessment was also conducted using questionnaire about the water sources. Data were entered and analyzed using SPSS version 20 software.

**Results:** The physico-chemical and microbiological quality of 71 water samples (tap n=29, spring n=15 and well n=27) were assessed. The mean turbidity of water samples was 19.35 + 5.75SD nephlometric turbidity unit (NTU), temperature 21.34+3.68 oc, pH 6.88+0.6, nitrate 10.02 + 8.72 mg/l, nitrite 0.33+0.64 mg/l, residual chlorine 0.01 + 0.06 mg/l, arsenic 0.2+0.00 mg/l and chromium 0.51+0.01 mg/l. Almost all samples were complying with the WHO acceptable range for nitrate arsenic and chromium among the physico-chemical parameters. However, turbidity was found to be unacceptably high in 21 (29.6%) samples, pH was unacceptably low in 26 (36.6%) of the samples and residual chlorine was unacceptably low in 69 (97.2%) of the samples. The majority of samples (n=46; 64.8%) had coliforms and 12 (16.9%) had Vibrio parahemolyticus.

**Conclusion:** Most of the physical and chemical parameters measured were within the recommended range except turbidity and residual chlorine. However, the majorities of drinking water samples were found to be contaminated and are potential risk to public health. Therefore, regular quality monitoring and frequent water treatment in the study area is mandatory.

## EVALUATION OF EQAS RESULTS, ON SEROTYPING AND ANTIMICROBIAL SUSCEPTIBILITY TESTING OF SALMONELLA AND SHIGELLA SPP. RETROSPECTIVE STUDY.

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**Background:** External Quality assurance scheme (EQAS) is the system which allows each laboratory to compare its overall performance with other internal and external existing laboratories, which are working in similar disciplines. Its comparative nature of participation, also engage the laboratories to work hard and minimize possible occurring errors, through time. A number of progresses were reported in different laboratories and countries after attending in one or more of such programs.

**Objective:** To evaluate EQAS results of Salmonella and Shigella species, that had been checked for the last five to six years under WHO- AFRO GSS EQAS program

**Methods:** Samples received for Salmonella and Shigella species serogrouping and/or for other enteric pathogens identifications in this EQAS program, were directly inoculated to the suitable and selective media according to the type of organisms. Serogroups were reported using terms according to Kauffmann-White-Le Minor procedures. For antimicrobial susceptibility testing drug diffusion method and CLSI interpretation guideline were used. Ampicillin, cefotaxime, ceftazidime, ceftriaxone, chloramphenicol, ciprofloxacin, gentamicin, nalidixic acid, streptomycin, sulfamethoxazole, tetracycline, trimethoprim and trimethoprim + sulphonamides antimicrobials were used for AST of Salmonella and Shigella strains.

Results: From all six years participation (2008-2013), the serogrouping results were correctly reported as 88.6% that was 62 out of 70. None of the deviations were recorded for Shigella species. Participation for Campylobacter species were done only twice per six years, only at 2009 and 2010; which the results of agreement from expected values were ½ (50%) and 2/2 (100%) respectively. From the overall results of antimicrobial susceptibility participation, 320 were correctly reported out of 356 antibiotics which accounts for 89.9%. In relation with this, the highest major discrepancy was observed on ciprofloxacin which was 6X, followed by tetracycline (5X), nalidixic acid (3X). The deviation on serogrouping, at each participation years is less than 10 % except, for the first year of participation (2008), which was 12.5% (1/8). In similar manner, the requirement of critical deviation, criteria were obtained at 2008 (2.5%), 2009 (3.7%) and at 2012 (4.8%), except at the year 2010 which was (8.3%).The detection power for serogrouping had shown slight progress from 87.5% at the year 2008 to 91.7% at consecutive years up to last year of participation that was 2013. In contrast, to serogrouping, antimicrobial susceptibility participation was dropped down slightly from 91% of the previous years to 85.7 % at the last participation year of 2012.

