

THE 5<sup>TH</sup> INTERNATIONAL

ONE  
HEALTH  
PLATFORM

# ne health CONGRESS

Canada  
**SASKATOON** 22-25 June  
**2018**

**OHS**  
ONE  
HEALTH  
SCIENCE

**AMR**  
ANTIMICROBIAL  
AGENTS AND  
RESISTANCE

**SPI**  
SCIENCE  
POLICY  
INTERFACE

Programme book

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## MESSAGE FROM THE CONGRESS ORGANIZERS

**On behalf of the Organizing Executive Board, we have the pleasure of welcoming you at the 5th International One Health Congress, organized by the One Health Platform, the University of Saskatchewan and our African partners: the Southern African Centre for Infectious Disease Surveillance (SACIDS), Global Health Kenya and One Health Central and Eastern Africa (OHCEA).**

The 5th International One Health Congress will build upon the excellent sessions and debates at previous International One Health Congresses organized in Melbourne, Bangkok and Amsterdam to give the floor to the most renowned experts and researchers. Since the first congress in 2011, the One Health approach has been increasingly accepted by major international health oriented organizations, academic research institutes, field workers and the pharmaceutical industry. We warmly welcome the growing movement of One Health advocates who strongly support the idea of an integrated approach to human, animal and environmental health as the best solution to complex and urgent health threats.

To capture the multi-faceted One Health paradigm, the 5th International One Health Congress has a multi-tracked programme. In the One Health Science sessions, world experts will showcase recent advances in pathogen discovery, diagnostics, drivers for emerging infections, vaccinology and political and social science. Seven sessions are specifically dedicated to antimicrobial resistance, in response to WHO's warning that AMR is indeed a global societal challenge and threat.

To foster the exchange of knowledge and practice at the interface of science and health policy, the 5th International One Health Congress also has a separate programme designed for public health officials. In this 'Science Policy Interface' or 'SPI' track, the world's leading experts will address some of the most intriguing One Health issues, while distinguished public health professionals will share their insights and experience. A series of plenary sessions will provide a platform for trans-disciplinary interaction, exchange of ideas and networking, in a true One Health spirit.

In many parts of the world, especially in developing countries and underserved communities, society is confronted with urban sprawl, spread of infectious diseases, rampant foodborne disease outbreaks, sick livestock and companion animals, and chronic water shortages. These challenges require global solutions in a One Health approach. The 5th International One Health Congress will therefore pay special attention to implementing One Health in underserved communities, in recognition of the complex interplay of environmental, animal and human health in underprivileged or subsistent societies around the world. At the same time, we wish to reinforce the increasing number of excellent One Health activities in developing countries. We are therefore extremely grateful that our congress enjoys the participation of so many One Health advocates from resource challenged areas.

We would like to thank everyone who has contributed to the preparations for this congress, with a special word of thanks to the members of the Congress Programme Committees for their tireless efforts and creative ideas that led to the development of four challenging programme tracks, and also to the session chairs for reviewing so many high-quality abstracts. Finally, we would like to acknowledge the financial support of our funding partners, without which we could not have organized this congress.

We wish you all an inspiring, fruitful and interactive conference.



Prof. Ab Osterhaus  
One Health Platform



Prof. John Mackenzie  
One Health Platform

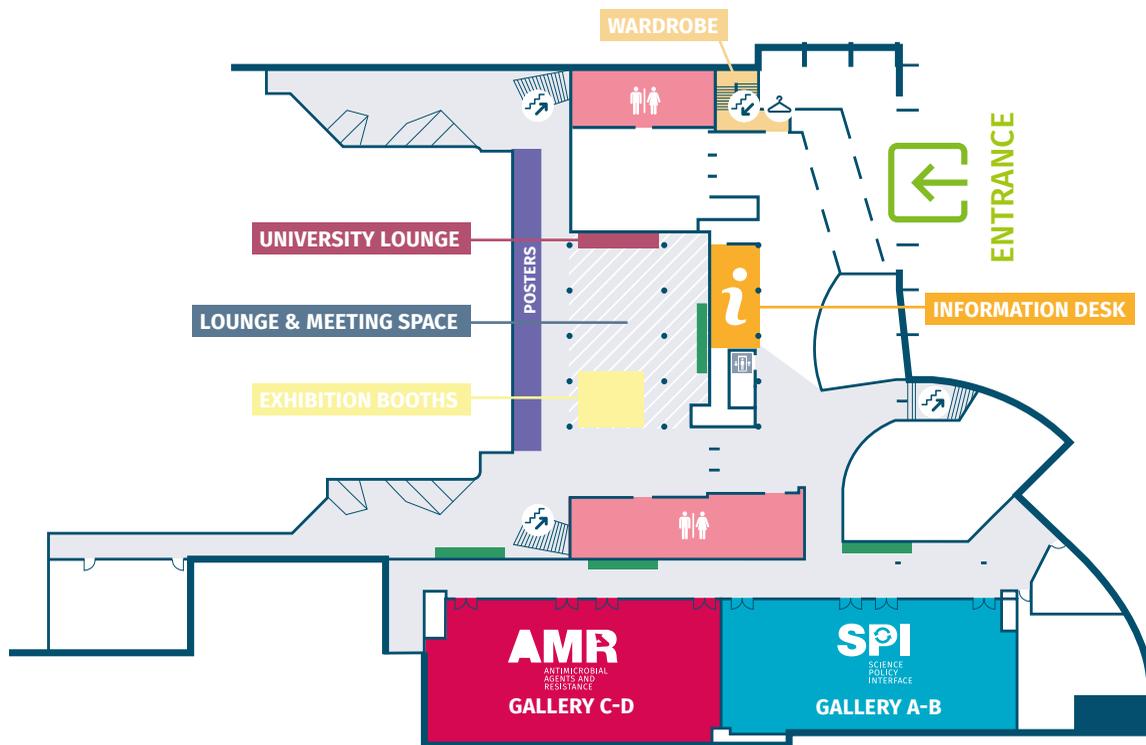


Prof. Karen Chad  
University of Saskatchewan

CO-CHAIRS 5TH INTERNATIONAL ONE HEALTH CONGRESS

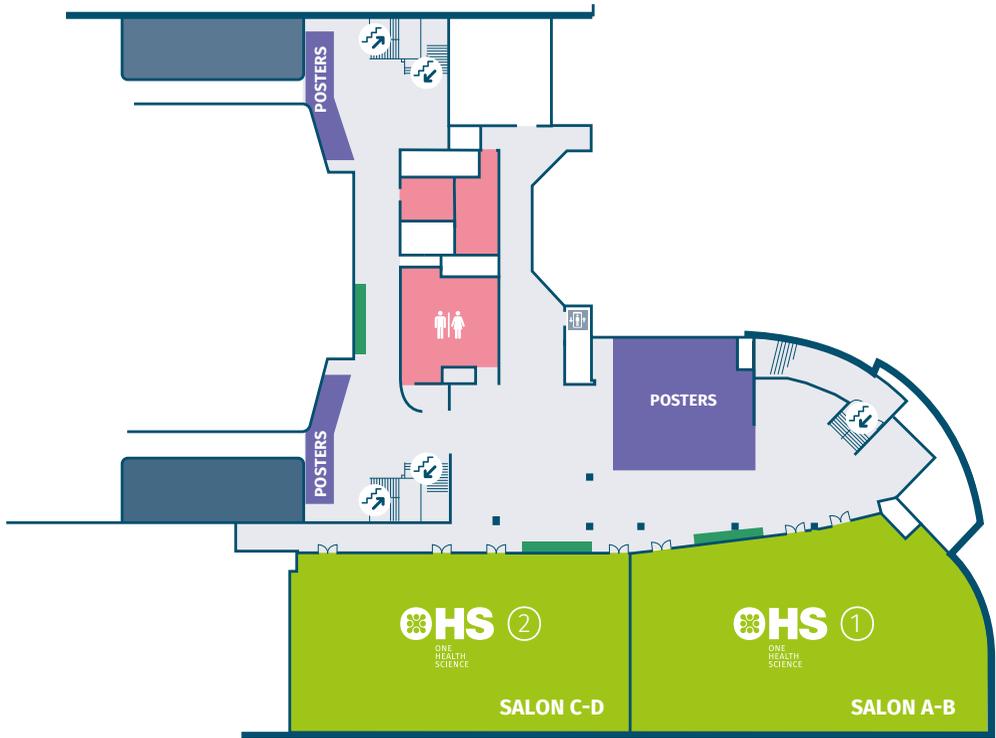
## VENUE FLOOR PLAN

FIRST FLOOR (ground floor)

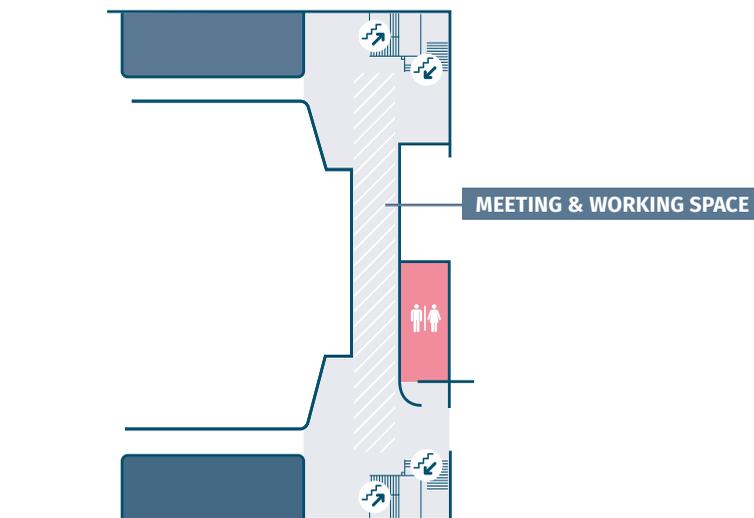


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|---|---|
| <span style="display: inline-block; width: 15px; height: 15px; background-color: #cccccc; border: 1px solid black;"></span> conference zone                 | <span style="display: inline-block; width: 15px; height: 15px; background-color: #2e8b57; border: 1px solid black;"></span> food & drinks   |
| <span style="display: inline-block; width: 15px; height: 15px; background-color: #ff9900; border: 1px solid black;"></span> information & registration desk | <span style="display: inline-block; width: 15px; height: 15px; background: repeating-linear-gradient(45deg, transparent, transparent 2px, #cccccc 2px, #cccccc 4px); border: 1px solid black;"></span> lounge & meeting space |
| <span style="display: inline-block; width: 15px; height: 15px; background-color: #90ee90; border: 1px solid black;"></span> OHS track 1 and 2               | <span style="display: inline-block; width: 15px; height: 15px; background-color: #ffff00; border: 1px solid black;"></span> exhibition booths   |
| <span style="display: inline-block; width: 15px; height: 15px; background-color: #00b0f0; border: 1px solid black;"></span> SPI track                       | <span style="display: inline-block; width: 15px; height: 15px; background-color: #800000; border: 1px solid black;"></span> university lounge   |
| <span style="display: inline-block; width: 15px; height: 15px; background-color: #dc143c; border: 1px solid black;"></span> AMR track                       | <span style="display: inline-block; width: 15px; height: 15px; background-color: #f4a460; border: 1px solid black;"></span> wardrobe  |
| <span style="display: inline-block; width: 15px; height: 15px; background-color: #483d8b; border: 1px solid black;"></span> poster sections                 |   |

SECOND FLOOR



THIRD FLOOR



## PROGRAMME AT A GLANCE

### FRIDAY 22 JUNE 2018

11:00-12:00	CONGRESS PRESS BRIEFING	GALLERY SUITE I
12:00-14:30	SPECIAL PLENARY SESSION-open to non-congress attendees <b>Chronic Wasting Disease-lessons learned from the BSE crisis</b>	SALON C-D
14:30-15:00	COFFEE BREAK	
15:00-17:00	SPECIAL PLENARY SESSION <b>One Health and zoonoses</b>	SALON A-B
17:00-18:30	SPECIAL PLENARY SESSION <b>Potential impact of vaccination on antibiotic usage and antibiotic resistance: the influenza case</b>	SALON A-B
18:30-20:00	OPENING CEREMONY	SALON A-B
20:00-22:00	WELCOME RECEPTION	

### SATURDAY 23 JUNE 2018

07:30-9:00	BREAKFAST PLENARY SESSION			SALON C-D
	<b>Tuberculosis: A One-health problem in underserved communities</b>			
09:15-10:15	KEYNOTE LECTURES			SALON A-B
10:15-10:45	COFFEE BREAK			
10:45-12:30	PARALLEL SESSIONS			
	<b>HS ①</b> SALON A-B Pathogen discovery	<b>HS ②</b> SALON C-D Surveillance and early detection	<b>AMR</b> GALLERY C-D Use of antibiotics in human and animals, in food and agriculture and the link to AMR and environmental impact	<b>SPI</b> GALLERY A-B The impacts of Zoonotic Diseases – Why should OH be of importance to policy makers? Lessons learnt from One Health crises.
12:30-14:00	LUNCH			
	SPECIAL PLENARY SESSION			SALON C-D
	<b>Changing the Future of Epidemic Response &amp; Pandemic Prevention</b>			
14:00-15:45	PARALLEL SESSIONS			
	<b>HS ①</b> SALON A-B Diagnostics	<b>HS ②</b> SALON C-D Intervention strategies	<b>AMR</b> GALLERY C-D Genomic epidemiology / evolution of AMR transmission	<b>SPI</b> GALLERY A-B Addressing zoonotic diseases at the animal-human-ecosystem interface. What are the threats? How to be prepared?