**Conclusion:** Even though, everyone has got a knowledge and awareness about the benefits of EQAS by default, its acceptance and implementation in developing countries is less communicated and exercised. The final recommendation in this project will be, all higher officials and policy makers in the field have to give attention for this and other similar EQAS program, and have to allocate adequate budget in a continuous basis.

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## VIROLOGICAL and BACTERIOLOGICAL QUALITY of DRINKING WATER in ETHIOPIA

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**Background:** Since unsafe water is responsible for serious illness, deaths due to highest burdens of diseases and greatest economic failure, monitoring the quality of water is essential. Water Quality monitoring is assessed widely using different indicators. Bacterial and viral indicators provide more complete picture of water quality. Virological quality of water hasn’t been assessed in most countries including Ethiopia. The use of E. coli CB390 minimizes resource and time to perform the tests in simultaneous detection of somatic and male-specific coliphages.

**Methodology:** A cross sectional study was conducted on 218 drinking waters samples collected from various regions of Ethiopia from February to June 2016 to assess water quality using coliphages by the help of CB390 E. coli host, plaque assay; Multiple tube fermentation method for coliforms and pour plate technique for counting heterotrophic bacteria at Ethiopian Public Health Institute. The data were analyzed using SPSS 20.

**Results:** Heterotrophic bacteria, total and thermotolerant coliforms, E. coli and phages were detected in 72.9 %, 51.8%, 38.5%, 23.9% and 2.3 % of the total samples respectively. Heterotrophic plate count greater than 100 CFU/ml were noted in 41 (18.8%) samples and detections of total and thermotolerant coliforms and E. coli in 38 (17.4%), 24 (11.0%) and 10 (4.6%) samples respectively and no detection of phages in chlorinated waters. While, Heterotrophic plate count greater than 100 CFU/mL were observed in 100 (45.9%) samples and detections of total and thermotolerant coliforms, E. coli and coliphages in 75 (34.4%), 60 (27.5%), 42 (19.3%) and 5 (2.3%) samples respectively for untreated waters.

**Conclusion:** Majority of the waters contained indicators above standard limits. This indicates that the sources are contaminated with environmental and fecal contaminants signifying poor quality and it is a potential threat to human and animals health. Hence regular water monitoring using various indicators should be a priority agenda by all stake holders.

## MYCOLOGICAL AND BACTERIOLOGICAL QUALITY and SAFETY of BOTTLED WATER IN ETHIOPIA

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**Background:** Safe water supply is vital and can result in significant benefits to health. However, contaminated bottled water poses a great health risk due to poor microbiological quality of water.

**Methods and Materials:** A retrospective study was conducted on 222 Bottled water samples collected from various regions of Ethiopia from January 2008 to December 2015, tested and recorded in Ethiopian Public Health Institute to determine heterotrophic plate count and Staphylococcus aureus by the help of pour plate method; for coliforms using multiple tubes fermentation techniques; for mould and yeast count using spread method, and for Salmonellae and Shigella spp. using ES ISO 6579. The data was analyzed using SPSS 20 statistical package.

**Results:** Among the total samples examined from 44 brands, detections of heterotrophic plate count, mould, yeast, total and thermotolerant coliforms, Escherichia coli and Staphylococcus aureus were observed in 114 (51.4%), 33 (14.9%). 5(2.3%), 2(0.9%), 1(0.5%), 1(0.5%) and 1(0.5%) samples respectively, but there were no detections of Salmonellae nor Shigellae species.

**Conclusion:** More than one-third of bottled water samples were mycologically and bacteriologically unsafe for human consumption. To prevent public health hazards, regular monitoring of bottled water using quality indicators should be a priority agenda.

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## SEROPREVALENCE AND MOLECULAR DIAGNOSIS OF BRUCELLOSIS IN GOATS MOROGORO, TANZANIA

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Brucellosis is a re-emerging zoonotic disease that causes a great socio-economic as well as a public health concern. Limited studies have been conducted to determine prevalence of brucellosis in small ruminants kept in a free range grazing systems of Tanzania. The present study was performed to establish the prevalence of anti-Brucella antibodies and molecular prevalence of Brucella spp. in goats in nine wards of three districts of Morogoro region. Blood samples from 478 goats were collected by venipuncture into vacutainer tubes. All samples were screened by Rose Bengal plate Test (RBPT) and a subset of 92 samples including the RBPT positive was further subjected to indirect Enzyme Linked Immunosorbent Assay (iELISA). All samples were PCR screened using real-time Polymerase Chain Reaction (qPCR) for presence of Brucella DNA. Structured questioners were administered to collect information on goat health, management, and determine the risk factors for Brucellosis in the community. Out of 478 goat sera, one (0.2%) serum showed positive reaction to both RBT and iELISA. Eighteen (3.8%) of all samples were positive for Brucella spp on qPCR, and Brucella abortus was the only species detected in all goat sera. Minority (2.2 %; one out of 46) of interviewees were aware of the human brucellosis whereas 15.2% (n=7) were aware of livestock brucellosis. Twenty six percent admitted to consume raw milk, 11 % consume raw blood, 80.4% reported to see goat abortion cases in their herds, 28.3 % observed cases of retained fetal membranes, and 42 % had no proper means of handling and disposal of animal fetal membranes. This study has indicated the presence of Brucella abortus in goats in Morogoro region. Transmission of the infection between animals and human is likely to occur due to low awareness of people toward the transmission, prevention and control means of the disease. Therefore, there is a need for implementing control measures and raising public health awareness in prevention of brucellosis in Tanzania.

## Sero-prevalence of bovine brucellosis and its associated risk factors in Western Gojjam zone, Mecha district, North Western Ethiopia.

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A cross-sectional study was conducted from November 2016 to April 2017 to determine the sero-prevalence of bovine brucellosis and to identify the potential risk factors in Mecha district, western Gojjam zone, Ethiopia. A total of 320 sera samples were collected from cows with more than six month of age and have no history of previous vaccination against brucellosis. Rose Bengal Plate Test (RBPT) were used for screening purpose while Complement Fixation Test (CFT) as confirmatory test at National Veterinary Institute (NVI), Ethiopia. Out of the 320 sera samples collected, 5% (N=16) were positive using RBPT of which 2.2% (N= 7) were confirmed positive by CFT. In this study, though statistically not significant, higher prevalence were found in cows with age group between 3 to 6 years (3%, N=5) than other age group and in cross breeds (2.6%, N=3) than local breeds (1.0%, N=4) ($p>0.05$). Among the expected risk factors, pregnant cows showed higher prevalence within the group (5.4%) than not pregnant (1.9%) and heifers (0%); cows with pluri-parous history than primi-parous and no parity cows (2.4%, 2% and 0% respectively); intensive farms (2.8%) than semi-intensive farms (1.7%) ($p>0.05$). On the other hand, using univariate logistic regression analysis, cows that have abortion history after 5 months pregnancy showed statistically significant Brucella sero-positivity than cows that abort at less than 5 months pregnancy period ($p<0.05$ and Odds Ratio =17.11). Assessment of knowledge and practices of animal owners on brucellosis in the study area shows that only 37.2% (N=51) knows brucellosis as a disease and 0.7% (N=1) used to wear protective materials during cows parturition support. In conclusion, the prevailing Brucella sero-positivity and weak prevention practices in the study area signifies double burden of the disease which affects both dairy cattle industry and public health. Therefore, awareness creation to animal owners and to the public at large regarding bovine brucellosis and implementation of proper hygienic practices in dairy farm management is crucial to minimize the diseases burden.

### The Canadian Food Inspection Agency Establishment-based Risk Assessment model: How to allocate inspection resources to highest-risk areas?