15:45-16:15	COFFEE BREAK			
16:15-18:00	<b>PARALLEL SESSIONS</b>			
	 <b>HS ①</b> <span>SALON A-B</span> Social science and politics	 <b>HS ②</b> <span>SALON C-D</span> Pathogenesis 1	<b>AMR</b> <span>GALLERY C-D</span> Real life applications of whole genome sequencing	<b>SPI</b> <span>GALLERY A-B</span> The drivers of emerging zoonotic diseases
18:00-19:30	<b>POSTER SESSION</b>			

## SUNDAY 24 JUNE 2018

07:30-9:00	<b>BREAKFAST PLENARY SESSION</b> <span style="float: right;">SALON C-D</span>			
	<b>Global Perspectives on Health and Security and the Future of Biological Threat Reduction</b>			
09:15-10:15	<b>KEYNOTE LECTURES</b> <span style="float: right;">SALON A-B</span>			
10:15-10:45	COFFEE BREAK			
10:45-12:30	<b>PARALLEL SESSIONS</b>			
	 <b>HS ①</b> <span>SALON A-B</span> Drivers for emerging diseases 1	 <b>HS ②</b> <span>SALON C-D</span> One health in underprivileged communities	<b>AMR</b> <span>GALLERY C-D</span> Prevalence and surveillance of resistance	<b>SPI</b> <span>GALLERY A-B</span> Resistance to antibiotics and antivirals: challenges for policy makers and scientists
12:30-14:00	LUNCH			
	<b>SPECIAL PLENARY SESSION</b> <span style="float: right;">SALON C-D</span>			
<b>Neglected Zoonotic Diseases in Resource-Poor, Marginalised and Under-Served Communities: Challenges in Infectious Disease Control</b>				
14:00-15:45	<b>PARALLEL SESSIONS</b>			
	 <b>HS ①</b> <span>SALON A-B</span> Drivers for emerging diseases 2	 <b>HS ②</b> <span>SALON C-D</span> Pathogenesis 2	<b>AMR</b> <span>GALLERY C-D</span> Novel strategies for amr interventions / preparedness	<b>SPI</b> <span>GALLERY A-B</span> One health and global health security-disaster risk reduction
15:45-16:15	COFFEE BREAK			

16:15-18:00	<b>PARALLEL SESSIONS</b>			
	 <b>HS ①</b> <span>SALON A-B</span> <b>Vaccines 1</b>	 <b>HS ②</b> <span>SALON C-D</span> <b>Infectious diseases from an ecohealth perspective 1</b>	<b>AMR</b> <span>GALLERY C-D</span> <b>Alternative approaches to tackling resistant infections</b>	<b>SPI</b> <span>GALLERY A-B</span> <b>Making one health operational: the barriers to change and glimmers of hope</b>
18:00-19:30	<b>SPECIAL PLENARY SESSION</b>			<span>SALON C-D</span>
	<b>Emerging and re-emerging infectious diseases: assessment, preparedness and eradication</b>			
20:00-23:00	<b>FAREWELL DINNER</b>			<span>REMAI MODERN ART GALLERY</span>

**MONDAY 25 JUNE 2018**

08:00-08:30	<b>BREAKFAST PLENARY SESSION</b>				<span>SALON C-D</span>
10:00-10:30	COFFEE BREAK				
10:30-12:15	<b>PARALLEL SESSIONS</b>				
	 <b>HS ①</b> <span>SALON A-B</span> <b>Vaccines 2</b>	 <b>HS ②</b> <span>SALON C-D</span> <b>Infectious diseases from an ecohealth perspective 2</b>	<b>AMR</b> <span>GALLERY C-D</span> <b>Rapid diagnostics</b>	<b>SPI</b> <span>GALLERY A-B</span> <b>One Health in underserved, resource-poor and marginalized communities / New strategies call for One Health solutions</b>	
12:15-13:45	<b>PARALLEL TRACKS</b>				
	<span>SALON A-B</span> Late breakers 1	<span>SALON C-D</span> Late breakers 2		<span>GALLERY A-B</span> Late breakers 3	
13:45-14:00	<b>CLOSING CEREMONY</b>				<span>SALON A-B</span>
14:00-14:30	LUNCH				
14:30-15:30	<b>PRESS CONFERENCE - LIVE STREAM</b>				<span>SALON C-D</span>
15:30-	<b>GUIDED EXCURSIONS</b>				



## COMMITTEES

### ORGANIZING EXECUTIVE BOARD

- Ab Osterhaus, RIZ HANNOVER, GERMANY, CO-FOUNDER ONE HEALTH PLATFORM FOUNDATION, CO-CHAIR 5TH INTERNATIONAL ONE HEALTH CONGRESS
- John Mackenzie, CURTIN UNIVERSITY, AUSTRALIA, CO-FOUNDER ONE HEALTH PLATFORM FOUNDATION, CO-CHAIR 5TH INTERNATIONAL ONE HEALTH CONGRESS
- Karen Chad, UNIVERSITY OF SASKATCHEWAN, CANADA, CO-CHAIR 5TH INTERNATIONAL ONE HEALTH CONGRESS
- Chris Vanlangendonck, CO-FOUNDER ONE HEALTH PLATFORM FOUNDATION DIRECTOR OF SEMIOTICS, BELGIUM
- Mark Rweyemamu, DIRECTOR OF THE SOUTHERN AFRICAN CENTRE FOR INFECTIOUS DISEASES AND SURVEILLANCE (SACIDS)
- Bruce Kaplan, ONE HEALTH INITIATIVE
- Baljit Singh, UNIVERSITY OF CALGARY, CANADA
- Doug Freeman, UNIVERSITY OF SASKATCHEWAN, CANADA, CHAIR LOCAL ORGANIZING COMMITTEE 5TH INTERNATIONAL ONE HEALTH CONGRESS
- Kim Ali, ON PURPOSE LEADERSHIP (PCO)

### LOCAL ORGANIZING COMMITTEE

- Doug Freeman, UNIVERSITY OF SASKATCHEWAN, CANADA, CHAIR LOCAL ORGANIZING COMMITTEE 5TH INTERNATIONAL ONE HEALTH CONGRESS
- Volker Gerdts, UNIVERSITY OF SASKATCHEWAN, CANADA
- Vikram Misra, UNIVERSITY OF SASKATCHEWAN, CANADA

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- John Mackenzie, CURTIN UNIVERSITY
- Martyn Jeggo, GEELONG CENTRE FOR EMERGING INFECTIOUS DISEASES, AUSTRALIA
- Amadou Alpha Sall, INSTITUT PASTEUR DE DAKAR, SENEGAL
- Mark Rweyemamu, DIRECTOR OF THE SOUTHERN AFRICAN CENTRE FOR INFECTIOUS DISEASES AND SURVEILLANCE (SACIDS)
- Linfa Wang, DUKE-NUS MEDICAL SCHOOL, SINGAPORE
- William B. Karesh, ECOHEALTH ALLIANCE
- Ottorino Cosivi, WHO-BRAZIL
- Andrew Dobson, PRINCETON UNIVERSITY, USA CASEY
- Barton Behravesh, CDC, USA
- Malik Peiris, UNIVERSITY OF HONG KONG
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- Craig Stephen, UNIVERSITY OF SASKATCHEWAN, CANADA
- Marietjie Venter, UNIVERSITY OF PRETORIA, SA
- Jonna Mazet, UC DAVIS, USA
- Penina Munyua, ONE HEALTH DIRECTOR CDC KENYA
- Sam Iverson, ENVIRONMENT AND CLIMATE CHANGE CANADA

### SCIENTIFIC PROGRAMME COMMITTEE ON ANTIMICROBIAL RESISTANCE

- Giuseppe Cornaglia, VERONA UNIVERSITY, ITALY
- Jorgen Schlundt, NANYANG TECHNOLOGICAL UNIVERSITY, SINGAPORE
- Cheryl Waldner, UNIVERSITY OF SASKATCHEWAN, CANADA
- Gerard Wright, M.G. DEGROOTE, INSTITUTE FOR INFECTIOUS DISEASE RESEARCH, CANADA
- Britta Lassman, INTERNATIONAL SOCIETY FOR INFECTIOUS DISEASES
- Rafael Canton, UNIVERSITY HOSPITAL OF MADRID, SPAIN
- Robert Skov, MVZ SYNLAB, LEVERKUSEN, GERMANY
- Surbhi Malhotra-Kumar, UNIVERSITY OF ANTWERP, BELGIUM
- Cornelia Lass-Floerl, UNIVERSITY OF INNSBRUCK, AUSTRIA
- Laura H. Kahn, PRINCETON UNIVERSITY, USA
- David Heymann, CHATHAM HOUSE LONDON
- Tamika Sims, INTERNATIONAL FOOD INFORMATION COUNCIL
- Jaap Wagenaar, UTRECHT UNIVERSITY, THE NETHERLANDS
- Richard Reid-Smith, CANADIAN INTEGRATED PROGRAM FOR ANTIMICROBIAL RESISTANCE SURVEILLANCE (CIPARS)

### SPI PROGRAMME COMMITTEE

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- Chris Vanlangendonck, DIRECTOR OF SEMIOTICS, BELGIUM
- Peter W.B. Phillips, UNIVERSITY OF SASKATCHEWAN, CANADA
- William B. Karesh, ECOHEALTH ALLIANCE
- Bart Staes, MEMBER OF EUROPEAN PARLIAMENT, BELGIUM
- Dennis Carroll, DIRECTOR GLOBAL HEALTH SECURITY AND DEVELOPMENT, USAID
- Moira McKinnon, MEDICAL PRACTITIONER, CANBERRA, AUSTRALIA



Actively engaging in 40 countries across the globe solving complex health problems



Training future health professionals to continue our work for years to come



Conducting research aimed at informing policy and providing lasting solutions

The **ONE HEALTH INSTITUTE** unites professionals across many disciplines, from veterinarians, physicians, epidemiologists, social scientists, and ecologists to government officials and community leaders, in countries around the world—all with the goal of creating lasting solutions and driving positive change.

The Institute grew out of the UC Davis School of Veterinary Medicine’s deep commitment to the One Health approach and is home to many Centers of Excellence including the Karen C. Drayer Wildlife Health Center and its many projects and programs.

ONE HEALTH  
**OneUCDAVIS**

[www.onehealth.institute](http://www.onehealth.institute)

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-  [onehealth@ucdavis.edu](mailto:onehealth@ucdavis.edu)

## SPEAKER GUIDELINES

All oral presenters in parallel sessions should adhere to a 15 minutes time limit, while late breaker presenters must adhere to a 10 minutes time limit. Following the individual presentations, there will be 5 minutes designated for questions. Because the meeting is multi-tracked and attendees will be moving from track to track, it is imperative that sessions remain on schedule.

The use of Microsoft PowerPoint is obliged to ensure compatibility with the computers at the venue. The use of personal laptop computers is not allowed.

Slide shows will be projected in 16:9 ratio. Slide sets in 4:3 ratio are accepted, but will not be projected optimally.

The oral presentations are collected centrally. To ensure that the meeting runs smoothly, presentations will be loaded on the venue computers in advance. Therefore, the authors are urged to submit their PowerPoint presentations to the congress registration and information desk by noon of the day prior to their session. No edits or updates will be accepted the day of the session. A technician will be available to answer any questions.