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The transmission of zoonotic pathogens to humans via the foodborne route no longer has to be proven. With the constantly growing demand for safe food products, this situation reinforces the need for implementing focused and innovative control and risk management strategies to address pathogen contamination and transmission issues along the food supply chain, in order to preserve the health of Canadians. Despite regulatory, monitoring and surveillance programs, about 4 million Canadians are affected by foodborne illnesses each year. Risk assessment models facilitate decisions on the allocation of inspection resources and provide decision makers with a justifiable basis for determining risk acceptability. As part of its risk-based food safety continuous improvement, the Canadian Food Inspection Agency (CFIA) developed a new inspection model to help allocate inspection resources and support public health protection. This will be achieved by quantitatively assessing factors that contribute to the infectious foodborne disease risk represented by over 3,000 federally-registered food establishments in Canada.

The model concept is based on the allocation of risks to food establishments based on their impact upon the consumers' health in Canada. The underlying principle is that the total impact expressed as Disability Adjusted Life Years (DALYs) remains constant, but the proportion allocated to individual facilities is fluid. This value takes into consideration the number of cases attributed to each food safety hazard yearly, their association to specific food commodities and products, and the health impact per case of illness for each hazard. The health impact is initially allocated to individual establishments based on the volume of each product type they manufacture. The establishment-level health impact is then adjusted considering the presence or absence of specific food safety risk factors and their relative weights.

The model has been tested in meat/poultry, dairy and fish/seafood establishments and is currently being piloted in maple, honey and egg products. The model performance is being assessed by comparing the model outputs with the scores given by senior inspectors to establishments that participate in the pilot projects. Data analysis showed the Spearman correlation coefficient to be positive for meat/poultry and dairy establishments ($r=0.64$; $p<0.001$) and moderately positive for fish/seafood establishments ($r=0.44$; $p=0.004$). Few discrepancies were observed when considering the facility type, volume/type of product, and the inspection compliance results. Pilots with other food commodities will further help enhance the CFIA risk assessment model that will be implemented as part of the regulatory oversight activities of the Agency.

## Antimicrobial resistance in zoonotic Campylobacter isolated from informal settlements in Nairobi.

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**Abstract:** Surveillance of antimicrobial resistance in Campylobacter shows important levels of resistance globally. One cause of the high level of resistance is the use of these drugs in livestock treatment. Resistance prevalence data are an important starting-point for assessing the risk associated with antimicrobial resistance. This study aimed at investigating the antimicrobial resistance of zoonotic Campylobacter isolated from livestock in Korogocho and Viwandani informal settlements. The objectives were to investigate antimicrobial usage in the community, to identify phenotypic antimicrobial resistance and resistance genes present in the isolates. This was a cross sectional study with questionnaires to livestock keepers and livestock sampling and laboratory investigation of antimicrobial resistance in the confirmed zoonotic Campylobacter isolates.

Zoonotic Campylobacter are important pathogens in livestock in Korogocho and Viwandani informal settlements in Nairobi. The high resistance pattern to antimicrobials especially the first line of treatment of Campylobacter infections in humans (macrolides and quinolones) seen in the results of this study may be explained by lack of prudent usage of antimicrobial usage on livestock at farm level in the study area. Seventy percent of livestock were treated by owners compared to 5.1% treated by professional veterinarians. The trend seen in this study agrees with reports of rampant use of antimicrobials in livestock in Kenya. This situation is further emphasized by the 63.8% who buy the antibiotics from agro vets compared to only 2.7% of the households that get their livestock examined and medication prescribed by a veterinarian. This study recommends education of the public on zoonoses, antimicrobial resistance and prudent use of antimicrobials.

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## A one year study of diversity/evolution of Listeria monocytogenes strains in slaughterhouses and meat facilities in province of Quebec: genomic characterization of virulence and resistance.