**Several conference sessions will be filmed. Footage shall be used for One Health Platform educational purposes only. Kindly inform the session chair if you object to being filmed.**

### CE ACCREDITATION

All authors of accepted oral presentations must include a disclosure slide (first or second slide) in their presentations.

## POSTER AREA

Accepted posters are on display for the full duration of the congress and are open for viewing during official congress hours.

### POSTER MOUNTING

Friday 22 June 2018: 10:00 - 18:00

### POSTER DISMANTLING

Monday 25 June 2018: 15:00 - 17:00

Poster tubes must not be left behind in the exhibition hall.

### POSTER SESSION

A dedicated poster session is scheduled on Saturday evening 23 June from 18:00 until 19:30. This will be your opportunity to interact with the poster authors while enjoying some free wine and cheese.

Poster authors who wish to make their posters electronically available to the congress audience are invited to head to the Congress Information Desk and hand in a pdf of their work.

### ABSTRACT BOOK

Download the congress abstract book from [abstracts.onehealthplatform.com](http://abstracts.onehealthplatform.com)

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# FOR ANIMALS FOR HEALTH FOR YOU



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**zoetis**

## CONFERENCE INFORMATION

### AIRPORT TRANSFER

Shuttle buses will operate between Saskatoon John G. Diefenbaker International Airport and the congress venue on 22 June and 25 June, after the last session. Shuttle services will not operate on other days.

### BADGE

Participants are requested to wear their conference badges at all times when visiting the conference floor and attending social events.

### CONFERENCE INFORMATION DESK

The congress team is ready to assist you throughout the duration of the 5th International One Health Congress. The congress information desk is located in the lobby of TCU place.

#### OPENING HOURS:

Friday 22 June 2018	09:30 – 20:00
Saturday 23 June 2018	08:30 – 18:00
Sunday 24 June 2018	08:30 – 18:00
Monday 25 June 2018	08:30 – 15:30

Out of office hours contact (in case of emergency only) contact Kim Ali at +1 306-220-8077 (mobile).

### EXHIBITION AND UNIVERSITY LOUNGE

The conference hosts a commercial and scientific exhibition as well as a University Lounge. The Lounge is specifically designed for academic institutes to demonstrate their dedication to One Health, engage with other leading universities and share information on courses, post-doc positions and consortia.

The exhibitions are centrally located on the congress floor.

#### OPENING HOURS:

Friday 22 June 2018	13.00 – 22.00 <i>open during welcome reception</i>
Saturday 23 June 2018	08:00 - 19:30
Sunday 24 June 2018	08:00 - 19:30
Monday 25 June 2018	08:00 - 14:30

### LANGUAGE

The official language of the conference is English.

### VENUE

TCU Place  
35 22nd Street East  
SK S7K 0C8  
Saskatoon, Canada  
tcuplace.com

### WIFI

The 5th International One Health Congress is pleased to provide all delegates with complimentary internet access during the conference.

Network: IOHC2018

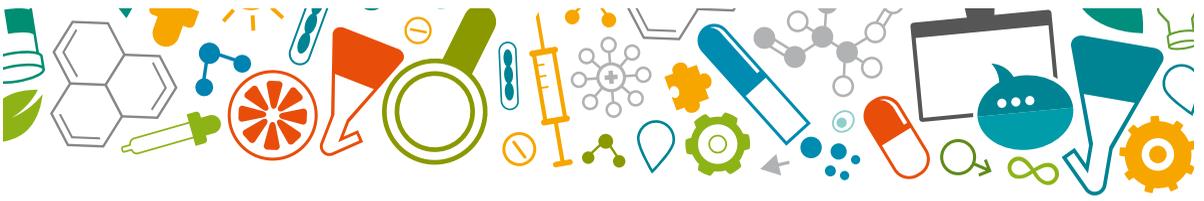
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### SOCIAL MEDIA

Follow the latest conference updates on Twitter: [#OneHealthPF #IOHC18](https://twitter.com/OneHealthPF)

Follow the latest conference updates on Facebook:

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## GENERAL INFORMATION

### SASKATOON

At 246,376 (2016 Census), Saskatoon is the largest city in the province of Saskatchewan and the is the 17th largest census metropolitan area in Canada. It is situated on the banks of the South Saskatchewan River which is crossed by seven bridges within city limits. The altitude of Saskatoon is 481.5 meters above sea level. The census metropolitan area of Saskatoon spans 5,214.52 sq. kilometres.

The City of Saskatoon maintains more than 1,000 hectares of parks and civic open spaces and 75 kilometers of trails throughout the city. The City's Urban Forestry Program is responsible for the management of a tree inventory exceeding 100,000 trees. Saskatoon has 198 parks and 870 hectares of parkland throughout the city, including 156 hectares of river valley parkland.

### BANKS AND CREDIT UNIONS

In the downtown core, financial institutions are generally open from 9am – 5pm Monday to Friday. Some branches in the outlying areas are open until 1pm on Saturdays.

### CLIMATE

The weather in Saskatoon is generally dry and sunny. The average high temperature in June is 23C (73F). Evenings are cool with an average low of 11.5C (53F), generally requiring a light sweater or jacket. The average annual precipitation of 357mm ensures lush gardens, parks, and golf courses.

### CREDIT CARDS / ATM

Automated Teller Machines (ATMs) dispensing CAD dollars are readily available at all host hotels, and at most restaurants and shopping malls. There is a currency exchange office (ICE) in the Saskatoon Airport open Monday to Friday: 4AM-6PM and Saturday –Sunday:4AM-2PM.

### CURRENCY

The currency system is based on Canadian dollars (CAD). U.S. currency can be exchanged at any bank, or credit union. Some businesses will accept U.S. dollars at the exchange rate.

### DRESS CODE

Dress code for the conference, lunches and social events is Business Casual.

### ELECTRICITY

Electrical outlets in Saskatoon provide the same current as the rest of Canada and the United States - 110 volts (60 cycles). Overseas travelers are advised to use an adapter with their small appliances if they are designed for a different standard.

### INFORMATION AND EMERGENCY

For non-emergency calls and general tourist information, contact Tourism Saskatoon at 1(306-242-1206).

The national emergency number is 911.

### HEALTH & ACCIDENT INSURANCE

The conference fee does not include insurance. All participants should arrange for their own insurance. Travelers do not normally require certificates of vaccination or immunization to enter Canada. Visitors from Canada should make sure that they have their provincial health card. It is advisable that all visitors take out a personal medical insurance policy.

Visitors receiving special medical treatment should bring a medical prescription in case they need to purchase particular medication.

### LOCAL TIME

Saskatoon observes Central Standard Time (CST) year round and clocks are not adjusted during Daylight Saving Time which is GMT +6.



# ELSEVIER SUPPORTS

# ONE HEALTH



## ONE HEALTH

A platform to share high quality scientific knowledge on inter- and intra-species pathogen transmission, bringing together leading experts in virology, pathology, immunology, bacteriology, parasitology, veterinary sciences, food safety, mathematical modelling, epidemiology, public health research and emergency preparedness.

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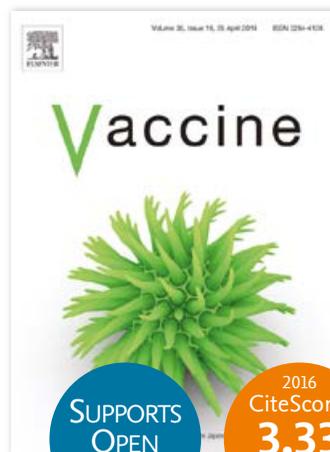
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**PASSPORTS**

All foreign visitors to Canada must possess a valid passport.

**PHARMACIES**

Pharmacies are located throughout Saskatoon and are open during normal shopping hours, Monday to Sunday (9 am – 9 PM). Some pharmacies in outlying areas are open 24 hours.

**RELIGION & WORSHIP**

The main religion practiced in Saskatoon is Christianity (Protestant, Roman Catholic, Christian, Orthodox). Other religions practiced are Buddhist, Islam, Sikh, Hindu, and Judaism.

**SMOKING POLICY**

The City of Saskatoon is a smoke-free city which makes all public places and private clubs smoke-free. This includes bars, nightclubs, bingos, bowling centers, private clubs & restaurants. In addition, smoking is not allowed in outdoor seating areas associated with these establishments or in temporary tent shelters at public events. Please note that smoking is not allowed in any of the conference venues.

**TAXIS**

There are two major taxi companies in Saskatoon - United Cabs – 306-652-2222 and Comfort Cabs – 306-664-6464. UBER and LYFT services are not yet available in Saskatoon.

**TELEPHONE**

The international access code for Canada is +1.

**WATER**

Saskatoon has one the safest water supplies in North America. A clean and safe water supply is one of the top priorities of the citizens of Saskatoon. We take pride in the quality of our water supply and tap water is safe for drinking, cooking, bathing and all other personal uses.



# MASTER OF PUBLIC HEALTH



The **Master of Public Health (MPH)** programme prepares students from diverse backgrounds and experience with the knowledge and competencies for the **effective practice of public health** and to **become the next generation of public health leaders** in order that public health issues and priorities are better understood, accepted and acted upon in Hong Kong, Asia and globally.

#### Modes of Study

- 1-year Full-time
- 2-year Part-time

#### Concentrations

- Public Health Practice
- Epidemiology and Biostatistics
- Control of Infectious Diseases
- Health Economics, Policy and Management

Effective February 3<sup>rd</sup>, 2018, HKU School of Public Health's MPH programme is an applicant for accreditation by the Council on Education for Public Health (CEPH). The accreditation review will address the MPH programme. Other degrees and areas of study offered by this institution will not be included in the unit of accreditation review. For more information on the accrediting process, please visit CEPH's website at <http://ceph.org/>

## Application opens in December of each year

#### Enquiry

All enquiries should be directed to the MPH Office of the School of Public Health.

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✉ [mphsph@hku.hk](mailto:mphsph@hku.hk)

🌐 <http://mph.sph.hku.hk>

📍 G/F, Patrick Manson Building (North Wing), 7 Sassoon Road, Pokfulam, Hong Kong

📘 HKU Master of Public Health



## REFRESHMENTS & FUNCTIONS

### COFFEE BREAKS

Coffee and tea will be served during morning and afternoon conference session breaks.

#### COFFEE BREAK HOURS:

Friday 22 June 2018	14:30 – 15:00
Saturday 23 June 2018	10:15 – 10:45 15:45 – 16:15
Sunday 24 June 2018	10:15 – 10:45 15:45 – 16:15
Monday 25 June 2018	10:00 – 10:30

### LUNCH

Lunchboxes are provided from various distribution points throughout the congress venue. For those who are attending the special plenary sessions over lunch time, lunch boxes will be distributed at the entrance of the meeting room.

#### LUNCH HOURS:

Saturday 23 June 2018	12:30 – 14:00
Sunday 24 June 2018	12:30 – 14:00
Monday 25 June 2018	14:00 – 14:30

### WELCOME RECEPTION

Friday 22 June 2018	20:00 – 22:00
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Directly following the Opening Ceremony, the Welcome Reception will be held on the first and second conference floors. Dress code is smart casual. You should wear your delegate name badge.

### FAREWELL DINNER

Monday 25 June 2018	20:00 – 23:00
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The Farewell Dinner is an official part of the congress programme, with the dress code being as per the Welcome Reception. Please wear your name badge.

The Farewell Dinner will be held outside the congress venue in the Remai Modern Art Gallery, which has just opened its doors to the public in October 2017. This brand-new museum of modern and contemporary art houses the most comprehensive collection of linocuts by Pablo Picasso (1881-1973).



In addition to the daily conference coffee breaks and lunch, both the Welcome Reception and Farewell Evening are included in the registration fee. Participants of the Breakfast Plenary Sessions on Saturday 23rd, Sunday 24th and Monday 25th June will be offered take away coffee and Danish at the entrance of the meeting room.

# One Health Outlook

*One Health Outlook* is a new open access journal published by BMC in collaboration with the One Health Platform. Edited by Ab Osterhaus *One Health Outlook* will have a broad scope to encompass all aspects of One Health.

Education and bringing people from different backgrounds together is what One Health is all about, and by removing barriers for readers, Open Access is ideally placed to promote the One Health ethos.

*One Health Outlook* welcomes papers from researchers looking at the interaction between human, animal, plant and environmental health; agriculture, food and water safety and soil health; disease surveillance, prevention and response, both infectious and chronic diseases; antimicrobial resistance; environmental toxicology detection and response; public policy and regulation; education, communications and outreach.

**Submit your paper today at**  
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## ABOUT THE ORGANIZERS

The 5th International One Health Congress is a co-organization of the One Health Platform Foundation and the University of Saskatchewan.



The One Health Platform is a strategic forum of stakeholders and a One Health reference network that aims to enhance our understanding of zoonoses, emerging infectious diseases and antimicrobial resistance, including the ecological and environmental factors which impact on these diseases. The One Health Platform engages in collaborative partnerships with existing international governmental and non-governmental organizations and institutions to set up a framework for information-sharing, cooperation and awareness raising activities.

More info about the One Health Platform is to be found on [www.onehealthplatform.com](http://www.onehealthplatform.com)

Join the One Health Platform on Facebook and Twitter



With more than 20,000 students and 7,000 faculty and staff, the University of Saskatchewan is one of Canada's leading medical-doctoral research-intensive universities, and offers the widest array of human and animal health science programs in the country. It is unique in Canada in having faculties, schools, institutes and centres that deliver undergraduate and graduate programs and coordinate integrative research in all areas related to the health of people, animals and the environment.

Efforts at the UofS to engage incoming students to professional programs in human, animal and environmental health have resulted in the One Health Club, an active group of university students interested in multidisciplinary collaboration. Their activities and projects bring together students from different colleges in order to network, and apply a systematic, collaborative approach to solving local complex problems. The club routinely organizes seminars and training sessions and coordinates clinics to deliver integrated health care to remote communities. [www.facebook.com/groups/onehealthinitiative/](https://www.facebook.com/groups/onehealthinitiative/)

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And Eastern Africa

## FULL CONGRESS PROGRAMME

FRIDAY 22 JUNE 2018

11:00-12:00	<b>CONGRESS PRESS BRIEFING</b>	GALLERY SUITE 1
CONGRESS CO-CHAIRS: <b>Prof. Ab Osterhaus</b> AND <b>Prof. John Mackenzie</b> The congress press briefing is open for members of the press attending the congress. Congress co-chairs Prof. Ab Osterhaus and Prof. John Mackenzie will provide an overview of the congress programme, highlighting key lectures and elaborating on major topics. The scope and objectives of the congress will be put in the wider framework of the threats of emerging and re-emerging diseases and the challenges the world faces when addressing antimicrobial resistance. Members of the press receive detailed information about speakers' backgrounds and expertises and on how to contact them during the congress. The press briefing will not be recorded and can therefore not be shared with journalists who are not attending the congress.		
12:00-14:30	<b>SPECIAL PLENARY SESSION-open to non-congress attendees</b>	SALON C-D
<b>Chronic Wasting Disease-lessons learned from the BSE crisis</b>		
CHAIR: <b>Adriano Aguzzi</b> , DIRECTOR INSITUTE OF NEUROPATHOLOGY, UNIVERSITY HOSPITAL ZÜRICH, SWITZERLAND		
1. First evidence of intracranial and peroral transmission of Chronic Wasting Disease into Cynomolgus macaques: a work in progress <b>Stephanie Czub</b> , CANADIAN FOOD INSPECTION AGENCY, ALBERTA, CANADA		
2. Battling Chronic Wasting Disease in Norway: an update on management and disease development after two years on the map <b>Carlos Gonçalo das Neves</b> , HEAD OF FOOD SAFETY & EMERGING HEALTH THREATS, NORWEGIAN VETERINARY INSTITUTE, NORWAY		
3. Detection of prions associated to Chronic Wasting Disease in animal blood and in association to environmental materials <b>Claudio Soto</b> , DIRECTOR THE GEORGE AND CYNTHIA MITCHELL CENTER, UNIVERSITY OF TEXAS/USDA, USA		
4. Investigations of Chronic Wasting Disease strains and transmission barriers <b>Glenn Telling</b> , PRION RESEARCH CENTER, COLORADO STATE UNIVERSITY, USA		
5. BSE, CWD and alternatively folded forms of the cellular 1 prion protein, PrPc <b>David Westaway</b> , CENTRE FOR PRIONS AND PROTEIN FOLDING DISEASES, UNIVERSITY OF ALBERTA, CANADA		
6. Why do we have a prion protein? <b>Adriano Aguzzi</b> , DIRECTOR INSITUTE OF NEUROPATHOLOGY, UNIVERSITY HOSPITAL ZÜRICH, SWITZERLAND		
7. No Accident: Public Policy and Chronic Wasting Disease <b>Darrel Rowledge</b> , DIRECTOR ALLIANCE FOR PUBLIC WILDLIFE, CANADA		
14:30-15:00	COFFEE BREAK	
15:00-17:00	<b>SPECIAL PLENARY SESSION</b>	SALON A-B
<b>One Health and zoonoses</b>		
CHAIR: <b>Mike Ryan</b> , WORLD HEALTH ORGANIZATION, GENEVA, SWITZERLAND		

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FRIDAY 22 JUNE 2018

17:00-18:30	<p><b>SPECIAL PLENARY SESSION</b> <span style="float: right;"><b>SALON A-B</b></span></p> <p><b>Potential impact of vaccination on antibiotic usage and antibiotic resistance: the influenza case</b></p> <p>CHAIRS: <b>Jorgen Schlundt</b>, NANYANG TECHNOLOGICAL UNIVERSITY, SINGAPORE <b>Ab Osterhaus</b>, RIZ HANNOVER, GERMANY</p> <ol style="list-style-type: none"> <li>1. Quantifying the problem of antibiotic resistance <b>Jorgen Schlundt</b>, NANYANG TECHNOLOGICAL UNIVERSITY, SINGAPORE</li> <li>2. The role of diagnostics and viral vaccines in reducing antibiotic resistance SPEAKER TO BE CONFIRMED</li> <li>3. Assessing the full economic value of vaccines in reducing AMR <b>Jonathan Rushton</b>, PROFESSOR OF ANIMAL HEALTH AND FOOD SYSTEMS ECONOMICS, UNIVERSITY OF LIVERPOOL, UK</li> <li>4. Vaccination and antibiotic resistance in developing countries <b>Mishal Khan</b>, CENTRE ON GLOBAL HEALTH SECURITY AT CHATHAM HOUSE, UK</li> <li>5. The influenza case: a systematic literature review on the impact of influenza vaccination on antibiotic use <b>Ab Osterhaus</b>, RIZ HANNOVER, GERMANY</li> </ol>
18:30-20:00	<p><b>OPENING CEREMONY</b> <span style="float: right;"><b>SALON A-B</b></span></p> <ul style="list-style-type: none"> <li>▪ Welcome and opening remarks by the congress organizers: Prof. <b>John Mackenzie</b>, <b>Ab Osterhaus</b> and <b>Karen Chad</b></li> </ul> <p>OPENING LECTURES:</p> <ol style="list-style-type: none"> <li>1. <b>Tedros Adhanom Ghebreyesus</b>, WORLD HEALTH ORGANIZATION (VIDEO STATEMENT)</li> <li>2. <b>Theresa Tam</b>, CHIEF PUBLIC HEALTH OFFICER OF CANADA</li> <li>3. <b>Jaspinder Komal</b>, EXECUTIVE DIRECTOR, ANIMAL HEALTH DIRECTORATE, CFIA; CVO AND OIE DELEGATE FOR CANADA</li> <li>4. <b>Rimma Driscoll</b>, VICE PRESIDENT, BUSINESS DEVELOPMENT AND ALLIANCES AT ZOETIS</li> </ol> <p>KEYNOTE ADDRESS:</p> <ul style="list-style-type: none"> <li>▪ One Health for a Challenged World by Nobel Laureate by <b>Peter Doherty</b>, UNIVERSITY OF MELBOURNE, AUSTRALIA</li> </ul>
20:00-22:00	<p><b>WELCOME RECEPTION</b></p>

## SATURDAY 23 JUNE 2018

07:30-9:00	<b>BREAKFAST PLENARY SESSION</b>	<b>SALON C-D</b>
<b>Tuberculosis: A One-health problem in underserved communities</b>		
ORGANIZED BY THE UNIVERSITY OF SASKATCHEWAN		
1. Tuberculosis in underserved communities in Canada		
<b>Vern Hoepfner</b> , UNIVERSITY OF SASKATCHEWAN, CANADA		
2. TAIMA TB - A partnership with Inuit to stop transmission of tuberculosis		
<b>Gonzalo Alvarez</b> , UNIVERSITY OF OTTAWA, CANADA		
3. One health and tuberculosis - comparison of M. tuberculosis and M. bovis		
<b>Steve Gordon</b> , UNIVERSITY COLLEGE DUBLIN, IRELAND		
4. Novel approaches to tuberculosis vaccine development using novel animal models		
<b>Jeff Chen</b> , VIDO-INTERVAC, CANADA		
09:15-10:15	<b>KEYNOTE LECTURES</b>	<b>SALON A-B</b>
CHAIR: <b>Rita Colwell</b> , JOHNS HOPKINS UNIVERSITY BLOOMBERG SCHOOL OF PUBLIC HEALTH, USA		
1. One Health as a Pillar of Policy, <b>Bill Karesh</b> , ECOHEALTH ALLIANCE		
2. Past, present and future of AMR, <b>Giuseppe Cornaglia</b> , UNIVERSITY OF VERONA, ITALY		
10:15-10:45	COFFEE BREAK	
10:45-12:30	<b>PARALLEL SESSIONS</b>	
<b>HS ONE HEALTH SCIENCE 1</b>		<b>SALON A-B</b>
<b>Pathogen discovery</b>		
CHAIR: <b>Linfa Wang</b> , DUKE-NUS MEDICAL SCHOOL, SINGAPORE		
CO-CHAIR: <b>Peng ZHOU</b> , CHINESE ACADEMY OF SCIENCES		
1. Plagiorchis sp. in small mammals of Senegal: an emerging food-borne trematodiasis?		
<b>Stefano Catalano</b> , ROYAL VETERINARY COLLEGE, UNIVERSITY OF LONDON		
2. Zika Virus Exposure In Malaysia; A Preliminary Study On Seroprevalence Among Local Population		
<b>Wan Nabilatul Huda Wan Ghazali</b> , INSTITUTE FOR MEDICAL RESEARCH, MALAYSIA		
3. A new concept for de-novo detection of viral pathogens with adaptive diagnostics and integrated data analysis approaches results in the recent discovery of two novel viruses		
<b>Leonie Franziska Forth</b> , FRIEDRICH-LOEFFLER-INSTITUT, GERMANY		
4. Novel orthobunyavirus identified in an African child with severe encephalopathy		
<b>Arthur Wouter Dante Edridge</b> , ACADEMIC MEDICAL CENTER, THE NETHERLANDS		
5. Seroprevalence of West Nile virus in wild birds in Bangladesh		
<b>Ausraful Islam</b> , ICDDR,B-BANGLADESH		



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SATURDAY 23 JUNE 2018

10:45-12:30

**HS ONE HEALTH SCIENCE 2**

SALON C-D

**Surveillance and early detection**

CHAIR: **Ab Osterhaus**, RIZ HANNOVER, GERMANY

CO-CHAIR: **Nistara Randhawa**, ONE HEALTH INSTITUTE UC DAVIS, USA

1. One Health-oriented outbreak response in Cameroon: A case study of the 2016 Monkeypox outbreak response in Cameroon  
**Moctar Mouiche**, MOSAIC, CAMEROON
2. Zoonotic Enteric Parasites in Humans, Animals, and Drinking Water in Mongolian Households and Their Associated Risk Factors  
**Anu Davaasuren**, THE NATIONAL CENTER FOR COMMUNICABLE DISEASES, MOH, ULAANBAATAR, MONGOLIA
3. Evidence of silent infection of domestic pigs with Highly Pathogenic Avian Influenza H5N1 and H1N1pdm09 in 'hot spot' Nigeria: Is a pandemic virus already in the pipeline?  
**Clement Adebajo Meseko**, NATIONAL VETERINARY RESEARCH INSTITUTE, NIGERIA
4. Phylogenetic analysis of viruses detected in mosquitoes, horses and humans supports epidemiological data indicating two different geographical origins for epidemics of encephalitis due to Murray Valley encephalitis virus  
**David William Smith**, PATHWEST LABORATORY MEDICINE WA, AUSTRALIA
5. Prevalence and characterization of Brucella spp. in slaughter animals in Gauteng Province abattoirs and assessment of zoonotic risk factors posed to abattoir workers  
**Francis Babaman Kolo**, UNIVERSITY OF PRETORIA, SOUTH AFRICA