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The occurrence of Listeria monocytogenes in the upstream of meat production environment is often unknown in many countries including Canada. Previous studies have demonstrated that environmental contamination is an important source of foodborne pathogen gaining entry into food processing plants. The aim of this study was to investigate L. monocytogenes genetic diversity throughout the meat processing environment and to describe evolution of genomic supported virulence and antibiotic resistance determinants. Four slaughterhouses and cutting facilities were sampled after cleaning and sanitation at four different periods of sampling with a minimum interval of three months between each sampling. A total of 2496 samples was collected over one year and analyzed for the presence of L. monocytogenes followed by phenotypic and genotypic characterization using serology, ribotyping and pulsed-field gel electrophoresis (PFGE). The whole genome of forty different? PFGE profiled strained sequenced with MiSeq Illumina technology and analyzed for virulence factors and antibiotic resistance attributes. A total of 57 PFGE profiles were found in all facilities which indicate an important diversity of strains in this environment. Among these strains a group of eleven strains emerged and interestingly, five out of them presented the same PFGE profile as those frequently isolated from food and those occasionally causing human listeriosis. The genomic analysis for presence and composition of particular virulence and antibiotic resistance factors will be shown during the presentation. These results strongly highlight the importance to consider the surveillance of L. monocytogenes in the upstream of food production in order to contribute to the reduction of food contamination and public health risks.

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## Non sorbitol fermenting Escherichia coli as indicator organism of microbial health risks associated with urban integrated farming in Dar es salaam, Tanzania

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Escherichia coli such as E. coli O157:H7 are important human pathogens among other common zoonotic pathogens carried by animals especially cattle. They are discharged through their faeces into the environment. With the increasing practice of urban farming, livestock manure is used as organic fertiliser in either fish ponds or vegetable gardens. This practice increases the risk of transmission of such pathogens to humans. This study aimed at determining the occurrence, antimicrobial resistance profiles and genetic relatedness of Non-Sorbitol Fermenting (NSF) E.coli isolates from manure, vegetables and fish. Microbiological standard methods were used to isolate and identify E. coli isolates from manure, vegetables and fish samples. Confirmed isolates on biochemical tests were tested for resistance against six antimicrobial agents using the disc diffusion method. Enterobacterial repetitive intergenic consensus polymerase chain reaction (ERIC-PCR) typing method was used to generate fingerprints and determine the genetic relatedness of the E. coli isolates. Out of 156 samples including 89 manure, 53 vegetables and 16 fish, 36 (23.1%) samples were positive for NSF E. coli from where a total of 48 E. coli different isolates were recovered that were subjected to antimicrobial susceptibility testing and genetic relatedness. Of these isolates, 25 (52.1%) were resistant to at least one antimicrobial agent and 12 (48.0%) showed Multidrug Resistance. ERIC-PCR profiles of E. coli isolates from manure, vegetables and fish showed genetic diversity with genetic relatedness ranging from 74.5% - 100%. Nine phylogenetic clusters (I - IX) determined at 90% threshold level of genetic relatedness were identified among the isolates. These results show potential health risk urban integrated farming pose, in the transmission of antimicrobial resistant pathogens with genetic diversity to humans and hence the need to monitor and improve husbandry practices in urban farming.

## Detection of mecA Gene in Methicillin Resistant and Sensitive Staphylococcus aureus Isolates from Dairy Cattle Milk

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Staphylococcus aureus is the main cause for clinical and subclinical mastitis in dairy cattle. Until recently, mastitis has only been medicated with antibiotics, despite the fact that misuse of antibiotics can cause S. aureus resistance from antibiotics. Methicillin resistant staphylococcus aureus (MRSA) is one of the strains of S. aureus which is resistant to methicillin. MRSA was detected for the first time in cattle milk with mastitis and it was a pathogenic bacterium to humans. While mecA gene is responsible for the resistance from beta-lactam antibiotics such as methicillin, it was also reported to be found in methicillin sensitive S. aureus. The objective of this research is to detect the existence of mecA gene in methicillin resistant and sensitive S. aureus which are isolated from dairy cattle milk.

MecA gene were detected from 32 methicillin resistant and sensitive S. aureus isolate from cattle milk from Boyolali, Pacitan, and Ponorogo. In those 32 S. aureus isolate, 28 are from subclinical mastitis cattle milk, 3 from normal cattle milk, and 1 from clinical mastitis milk. Reidentification of S. aureus was done by culture process on blood agar plate, gram stain, catalase test, coagulase test, mannitol fermentation ability with Mannitol Salt Agar (MSA), and voges proskauer test. Identification of S. aureus in a molecular level was done by detecting 23S rRNA gene using polymerase chain reaction (PCR). The determination of resistant and sensitive S. aureus by testing the bacterium on Mueller-Hinton Agar (MHA) using methicillin disc was done subsequently. PCR molecular detection was used to identify mecA gene as the target gene. PCR product of mecA gene was then sequenced to determine whether the amplified DNA fragment was actually mecA gene or not.