10:45-12:30

**AMR ANTIMICROBIAL AGENTS AND RESISTANCE**

GALLERY C-D

**Use of antibiotics in human and animals, in food and agriculture and the link to AMR and environmental impact**

CHAIR: **Jorgen Schlundt**, NANYANG TECHNOLOGICAL UNIVERSITY, SINGAPORE

CO-CHAIR: **Jaap Wagenaar**, UTRECHT UNIVERSITY, THE NETHERLANDS

1. Reduced and responsible use of antibiotics in food-producing animal in The Netherlands  
**Christianne J.M. Bruschke**, MINISTRY OF AGRICULTURE, NATURE AND FOOD QUALITY, THE NETHERLANDS
2. Antimicrobial resistance in wildlife species: the potential for sentinel surveillance in a ONE HEALTH perspective  
**Carlos G. Das Neves**, NORWEGIAN VETERINARY INSTITUTE, NORWAY
3. Comparative human exposure to antimicrobial-resistant Campylobacter species, Escherichia coli, Salmonella enterica from food animals using integrated assessment modelling: A farm to fork approach  
**Colleen Patricia Murphy**, PUBLIC HEALTH AGENCY OF CANADA
4. Assessing Impacts of Antibiotic Therapy in Neonatal Dairy Calves on Gut and Animal Health  
**Olivia Char Lottes**, WASHINGTON STATE UNIVERSITY, USA
5. Prevalence and Antimicrobial Resistance profile of Salmonella spp. in retail meats of Super Shop: a food safety risk  
**Mohammed Abdus Samad**, BANGLADESH LIVESTOCK RESEARCH INSTITUTE, BANGLADESH

SATURDAY 23 JUNE 2018

10:45-12:30

**SPI** SCIENCE POLICY INTERFACE

GALLERY A-B

**The impacts of Zoonotic Diseases – Why should OH be of importance to policy makers? Lessons learnt from One Health crises.**CHAIR: **John Mackenzie**, CURTIN UNIVERSITY, AUSTRALIACO-CHAIR: **Casey Barton-Beravesh**, CDC, USA

1. New World Screwworm Eradication in South Florida – A One Health Success Story  
**Lisa Conti**, ONE HEALTH INITIATIVE
2. Rift Valley Fever as a public health emergency  
**Pierre Formenty**, TEAM LEAD – VIRAL HAEMORRHAGIC FEVERS (VHF), WORLD HEALTH ORGANIZATION
3. Ebola: what went wrong and where do we go now?  
**Simon Mardel**, MANCHESTER UNIVERSITY NHS FOUNDATION TRUST
4. Lessons learned from the H1N1 influenza pandemic: are we prepared for a new outbreak  
**Theresa Tam**, CHIEF PUBLIC HEALTH OFFICER OF CANADA
5. How can we improve global response strategies?  
**Patrick Drury**, WORLD HEALTH ORGANIZATION

12:30-14:00

LUNCH

SPECIAL PLENARY SESSION

SALON C-D

**Changing the Future of Epidemic Response & Pandemic Prevention**CHAIR: **Jonna AK Mazet**, UC DAVIS, USA

1. Shifting the response paradigm from reactive to proactive  
**Jonna AK Mazet**, UC DAVIS, USA
2. Rapid response & control lessons from Ebola in DRC  
**Charles Kumakamba**, DEMOCRATIC REPUBLIC OF CONGO
3. Nipah in Bangladesh: when epidemics become endemic  
**Ariful Islam**, ICDDR,B - BANGLADESH
4. Accurately forecasting viral spread  
**Nistara Randhawa**, ONE HEALTH INSTITUTE UC DAVIS, USA
5. Strategy to understand new high consequence viral species  
**Tracey Goldstein**, ONE HEALTH INSTITUTE UC DAVIS, USA
6. The Global Virome Project: assessing & mitigating risk from emerging zoonotic threats  
**Jonna AK Mazet**, UC DAVIS, USA

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SATURDAY 23 JUNE 2018

14:00-15:45

## PARALLEL SESSIONS

### HS ONE HEALTH SCIENCE 1

SALON A-B

#### Diagnostics

CHAIR: **Martyn Jeggo**, GEELONG CENTRE FOR EMERGING INFECTIOUS DISEASES, AUSTRALIA

CO-CHAIR: **Dang Xuan Sinh**, CENTER FOR PUBLIC HEALTH AND ECOSYSTEM RESEARCH, HANOI, VIETNAM

1. Recombinant techniques to address the challenges in development of assays for diagnosis and surveillance of emerging zoonotic diseases  
**Felicity Jane Burt**, UNIVERSITY OF THE FREE STATE, SOUTH AFRICA
2. Comparison of two RdRp PCR assays for the detection of MERS related Coronaviruses  
**Sininat Petcharat**, KING CHULALONGKORN MEMORIAL HOSPITAL, THAILAND
3. The accuracy of pre-vaccination screening for Q fever and the extent of exposure – Bayesian latent class analysis  
**Solomon Meseret Woldeyohannes**, UNIVERSITY OF QUEENSLAND, AUSTRALIA
4. Reproducibility of results and performance of TB diagnostics in East Africa Public Health Laboratory Networking Project sites in Kenya: Implication on Policy Resolution for Strategic TB Diagnosis  
**Willie Abela Githui**, KENYA MEDICAL RESEARCH INSTITUTE
5. Development of lateral flow immunochromatographic test for multiple detection of Salmonella Species in poultry food product  
**Rafik Sayed**, CENTRAL LABORATORY FOR EVALUATION OF VETERINARY BIOLOGICS, EGYPT

14:00-15:45

### HS ONE HEALTH SCIENCE 2

SALON C-D

#### Intervention strategies

CHAIR: **Sarah Cleaveland**

CO-CHAIR: **Rachel Hopper**, LIVERPOOL SCHOOL OF TROPICAL MEDICINE, UK

1. Adapting the determinants of health perspectives to developing and implementing integrated priorities to address social and ecological expectations for fisheries and community health  
**Craig Stephen**, UNIVERSITY OF SASKATCHEWAN, CANADA
2. Control versus elimination of *Taenia solium* in eastern Zambia: Preliminary assessment of a two-year interventional program in the Katete and Sinda districts in the Eastern Province of Zambia  
**Emma Clare Hobbs**, INSTITUTE OF TROPICAL MEDICINE, ANTWERP, BELGIUM
3. An integrated human-animal health approach to reduce the disease burden of psittacosis  
**Lenny Hogerwerf**, NATIONAL INSTITUTE FOR PUBLIC HEALTH AND THE ENVIRONMENT, THE NETHERLANDS
4. Factors associated with improved uptake of Johne's Disease control mechanisms on Australian dairy farms: Regulatory insights from evolving control strategies  
**Paul Douglas Burden**, UNIVERSITY OF CALGARY, CANADA
5. Harm reduction: A strategy for One Health action in the face of uncertainty and conflict  
**Christa Gallagher**, ROSS UNIVERSITY SCHOOL OF VETERINARY MEDICINE. ST. KITTS AND NEVIS

SATURDAY 23 JUNE 2018

14:00-15:45

**AMR** ANTIMICROBIAL AGENTS AND RESISTANCE

GALLERY C-D

**Genomic epidemiology / evolution of AMR transmission**CHAIR: **Robert Skov**, MVZ SYNLAB, LEVERKUSEN, GERMANYCO-CHAIR: **Jesper Larsen**, STATENS SERUM INSTITUT, DENMARK

1. The human resistome within the Dutch pork production chain, a metagenome-wide study among farmers and slaughterhouse workers  
**Liese Van Gompel**, UTRECHT UNIVERSITY, THE NETHERLANDS
2. Genomic and evolutionary analysis of Clostridium difficile sequence type 11: a genetically diverse lineage of significant One Health importance  
**Daniel R Knight**, UNIVERSITY OF WESTERN AUSTRALIA, AUSTRALIA
3. Whole genome sequencing reveals limited contribution of non-intensive chicken farming to extended-spectrum beta-lactamase producing Escherichia coli colonization in humans in southern Vietnam  
**Trung Nguyen Vinh**, OXFORD UNIVERSITY CLINICAL RESEARCH UNIT, VIETNAM
4. Associations between antimicrobial use and the fecal resistome on broiler farms in nine European countries  
**Roosmarijn Luiken**, UTRECHT UNIVERSITY, THE NETHERLANDS
5. Epidemic clones of community-acquired methicillin-resistant Staphylococcus aureus in slaughter pigs, Cuba  
**Michel Baez Arias**, NATIONAL CENTRE OF ANIMAL AND PLANT HEALTH (CENSA), CUBA

14:00-15:45

**SPI** SCIENCE POLICY INTERFACE

GALLERY A-B

**Addressing zoonotic diseases at the animal-human-ecosystem interface. What are the threats? How to be prepared?**CHAIR: **Ab Osterhaus**, RIZ HANNOVER, GERMANYCO-CHAIR: **Doug Freeman**, UNIVERSITY OF SASKATCHEWAN

1. Avian Influenza Surveillance in Live Birds Markets in Thailand  
**Ong-orn Prasarnphanich**, UNITED STATES CENTERS FOR DISEASE CONTROL AND PREVENTION SOUTHEAST ASIA REGIONAL OFFICE
2. Challenges in Complexity: How Brucellosis Thrives in the Science-Policy Interface Space  
**Darrell Abernethy**, FACULTY OF VETERINARY SCIENCE, UNIVERSITY OF PRETORIA
3. Achieving Rabies Zero by 2030  
**Waqas Ahmad**, UNIVERSITY OF VETERINARY AND ANIMAL SCIENCES, PAKISTAN
4. Future Earth's Top Ten Challenges for One Health  
**Peter Daszak and William B. Karesh**, ECOHEALTH ALLIANCE

15:45-16:15

COFFEE BREAK

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## SATURDAY 23 JUNE 2018

16:15-18:00	<b>PARALLEL SESSIONS</b>
	<b>HS ONE HEALTH SCIENCE 1</b> <span style="float: right;">SALON A-B</span>
	<b>Social science and politics</b>
	<p>CHAIR: <b>Jonathan Rushton</b>, UNIVERSITY OF LIVERPOOL, UK</p> <p>CO-CHAIR: <b>Mieghan Bruce</b>, MURDOCH UNIVERSITY, AUSTRALIA</p> <ol style="list-style-type: none"> <li>1. Antimicrobials In Society: A One Health Approach in Kampala, Uganda <b>Laurie Denyer Willis</b>, LONDON SCHOOL OF HYGIENE AND TROPICAL MEDICINE, UK</li> <li>2. (Re)Claiming Water Stewardship in a Changing Climate – Learning from the Margins <b>Corinne J Schuster-Wallace</b>, MCMASTER UNIVERSITY, CANADA</li> <li>3. MAN-IMAL: An experimental One Health degree program around animal-man-food <b>Francois Meurens</b>, ONIRIS-NANTES ATLANTIC NATIONAL COLLEGE OF VETERINARY MEDICINE, FRANCE</li> <li>4. Human Behavioural Research at the Animal-Human Interface: Hunting and Trading of Bushmeat in Lao PDR <b>Soubanh Silithammavong</b>, METABIOTA, USA</li> <li>5. Evaluation Of One Health-Ness: Insights Into Interdisciplinary And Cross-Sectoral Integration <b>Simon Rüegg</b>, UNIVERSITY OF ZURICH, SWITZERLAND</li> </ol>
16:15-18:00	<b>HS ONE HEALTH SCIENCE 2</b> <span style="float: right;">SALON C-D</span>
	<b>Pathogenesis 1</b>
	<p>CHAIR: <b>Marietjie Venter</b>, UNIVERSITY OF PRETORIA, SA</p> <p>CO-CHAIR: <b>Felicity Burt</b>, UNIVERSITY OF THE FREE STATE, SOUTH AFRICA</p> <ol style="list-style-type: none"> <li>1. Cytokine patterns in Hemorrhagic Fever with Renal syndrome and Crimean-Congo Hemorrhagic Fever <b>Katerina Tsergouli</b>, ARISTOTLE UNIVERSITY OF THESSALONIKI, GREECE</li> <li>2. Replication of naturally occurring MERS-CoV protein 4a deletion variants in vitro and in vivo <b>Mart Matthias Lamers</b>, ERASMUS MC, THE NETHERLANDS</li> <li>3. The effect of antiretroviral naïve HIV-1 infection on the ability of Natural Killer cells to produce IFN-<math>\gamma</math> upon exposure to Plasmodium falciparum- infected Erythrocytes <b>Carole Stephanie Sake Ngane</b>, UNIVERSITY OF YAOUNDÉ I, CIRCB, CAMEROON</li> <li>4. Inflammatory effects of glyphosate and endotoxin exposure on human alveolar epithelial cells <b>Upkardeep Singh</b>, UNIVERSITY OF SASKATCHEWAN, CANADA</li> <li>5. Dynamic interaction of rabies virus with endosomes and end binding partners (EB3 and p140cap) of Cytoskeleton <b>Waqas Ahmad</b>, UNIVERSITY OF VETERINARY AND ANIMAL SCIENCES, JHANG CAMPUS, PAKISTAN</li> </ol>

SATURDAY 23 JUNE 2018

16:15-18:00

**AMR** ANTIMICROBIAL AGENTS AND RESISTANCE

GALLERY C-D

**Real life applications of whole genome sequencing**CHAIR: **Roberto Melano**, PUBLIC HEALTH ONTARIO, CANADA

1. Comparative Genomics of Vancomycin-Resistant Enterococcus spp. isolated from Wastewater Treatment Plants  
**Haley Ann Sanderson**, QUEEN'S UNIVERSITY, CANADA
2. Integrating whole genome sequencing data into quantitative microbial risk assessment modeling: a case study for Salmonella Heidelberg resistant to third-generation cephalosporins in Canadian broiler chicken production  
**Lucie Collineau**, PUBLIC HEALTH AGENCY OF CANADA
3. Whole Genome Sequence Profiling of Antibiotic Resistant Staphylococcus aureus isolates from Livestock and Farm Attendants in Ghana  
**Beverly Egyir**, NOGUCHI MEMORIAL INSTITUTE FOR MEDICAL RESEARCH, GHANA
4. Phenotypic and genomic analysis of antimicrobial resistant E. coli isolated from ready-to-eat food in Singapore  
**Siyao Guo**, NANYANG TECHNOLOGICAL UNIVERSITY FOOD TECHNOLOGY CENTRE, SINGAPORE
5. Antibiotic use and biosecurity in pig farming are determinants for antimicrobial resistance, a metagenome-wide association study in nine European countries  
**Liese van Gompel**, UTRECHT UNIVERSITY, THE NETHERLANDS

16:15-18:00

**SPi** SCIENCE POLICY INTERFACE

GALLERY A-B

**The drivers of emerging zoonotic diseases**CHAIR: **Moira McKinnon**, MEDICAL PRACTITIONER, CANBERRA, AUSTRALIA

1. The migration, climate change, and vector-borne disease nexus  
**Kanya C. Long**, WORLD BANK
2. AMR containment and Prevention considering the Drivers of EID in Thailand  
**Suwit Wibulpolprasert**, MINISTRY OF PUBLIC HEALTH, THAILAND
3. The Long and Hard Road to Evidence Based policy  
**Bonnie Henry**, PROVINCIAL HEALTH OFFICER BRITISH COLUMBIA, CANADA
4. Communicating the evidence to policy makers and populations. Who is the right audience?  
**Mark Rweyemamu**, DIRECTOR OF THE SOUTHERN AFRICAN CENTRE FOR INFECTIOUS DISEASES AND SURVEILLANCE (SACIDS)

18:00-19:30

**POSTER SESSION**

- Opportunity for congress delegates to interact with poster authors
- Wine and cheese, offered by the organizers

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## SUNDAY 24 JUNE 2018

07:30-9:00	<p><b>BREAKFAST PLENARY SESSION</b> <span style="float: right;"><b>SALON C-D</b></span></p> <p><b>Global Perspectives on Health and Security and the Future of Biological Threat Reduction</b></p> <p>ORGANIZED BY THE WEAPONS THREAT REDUCTION PROGRAM, GLOBAL AFFAIRS CANADA</p> <p>CHAIR: <b>Trevor Smith</b>, GLOBAL AFFAIRS CANADA</p> <ol style="list-style-type: none"> <li>1. Zoonotic disease outbreaks: natural infection or deliberate release? A quick review of the likely threats for pandemics or deliberate release. <b>SPEAKER TO BE CONFIRMED</b></li> <li>2. With IHR and the GHSA, are we prepared for public health emergencies including deliberate release? <b>Maurizio Barbeschi</b>, HEAD OF THE WHO, HEALTH EMERGENCIES PROGRAMME, SWITZERLAND (TBC)</li> <li>3. Biological threat reduction strategies <b>Keith Hamilton</b>, SCIENTIFIC AND TECHNICAL DEPARTMENT, WORLD ORGANISATION FOR ANIMAL HEALTH (OIE), FRANCE</li> <li>4. Developing procedural updates – Integration of scientific advances in the field of biological threat reduction <b>SPEAKER TO BE CONFIRMED</b></li> </ol>
09:15-10:15	<p><b>KEYNOTE LECTURES</b> <span style="float: right;"><b>SALON A-B</b></span></p> <p>CHAIR: <b>Peninah Munyua</b>, CDC KENYA</p> <ol style="list-style-type: none"> <li>1. <b>Cristina Romanelli</b>, CONVENTION ON BIOLOGICAL DIVERSITY (CBD)</li> <li>2. <b>Michael Ryan</b>, WORLD HEALTH ORGANIZATION</li> </ol>
10:15-10:45	<p>COFFEE BREAK</p>
10:45-12:30	<p><b>PARALLEL SESSIONS</b></p> <p><b>HS ONE HEALTH SCIENCE 1</b> <span style="float: right;"><b>SALON A-B</b></span></p> <p><b>Drivers for emerging diseases 1</b></p> <p>CHAIR: <b>Rita Colwell</b>, JOHNS HOPKINS UNIVERSITY BLOOMBERG SCHOOL OF PUBLIC HEALTH, USA CO-CHAIR: <b>Antar Jutla</b>, WEST VIRGINIA UNIVERSITY, USA</p> <ol style="list-style-type: none"> <li>1. Quantifying the health, economic, and ecosystem impacts of land-use change as a driver of disease emergence in Southeast Asia <b>Carlos Zambrana-Torrel</b>, ECOHEALTH ALLIANCE, USA</li> <li>2. Impacts of urbanization and conversion of rainforests into large industrial oil palm plantations on the ecology of Aedes vectors in arbovirus foci, Côte d'Ivoire <b>Julien Zahouli Bi Zahouli</b>, CENTRE SUISSE DE RECHERCHES SCIENTIFIQUES EN CÔTE D'IVOIRE, IVORY COAST</li> <li>3. The use of a nationwide pig movement network to predict the spatial risk of Nipah virus outbreaks in Thailand <b>Anuwat Wiratsudakul</b>, FACULTY OF VETERINARY SCIENCE, MAHIDOL UNIVERSITY, THAILAND</li> <li>4. Ecosystem Change and Zoonoses Emergence <b>Barry John McMahon</b>, UNIVERSITY COLLEGE DUBLIN, IRELAND</li> <li>5. Identification of molecular determinants of aquatic and terrestrial morbillivirus cross-species infections <b>Wendy Karen Jo Lei</b>, UNIVERSITY OF VETERINARY MEDICINE HANNOVER, GERMANY</li> </ol>

SUNDAY 24 JUNE 2018

10:45-12:30

**HS ONE HEALTH SCIENCE 2**

SALON C-D

**One health in underprivileged communities**

CHAIR: **Mark Rweyemamu**, DIRECTOR OF THE SOUTHERN AFRICAN CENTRE FOR INFECTIOUS DISEASES AND SURVEILLANCE (SACIDS)

CO-CHAIR: **Rafael Maciel de Freitas**, INSTITUTO OSWALDO CRUZ, BRAZIL

1. Molecular detection and characterization of *Anaplasma phagocytophilum* strains associated with different hosts in Bushbuckridge, Mpumalanga, South Africa  
**Agatha Onyemowo Kolo**, UNIVERSITY OF PRETORIA, SOUTH AFRICA
2. Assessment of aerosolization of Avian Influenza A associated with market hygiene and practices and potential occupational exposure of live bird market workers in Bangladesh  
**Mahbubur Rahman**, Institute of Epidemiology, DISEASE CONTROL AND RESEARCH, BANGLADESH
3. Transformation within Indigenous Lived Experiences and the Journey from a Pedagogy of Oppression to a Pedagogy of Hope and Freedom  
**Anne Poelina**, THE UNIVERSITY OF NOTRE DAME, AUSTRALIA
4. Tackling the second deadliest Neglected Tropical Disease: Predicting and reducing the impact of snakebite on human and animal health through One Health analyses of hotspots and access to care  
**Rafael Ruiz de Castaneda**, INSTITUTE OF GLOBAL HEALTH, FACULTY OF MEDICINE, UNIVERSITY OF GENEVA, SWITZERLAND
5. What will it take to eliminate rabies in Africa?  
**S Mwangi Thumbi**, WASHINGTON STATE UNIVERSITY, KENYA

10:45-12:30

**AMR ANTIMICROBIAL AGENTS AND RESISTANCE**

GALLERY C-D

**Prevalence and surveillance of resistance**

CHAIR: **Gerard Wright**, M.G. DEGROOTE INSTITUTE FOR INFECTIOUS DISEASE RESEARCH, CANADA

CO-CHAIR: **Georgina Cox**, UNIVERSITY OF GUELPH, CANADA

1. Temporal Changes in Antibiotic Resistance in Common Bottlenose Dolphins (*Tursiops truncatus*), a Sentinel Species  
**Adam M Schaefer**, FLORIDA ATLANTIC UNIVERSITY, USA
2. Antimicrobial Resistance in *Salmonella enterica* Isolates from Wildlife in Virginia  
**Karen Gruszynski**, LINCOLN MEMORIAL UNIVERSITY, USA
3. Antibiotic resistance and epidemiology of *Campylobacter* recovered from humans, animals and environmental sources in Ghana  
**Akosua Bonsu Karikari**, UNIVERSITY FOR DEVELOPMENT STUDIES, SCHOOL OF MEDICINE AND HEALTH SCIENCES, GHANA
4. A longitudinal evaluation of *Salmonella* Typhimurium AMR prevalence and transmission using whole genome sequencing and phenotyping in a poultry population with no antimicrobial selection pressure  
**Helen Kathleen Crabb**, THE UNIVERSITY OF MELBOURNE, AUSTRALIA
5. Antimicrobial resistance in *Escherichia coli* from dairy farms of Quebec, Canada, and identification of Extended-Spectrum- $\beta$ -lactamase/AmpC resistance  
**Jonathan Massé**, THE UNIVERSITY OF MONTREAL, CANADA



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SUNDAY 24 JUNE 2018

10:45-12:30

**SPI** SCIENCE POLICY INTERFACE

GALLERY A-B

### Resistance to antibiotics and antivirals: challenges for policy makers and scientists

CHAIR: **Laura H. Kahn**, PRINCETON UNIVERSITY, USA

CO-CHAIR: **Christianne Bruschke**, CHIEF VETERINARY OFFICER, THE NETHERLANDS

1. Antimicrobial Resistance and One Health solutions

**Joergen Schlundt**, UNIVERSITY OF SINGAPORE

2. Antimicrobial resistance: Canada's science and policy challenges

**Aline Dimitri**, CANADIAN FOOD INSPECTION AGENCY, CANADA

3. The Nordic countries strategy for AMR: challenges at "high latitudes" for policy makers, scientists and society

**Carlos Gonçalo das Neves**, NORWEGIAN VETERINARY INSTITUTE, NORWAY

4. WHO guidelines on use of medically important antimicrobials in food-producing animals

**Scott McEwen**, UNIVERSITY OF GUELPH, CANADA

5. Trade Implications of Antimicrobial Resistance in the International Food Chain

**Anna George**, MURDOCH UNIVERSITY, AUSTRALIA

12:30-14:00

LUNCH

SPECIAL PLENARY SESSION

SALON C-D

### Neglected Zoonotic Diseases in Resource-Poor, Marginalised and Under-Served Communities: Challenges in Infectious Disease Control

CHAIR: **Martyn Jeggo**, GEELONG CENTRE FOR EMERGING INFECTIOUS DISEASES, AUSTRALIA

1. Where we left off: main conclusions of the 2014 International meeting on the control of Neglected Zoonotic Diseases

**Mike Ryan**, WORLD HEALTH ORGANIZATION

2. Combatting Neglected Zoonotic Diseases at the human/animal interface: an overview

**Ab Osterhaus**, RIZ HANNOVER, GERMANY

3. Challenges and opportunities to preventing and responding to outbreaks of helminth/bacterial/viral infections in livestock