The result of this research showed that all of the S. aureus isolates (100%) could be indentified conventionally as well as molecularly. 16 (50%) methicillin resistant and 16 (50%) methicillin sensitive were identified from the S. aureus isolates. MecA gene cannot be identified in all of the S. aureus isolates, both methicillin resistant and sensitive. 93.75% MRSA were found in the subclinical mastitis milk.

Parasitic and Environmental Zoonoses

## Developing sustainable food value chains – The Gulf Challege –

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**ABSTRACT:** The development of sustainable food value chains can offer important pathways out of poverty for the millions of poor households in developing countries. Food value chains are complex systems. The real causes for their observed underperformance may not always be obvious. Typically, multiple challenges have to be tackled simul- taneously in order to truly break poverty cycles. This in turn implies the need for collaboration among the various stakeholders in a value chain, including farmers, agribusinesses, governments and civil society. Further compounding the challenge, improvements to the value chain must be economically, socially and environmentally sustainable: the so-called triple bottom line of profit, people and planet. Around the world, development practitioners in public, private and non-governmen- tal organizations are constantly designing and implementing innovative solutions to address these challenges. These practitioners facilitate the upgrading of products, technologies, business models, policy environments and so on. Some of these solu- tions fail to have a lasting impact, while others succeed in improving the system at scale and in a sustainable manner. Either way, valuable lessons are learned. In its role as a global knowledge broker aiming to enable the development of inclusive and efficient agricultural and food systems, the Food and Agriculture Organization of the United Nations (FAO) has initiated a new set of lessons. The first in the set contributes to the achievement of FAO’s Strategic Objective Four: Enable inclusive and efficient agricultural and food systems. It sets out the overall framework and a set of principles to guide sustainable food value chain development in practice. It is expected such lessons will facilitate the spread among practitioners of new ideas and knowledge related to the development of sustainable food value chains. If successful, it is hoped that this will lead to greater, faster and more lasting impacts in terms of growth in profitability of agribusiness and farming, creation of decent employment, generation of public revenue, strengthening of the food supply and improvement in the natural environment. Various successful examples of‘Developing sustainable food value chains’ will be presented, including: The potato value chain in India, the pineapple value chain in Ghana, the tea value chain in Kenya, the rice value chain in Senegal, the coffee value chain in Central America. The challenge for the Gulf countries, would be to explore the potentia role of local traditional foods, such as dates, camel meat or even seafood.

in the control programs with anti-helminth drugs and also consider other complementary measures including sanitation, provision of clean water supply, and snail control.

## A comparative study for cultural, serological and Molecular characterization of brucellosis in camel (Camelus dromedaries) in the Sudan

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Sudan has the second largest camel population in the world, estimated at nearly 4,500,000, and the country is home to some of the most well-known camel herds, the Kababish, Shukria, Hadendowa and others. Tribal groups in Sudan breed distinctive types of camels; Well-known among these are the Anafi and Bishareen, prized for their racing and riding capacities, the Rashaidi, a powerful transport camel with superior drought resistance and high meat yields.

Brucellosis in camels can be encountered in different camel breeds in different states in Sudan. High animal and herd prevalence have been reported from different localities, which not only cause a continuous risk for human infection, but also increase the spread of infection regularly to all other animal species. This research aims at providing information on diagnostic tools on diagnoses of brucellosis in camel milk in Sudan.

A Prospective study was conducted from January to May 2015 for diagnosis of brucellosis from dairy camel herds in Khartoum State in Sudan. This work aimed to elucidate the disease sero-prevalence in these dairy farms and to isolate Brucella spp. from camels' milk.

Three hundred and forty-five both milk and blood samples were collected from dairy camels in sterile containers. All milk samples were subjected to conventional bacteriological standard methods for brucella isolation, characterization and typing. Brucella abortus biovar 6 was isolated from 20 samples from camel's milk.

Molecular characterization of all the isolates using a multiplex PCR assay (Bruce-ladder), using IS711 primers revealed that all the 20 brucella isolates were Brucella abortus biovar 6. The PCR used for confirmation of camel milk isolates was found to be in 100% agreement with the conventional biotyping methods.

For conduction of serological investigations three tests were used which were the Rose Bengal Pate Test (RBPT), Serum Agglutination test (SAT), Competitive Enzyme Linked immunoSorbent Assay (cELISA), Milk Ring Test (MRT) and Milk ELISA. All the five tests were performed for detection of anti-brucella antibodies.

Of the 345 milk samples, 20 (5.8%) samples were bacteriologically proven and 68 (19.7%) samples were found to be serologically positive by modified MRT and 23 (6.7%) were positive by milk ELISA.

The results of the 345 serum samples revealed 82 (23.8%) positive with RBPT, 58 (16.8%) positive with SAT and 62 (18%) positive with cELISA.

This study ascertains the existence of brucella spp. in dairy camel and in their milk which is usually consumed as raw unpasteurized. Infected camels constitute one of the main sources of public health and animal health potential hazards.

It is highly recommended that integrated efforts should be taken to control this important disease in camel herds and to eliminate the potential public health threat from their marketed milk and other dairy products by proper pasteurization techniques and other proper implementation of hygenic measures.

### Phenotypic and genomic characterization of antimicrobial resistance of Salmonella enterica strains isolated along the beef chain in Mexico

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**Background:** Multidrug resistant Salmonella (MDRS) strains of different serovars are increasingly common worldwide. Food animals are recognized as a source of MDRS. Hence, it is important to address both phenotypic and genotypic characterization of food-associated strains, which can vary in a location-dependent fashion. The latter could help in determining factors involved in antimicrobial resistance dissemination and the potential transfer mechanisms of resistance genes. The purpose of this study is to identify and compare predominant strains isolated along the beef chain in Mexico regarding their phenotypic and genotypic antimicrobial resistance (AMR) profiles.

**Methodology/Principal Finding:**The study involved 43 Salmonella isolates from beef cattle feces, carcass swabs, primal cut swabs, and ground beef, corresponding to serovars Montevideo (n=26), Give (n=6), Derby (n=4), Muenster (n=3), Senftenberg (n=2), London and Roodepoort (n=1, each). The strains were subjected to whole genome sequencing (WGS) and antibiotic susceptibility testing (AST). The most frequent AMR phenotypes included tetracycline (37/43), sulfonamides (33/43), aminoglycosides (29/43), phenicols (19/43), and extended spectrum betalactams (17/43). Additionally, about 60% of the strains were MDRS, showing resistance to ≥3 antibiotic classes. These results were in line with the observed AMR genotypes, which included a widespread distribution across isolates of resistance genes for the above-mentioned phenotypes (tetA, aadA, aadA2, aph(3”)-Ib), dfrA12, dfrA17, sul1, sul2, bla-TEM-1, blaCARB-2). Moreover, all strains from serovars Give carried class-1 integrons (1014 bp) that harbored one cassette (aminoglycoside resistance). Strains of Muenster and one Derby isolate also carried a similar class-1 integron, which included an additional cassette for sulfonamide resistance. Remarkably, all the isolates encoded efflux pumps of the ABC, MFS, RND, and MATE families, which could also contribute to the observed AMR phenotypes. There was intra-serovar variation in both phenotypic and genotypic results. For instance, there were two distinguishable groups of Montevideo strains, one with an MDR profile (n=16) and another (n=10) that showed resistance only to tetracycline and had a single resistance gene against aminoglycosides (aadA). In silico plasmid profiling showed these mobile elements contribute mostly with resistance genes and integrons.