**Vivek Kapur**, PENNSYLVANIA STATE UNIVERSITY, USA

4. Need to acquire community support to implementing effective control programmes

SPEAKER TO BE CONFIRMED

SUNDAY 24 JUNE 2018

14:00-15:45

## PARALLEL SESSIONS

## OHS ONE HEALTH SCIENCE 1

SALON A-B

## Drivers for emerging diseases 2

CHAIR: **Peter Daszak**, PRESIDENT OF THE ECOHEALTH ALLIANCECO-CHAIR: **Ottorino Cosivi**, WHO-BRAZIL

1. Leveraging viral phylodynamics to inform spatiotemporal transmission of viral infectious diseases in Africa: 2009 Influenza A/H1N1 in Africa  
**Fredrick Nzabanyi Nindo**, UNIVERSITY OF CAPE TOWN, SOUTH AFRICA
2. Risk of pneumonia among residents living near goat and poultry farms  
**Pim Martijn Post**, DUTCH NATIONAL INSTITUTE FOR PUBLIC HEALTH AND THE ENVIRONMENT (RIVM), THE NETHERLANDS
3. Effect of Habitat Modification on Risk of Scrub Typhus, An Emerging Infectious Disease in Bhutan  
**Tandin Zangpo**, KHESAR GYALPO UNIVERSITY OF MEDICAL SCIENCES OF BHUTAN
4. A One Health Understanding of the Rodent Meat Value Chain in the Mekong Delta, Vietnam: Implications for Zoonotic Disease Risk Mitigation (Wellcome Trust VIZIONS)  
**Jason Euren**, METABIOTA, USA
5. Climate variability and infectious diseases nexus: Evidence from Sweden  
**Mwenya Mubanga**, UPPSALA UNIVERSITY, SWEDEN

14:00-15:45

## OHS ONE HEALTH SCIENCE 2

SALON C-D

## Pathogenesis 2

CHAIR: **Malik Peiris**, UNIVERSITY OF HONG KONGCO-CHAIR: **Wendy Karen Jo Lei**, RESEARCH CENTER FOR EMERGING INFECTIONS AND ZOOSES, HANNOVER, GERMANY

1. Species specific binding of the MERS-coronavirus S1<sup>A</sup> protein  
**W Widagdo**, ERASMUS MC, THE NETHERLANDS
2. Using Bioluminescent Salmonella Strains to Study Host-Pathogen Interaction in Chicken will Allow One-Health-Approach  
**Dinesh Hirantha Wellawa**, VACCINE AND INFECTIOUS DISEASE ORGANIZATION, CANADA
3. Influenza A viruses activate host PI3K/Akt survival pathway for pro-viral advantage in chicken but not in duck cells  
**Sanjeeva Kumar**, UNIVERSITY OF NOTTINGHAM, UK
4. Environmental CO<sub>2</sub> Modification of Innate Immune responses to LPS and Organic Dust  
**David Schneberger**, UNIVERSITY OF SASKATCHEWAN, CANADA
5. Rabies virus interrupts cofilin pathway and induces depolymerization of actin in hippocampal region  
**Waqas Ahmad**, UNIVERSITY OF VETERINARY AND ANIMAL SCIENCES, JHANG CAMPUS, PAKISTAN

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SUNDAY 24 JUNE 2018

14:00-15:45	<p><b>AMR</b> ANTIMICROBIAL AGENTS AND RESISTANCE <span style="float: right;">GALLERY C-D</span></p> <p><b>Novel strategies for amr interventions / preparedness</b></p> <p>CHAIR: <b>Laura H. Kahn</b>, PRINCETON UNIVERSITY, USA          CO-CHAIR: <b>Reema Persad-Clem</b>, UC BERKELEY, USA</p> <ol style="list-style-type: none"> <li>1. Operationalising One Health Approaches to Surveillance for Antimicrobial Resistance <b>Toby Leslie</b>, THE FLEMING FUND, UK</li> <li>2. #AMR: Exploring the role of social media in addressing antimicrobial resistance <b>M9egan Lesley Moore</b>, UNIVERSITY OF SASKATCHEWAN, CANADA</li> <li>3. Development of 2-Aminoimidazole Compounds that Enhance Antibiotic Activities to Reduce Antibiotic Usage <b>Malcolm Thomas</b>, AGILE SCIENCES, INC, USA</li> <li>4. A novel participatory strategy to reduce antimicrobial use in agricultural systems <b>Debra Anne McCorkindale</b>, VETSOUTH LIMITED WINTON, NEW ZEALAND</li> <li>5. Can inhibition of transmission of KPC and CTX-M producing plasmids reduce the spread of AMR? <b>Michelle M.C. Buckner</b>, UNIVERSITY OF BIRMINGHAM, UK</li> </ol>
14:00-15:45	<p><b>SPI</b> SCIENCE POLICY INTERFACE <span style="float: right;">GALLERY A-B</span></p> <p><b>One health and global health security-disaster risk reduction</b></p> <p>CHAIR: <b>William B. Karesh</b>, ECOHEALTH ALLIANCE          CO-CHAIR: <b>Trevor Smith</b>, DEPUTY EXECUTIVE DIRECTOR AND GENERAL COUNSEL, GLOBAL AFFAIRS CANADA</p> <ol style="list-style-type: none"> <li>1. Biological threats: a global perspective <b>Rebecca Katz</b>, CO-DIRECTOR, CENTER FOR GLOBAL HEALTH SCIENCE AND SECURITY AT GEORGETOWN UNIVERSITY, USA</li> <li>2. The Global Health Security Agenda <b>Outi Kuivasniemi</b>, DEPUTY DIRECTOR FOR INTERNATIONAL AFFAIRS, MINISTRY OF SOCIAL AFFAIRS AND HEALTH, FINLAND</li> <li>3. Weapons Threat Reduction Program <b>Trevor Smith</b>, SENIOR PROGRAM MANAGER, BIOLOGICAL &amp; CHEMICAL SECURITY, UNSCR 1540 IMPLEMENTATION, GLOBAL AFFAIRS CANADA</li> <li>4. Objectives and achievements of the Defense Threat Reduction Agency <b>Lance Brooks</b>, DIVISION CHIEF COOPERATIVE BIO ENGAGEMENT PROGRAM, DEPARTMENT OF DEFENSE, USA</li> </ol>
15:45-16:15	COFFEE BREAK

SUNDAY 24 JUNE 2018

16:15-18:00

## PARALLEL SESSIONS

 **HS ONE HEALTH SCIENCE 1**

SALON A-B

**Vaccines 1**CHAIR: **TBC**CO-CHAIR: **Volker Gerdtz**, UNIVERSITY OF SASKATCHEWAN, CANADA

1. Portfolio Approach, Development and Stockpile of MERS-CoV Vaccines: A Case Study  
**Simone Blayer**, CEPI, UK
2. Protective non-specific effect of rabies vaccine in humans, dogs and cattle: One Health implications  
**Anne Conan**, ROSS UNIVERSITY SCHOOL OF VETERINARY MEDICINE, SAINT KITTS AND NEVIS
3. Brucellosis in the changing peri-urban dairy systems of West Africa  
**Laura Ann Craighead**, RVC, UK
4. Evaluation of Post-Exposure Prophylaxis in Vietnam  
**Huong Nguyen**, NATIONAL INSTITUTE OF HYGIENE AND EPIDEMIOLOGY, VIETNAM
5. A systematic review of strategies for reducing missed opportunities for vaccination  
**Anelisa Jaca**, SOUTH AFRICAN MEDICAL RESEARCH COUNCIL, SOUTH AFRICA

16:15-18:00

 **HS ONE HEALTH SCIENCE 2**

SALON C-D

**Infectious diseases from an ecohealth perspective 1**CHAIR: **Craig Stephen**, UNIVERSITY OF SASKATCHEWAN, CANADACO-CHAIR: **Patrick Leighton**, UNIVERSITY OF MONTREAL, CANADA

1. Integrating Ecosystem Approaches to Health: A One Health Investigation of Rift Valley Fever Virus  
**Melinda K Rostal**, ECOHEALTH ALLIANCE, USA
2. The Other Side of One Health: A Brucellosis story  
**Barbara Akorfa Glover**, UNIVERSITY OF PRETORIA, SOUTH AFRICA
3. One ring to rule them all: Uniting human, animal, and environmental data using the Checklist for One Health Epidemiological Reporting of Evidence (COHERE)  
**Peter M. Rabinowitz**, CENTER FOR ONE HEALTH RESEARCH, UNIVERSITY OF WASHINGTON, USA
4. Ecohealth Project at the community level: Disease Research and development at the human-domestic animal and wildlife interface, Uganda  
**Innocent Bidason Rwego**, UNIVERSITY OF MINNESOTA, UGANDA
5. "Whenever I see a fruit bat, I think Hendra" – Attitudes and risk perception of Australian horse owners towards flying foxes in relation to Hendra virus  
**Anke Wiethoelter**, UNIVERSITY OF MELBOURNE, AUSTRALIA

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SUNDAY 24 JUNE 2018

16:15-18:00	<p><b>AMR</b> ANTIMICROBIAL AGENTS AND RESISTANCE <span style="float: right;">GALLERY C-D</span></p> <p><b>Alternative approaches to tackling resistant infections</b></p> <p>CHAIR: <b>Britta Lassman</b>, INTERNATIONAL SOCIETY FOR INFECTIOUS DISEASES          CO-CHAIR: <b>Mohamed Sirdar</b>, UNIVERSITY OF PRETORIA, SOUTH AFRICA</p> <ol style="list-style-type: none"> <li>1. Antibiotics usage by pastoralists in livestock in North-central Nigeria: The socio-cultural drivers for antibiotic resistance emergence and public health implications  <b>Nma Bida Alhaji</b>, NIGER STATE GOVERNMENT, NIGERIA</li> <li>2. Extent of dispensing prescription-only medications without a prescription in community drug retail outlets in Addis Ababa, Ethiopia: a simulated-patient study  <b>Begashaw Melaku Gebresillassie</b>, UNIVERSITY OF GONDAR, ETHIOPIA</li> <li>3. Towards a Global Database of Emerging Antibiotic Resistance  <b>Brooke Watson</b>, ECOHEALTH ALLIANCE, USA</li> <li>4. Current Patterns of Antibiotic Resistance in High Density Livestock-Human Populations in Western Kenya  <b>Steven Alan Kemp</b>, UNIVERSITY OF LIVERPOOL, UK</li> <li>5. Antimicrobial use behaviours, the economics of animal disease and perceptions of antimicrobial policy in pig production in Vietnam  <b>Lucy Alice Coyne</b>, UNIVERSITY OF LIVERPOOL, UK</li> </ol>
16:15-18:00	<p><b>SPI</b> SCIENCE POLICY INTERFACE <span style="float: right;">GALLERY A-B</span></p> <p><b>Making one health operational: the barriers to change and glimmers of hope</b></p> <p>CHAIR: <b>Robert Salerno</b>, DAI GLOBAL HEALTH          CO-CHAIR: <b>Osman Dar</b>, ONE HEALTH PROJECT DIRECTOR, CHATHAM HOUSE CENTRE ON GLOBAL HEALTH SECURITY, UK</p> <ol style="list-style-type: none"> <li>1. Introduction to the session's concept and Objectives  <b>Robert Salerno</b>, DAI GLOBAL HEALTH</li> <li>2. A decade of implementing One Health in Kenya: Translating research into practice  <b>Peninah Munyua</b>, KENYA CDC</li> <li>3. One Health Secretariat: A Formalized coordinating Entity for Operationalizing One Health in Bangladesh  <b>Meerjady Sabrina Flora</b>, IEDCR, BANGLADESH</li> <li>4. Making One Health operational within the Caribbean Region  <b>Chris Oura</b>, UNIVERSITY OF THE WEST INDIES, TRINIDAD</li> <li>5. Characterizing the interventions of the private sector extractive industries during the Ebola virus disease crisis in West Africa  <b>Susan Scribner</b>, VICE PRESIDENT HEALTH SYSTEMS SOLUTIONS, DAI GLOBAL HEALTH</li> <li>6. Tripartite Guidance: Taking One Health Approaches to Address Zoonotic Diseases in Countries: A "Glimmer of Hope"  <b>Elizabeth Mumford</b>, WORLD HEALTH ORGANIZATION</li> <li>7. Panel discussion and open Q&amp;A</li> </ol>