**Conclusions/Significance:** This study shows beef cattle is a significant source of MDRS. The concordance between phenotypic and genotypic results indicate resistance genes may be subjected to positive selection in the studied niche. Moreover, results suggest plasmids are likely to play a major role in the dissemination and transfer of AMR determinants among beef cattle-associated Salmonella in Mexico.

## Clinical Data and Antimicrobial Susceptibility of Multidrug-Resistant Pseudomonas aeruginosa Isolates in Qatar

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**Background:** Pseudomonas aeruginosa is the 2nd most frequent pathogen isolated from health care associated pneumonia, skin and soft tissue infection. There is insufficient data on epidemiology of multidrug resistance P. aeruginosa (MDR-PA) available in Qatar. Aim(s)/Objective(s): The present study aiming to determine anti- microbial susceptibilities, molecular epidemiology and risk factors of MDR-PA from patients, Hamad Medical Corporations (HMC), Doha, Qatar.

**Method(s):** Antimicrobial susceptibility testing: By Phoenix and results were confirmed by E-test. Descriptive analysis of the risk factors and clinical outcome of every file of MDR-PA positive patients were collected.

**Results:** Overall prevalence of MDR-PA was 8% (205/2552). Majority 74.6% were male, age range 1.5–90 years with a mean age of 45.75 years (SD = 62.58). 64% of patients >50 years, 68% patients non-Qatari, and majority 74.0% were inpatient.

Among the infected patients within last 90 days, 85% exposure to antibiotics, and 67% have history of MDR. 97% were hospital acquired. Among the patients of MDR-PA, 56% were colonization and 44% were infection.

The overall, 96.6% MDR-PA isolates shown resistance to cefepime, 91.2% ciprofloxacin, 90.7% piperacillin/tazobactam, 90.2% meropenem, 73.2% gentamicin, 58% amikacin, 54.6% tobramycin, and only 3.4% to colistin.

**Clinical outcome:** Overall 60% were cured, 36% died and 4% relapsed. Discussion and/or Conclusion(s): Our study showed a relatively low prevalence (8%), but there were five isolates resistant to all antibiotics tested in Qatar (Pandrug-resistance). Colistin shows high sensitivity (96.6%) and can be used for managing severe patients with suspected infections with MDR-PA.

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## INTERRUPTION OF TRANSMISSION OF Onchocerca volvulus IN GALABAT SUB-FOCUS

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**Back ground and Objective:** Control of Onckocercasis in galabt focus at Gedaref state started in 2007 by adopting of strategy of mass drug administration (MDA).The drug distributed once per year. In 2010 Federal Ministry of Health shifted the MDA to biannual treatments in order to eliminate the disease. As a base line the in 2007 assessment of transmission of the disease carried out to detect the infective stage of O.V. the head capsules of the vector S.Damnosum s.l by method of 0-150 PCRshowing 6.9 ( cl1.1-1.64) infective flies per 10 000 with moderate transmission. The objective of this work is to evaluate the effect of the Ivermectin against O.V. after three years of annual treatments and five years of biannual treatments.

**Materials and Methods:** In this study S.damnosum s.l collected from three sentential villages , flies preserved in Isopropanol for further studies. The flies divided into pools of 100 or less. DNA from head was extracted .Purification of DNA done by 0-150 PCR followed by PCR-based Eliza. Serological studies which used to determine transmission activity and the samples required is 3000 dry blood spots(DPS)from children >3years and <10 years. The OV 16 Eliza assay use recombinant antigen of O.V. to measure prevalent of immunoglobulin G4 (IgG4) antibodies. Parasitological studies, which done from adults more than 20 years. The three sentinels villages and another seven villages were selected five of them previously studied skin microfilaria, and the other two near Ethiopian borders.

**Results:** 0 - 150 PCR screening analysis showed no evidence of O.volvulus L3 larvae, this indicate zero prevalence of infective black flies. Serological results from 4244 DPS were all negative. Results of parasitological studies among 1046 skin snip with zero infection.

**Conclusion:** It is clear that from all these results the Onchocerciasis had been interrupted from Galabat focus –Gedref State.

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