SUNDAY 24 JUNE 2018

18:00-19:30

SPECIAL PLENARY SESSION

SALON C-D

**Emerging and re-emerging infectious diseases: assessment, preparedness and eradication**CHAIRS: **Mike Ryan**, THE WORLD HEALTH ORGANIZATION**William B. Karesh**, ECOHEALTH ALLIANCE

1. Introducing emerging and re-emerging infectious diseases / The threat of an Influenza Pandemic  
**Ab Osterhaus**, RIZ HANNOVER, GERMANY
2. Eradication of infectious diseases: past, present and future  
**Nick Juleff**, SENIOR PROGRAM OFFICER ANIMAL HEALTH PORTFOLIO, BILL & MELINDA GATES FOUNDATION
3. Risk reduction of health emergencies and impact of climate change on health: implications of relevant international frameworks  
**Chadia Wannous**, TOWARDS A SAFER WORLD NETWORK FOR PANDEMIC PREPAREDNESS (TASW)
4. Strengthening global biological security  
**Trevor Smith**, SENIOR PROGRAM MANAGER, BIOLOGICAL & CHEMICAL SECURITY, UNSCR 1540 IMPLEMENTATION, GLOBAL AFFAIRS CANADA
5. Community-based surveillance for early detection of EID  
**Letrak Srikitjakarn**, PARTICIPATORY ONE HEALTH DISEASE DETECTION (PODD)  
**Esron Karimuribo**, ENHANCING COMMUNITY-BASED DISEASE OUTBREAK DETECTION AND RESPONSE IN EAST AND SOUTHERN AFRICA (DODRES)
6. Health emergency challenges from the animal health pharma perspective  
**Theo Kanellos**, DIRECTOR OF STRATEGIC ALLIANCES AT ZOETIS, IRELAND
7. Health emergency challenges from the human health pharma perspective  
**Brian Lesser**, LIFECYCLE LEADER, CAPENDO, GENENTECH, USA

20:00-23:00

FAREWELL DINNER

REMAI MODERN ART GALLERY

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## MONDAY 25 JUNE 2018

	<b>BREAKFAST PLENARY SESSION</b>	<b>SALON C-D</b>
	CHAIR: <b>Jonna Mazet</b> , UC DAVIS, USA	
08:00-08:30	The importance of adjuvants in the vaccine design for the effective control of transboundary and emerging infectious diseases <b>Mahesh Kumar</b> , SENIOR VICE PRESIDENT, GLOBAL BIOLOGICS RESEARCH AT ZOETIS	
08:30-09:00	The scientific and economic rationale for the Global Virome Project <b>Peter Daszak</b> , PRESIDENT ECOHEALTH ALLIANCE	
09:00-09:30	Blockchain and Implications for One Health, <b>Travis Street</b> , UNIVERSITY OF SURREY, UK	
09:30-10:00	Indigenous Wellnes, <b>Carol Hopkins</b> , NATIONAL NATIVE ADDICATIONS PARTNERSHIP FOUNDATION (NNAPF)	
10:00-10:30	COFFEE BREAK	
10:30-12:15	<b>PARALLEL SESSIONS</b>	
	<b>HS ONE HEALTH SCIENCE 1</b>	<b>SALON A-B</b>
	<b>Vaccines 2</b>	
	CHAIR: <b>Lorne Babiuk</b> , UNIVERSITY OF ALBERTA, CANADA	
	CO-CHAIR: <b>Teresia Maina</b> , UNIVERSITY OF SASKATCHEWAN, CANADA	
	1. Development of a highly pathogenic avian H7N9 influenza disease model in mouse <b>Shelby Layne Landreth</b> , UNIVERSITY OF SASKATCHEWAN, CANADA	
	2. A trial to assess the thermotolerance of an inactivated rabies vaccine <b>Felix John Lankester</b> , WASHINGTON STATE UNIVERSITY, TANZANIA	
	3. Acceptance Of Heterologous Prime-Boost Vaccination Regimens – An Assessment <b>Peter Steinmann</b> , SWISS TROPICAL AND PUBLIC HEALTH INSTITUTE, SWITZERLAND	
	4. Identifying Genomic Predictors of Vaccine Response in Swine <b>Peris Mumbi Munyaka</b> , UNIVERSITY OF ALBERTA, CANADA	
	5. Q fever vaccine failure rate, duration of longevity of immunity and associated demographic factors in Australia, <b>Solomon Meseret Woldeyohannes</b> , UNIVERSITY OF QUEENSLAND, AUSTRALIA	
10:30-12:15	<b>HS ONE HEALTH SCIENCE 2</b>	<b>SALON C-D</b>
	<b>Infectious diseases from an ecohealth perspective 2</b>	
	CHAIR: <b>Jonna Mazet</b> , UC DAVIS, USA	
	CO-CHAIR: <b>James Bangura</b> , UC DAVIS ONE HEALTH INSTITUTE, FREETOWN, SIERRA LEONE	
	1. The role of mainland-island bat movement in the dissemination of viruses of public health concern in the Caribbean, Janine Seetahal, THE UNIVERSITY OF THE WEST INDIES, TRINIDAD & TOBAGO	
	2. Nematode co-infections, environmental factors and weather impact infection with the zoonotic bacterium, Bartonella tribocorum, in urban Norway rats (Rattus norvegicus) <b>Jamie Lee Rothenburger</b> , UNIVERSITY OF CALGARY FACULTY OF VETERINARY MEDICINE, CANADA	
	3. Environmental Change Increases Human-Macaque Interactions and the Risk of Zoonotic Disease Spillover, <b>Ariful Islam</b> , INSTITUTE OF EPIDEMIOLOGY, DISEASE CONTROL AND RESEARCH, BANGLADESH	
	4. Explaining variation in human and animal zoonotic infection risk in northern Tanzania: defining agro-ecological systems and their contribution to risk <b>William Anson de Glanville</b> , UNIVERSITY OF GLASGOW, UK	
	5. Building collaborative capacity to evaluate zoonotic viral sharing among bats, primates, and people in Tanzania, <b>Elizabeth VanWormer</b> , UNIVERSITY OF NEBRASKA, LINCOLN, USA	

MONDAY 25 JUNE 2018

10:30-12:15

**AMR** ANTIMICROBIAL AGENTS AND RESISTANCE

GALLERY C-D

**Rapid diagnostics**CHAIR: **TBC**CO-CHAIR: **Moon Tay Yue Feng**, NANYANG TECHNOLOGICAL UNIVERSITY, SINGAPORE

1. Analysis of single nucleotide polymorphism in KatG gene in isoniazid resistant Mycobacterium Tuberculosis  
**Muhammad Arif**, UNIVERSITY OF MALAKAND, PAKISTAN
2. Exploiting the potential of flow cytometry in rapid antimicrobial susceptibility testing  
**Timothy John Jay Inglis**, UNIVERSITY OF WESTERN AUSTRALIA, AUSTRALIA
3. Novel and Rapid Multiplex Allele-Specific PCR (MAS-PCR) Test for Rapid Detection of MDR and XDR-TB from the Sputum of Lung TB Patients in Makassar, Indonesia  
**Muhammad Nasrum Massi**, HASANUDDIN UNIVERSITY, INDONESIA
4. Presence of oqxA and oqxB genes in a multidrug resistant Salmonella Typhimurium isolate recovered from swine in Brazil  
**Daniel F. Monte**, UNIVERSITY OF SÃO PAULO, BRAZIL
5. Inter-laboratory validation for antimicrobial susceptibility testing of highly pathogenic bacteria performed by an European laboratory network  
**Tara Wahab**, PUBLIC HEALTH AGENCY OF SWEDEN

10:30-12:15

**SPI** SCIENCE POLICY INTERFACE

GALLERY A-B

**One health in underserved, resource-poor and marginalized communities / new strategies call for one health solutions**CHAIR: **Marietjie Venter**, UNIVERSITY OF PRETORIA, SACO-CHAIR: **Jay Varma**, SENIOR ADVISOR, AFRICA CDC

1. Africa CDC: Challenges and Opportunities for Advancing One Health in Africa  
**Jay Varma**, SENIOR ADVISOR, AFRICA CENTRES FOR DISEASE CONTROL AND PREVENTION
2. First Nations of Canada and the One Health approach  
**Addie Pryce**, ASSEMBLY OF FIRST NATIONS, CANADA
3. One Health, rabies response and more-than-human considerations in Indigenous communities in Northern Australia  
**Chris Degeling**, UNIVERSITY OF WOLLONGONG, AUSTRALIA
4. Aligning Science and Policy in the Fight Against Emerging Infectious Threats  
**Craig Vanderwagen**, FORMER ASSISTANT SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES, USA  
**Gerald Parker**, ASSISTANT DEAN OF THE VETERINARY SCHOOL FOR ONE HEALTH INITIATIVES AT TEXAS A AND M UNIVERSITY, USA
5. CORDS: Empowering Communities for the Containment of Infectious Outbreaks through a Global Multidisciplinary Collaboration between Regional Networks  
**Christophe Longuet**, CONNECTING ORGANISATION FOR REGIONAL DISEASES SURVEILLANCE (CORDS)



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## MONDAY 25 JUNE 2018

12:15-13:45	<b>PARALLEL TRACKS</b>	<b>SALON A-B</b>
	<b>Late breakers 1</b>	
	CHAIR: <b>John Mackenzie</b> , CURTIN UNIVERSITY, AUSTRALIA	
	1. Coronavirus bio-surveillance of the insectivorous bats at the Matlapitsi cave in the Limpopo province, South Africa	
	<b>Marike Geldenhuys-Venter</b> , UNIVERSITY OF PRETORIA, SOUTH AFRICA	
	2. Zika Virus Surveillance at the Animal-Human Interface in Brazil, Colombia, and Peru, 2017-2018	
	<b>Stephanie Salyer</b> , CENTERS FOR DISEASE CONTROL AND PREVENTION, US	
	3. Avian-origin PB1 gene confers selective advantages to 2009 pandemic H1N1 virus RNA transcription and replication	
	<b>Fangzheng Wang</b> , UNIVERSITY OF SASKATCHEWAN, CANADA	
	4. Learning from an evolutionary host: IRF3 signaling is critical to prevent Middle East respiratory syndrome (MERS) coronavirus propagation in big brown bat cells	
	<b>Arinjay Banerjee</b> , UNIVERSITY OF SASKATCHEWAN, CANADA	
	5. Anti-viral activity of HDAC6 against influenza A virus mediated via suppression of viral RNA polymerase subunit PA	
	<b>Yong-Sam Jung</b> , NANJING AGRICULTURAL UNIVERSITY, CHINA	
	6. Rapid and sensitive molecular detection of viruses, bacteria, and parasites without sophisticated laboratory equipment	
	<b>Joanne Macdonald</b> , UNIVERSITY OF THE SUNSHINE COAST, AUSTRALIA	
12:15-13:45	<b>Late breakers 2</b>	<b>SALON C-D</b>
	CHAIR: <b>Ab Osterhaus</b> , RIZ HANNOVER, GERMANY	
	1. One Health in History: Bison, Parks Canada and the Emergence of Tuberculosis in the Canadian Arctic	
	<b>James W Daschuk</b> , UNIVERSITY OF REGINA, CANADA	
	2. Alveolar echinococcosis – An emerging zoonosis in North America?	
	<b>Janna Schurer</b> , TUFTS UNIVERSITY-UGHE ONE HEALTH COLLABORATIVE, US	
	3. Students' experiences during One Health field attachment: A case study of One Health Institute in Makerere University, Uganda	
	<b>Esther Buregyeya</b> , MAKERERE UNIVERSITY SCHOOL OF PUBLIC HEALTH, UGANDA	
	4. A novel vaccine candidate for Salmonella gastroenteritis	
	<b>Akosiererem Senibo Sokaribo</b> , UNIVERSITY OF SASKATCHEWAN, CANADA	
	5. Core Competencies in One Health Education: What Are We Missing?	
	<b>Eri Togami</b> , University of California, DAVIS, US	
	6. West Nile disease: possible epizootic transmission cycle in Southern Pakistan	
	<b>Erum Khan</b> , AGA KHAN UNIVERSITY, PAKISTAN	

MONDAY 25 JUNE 2018

12:15-13:45	<b>Late breakers 3</b>	GALLERY A-B
CHAIR: <b>Karen Chad</b> , UNIVERSITY OF SASKATCHEWAN		
1. Genetic diversity of VCC-1 carbapenemase-producing <i>Vibrio cholerae</i> in costal waters of Germany <b>Jens Andre Hammerl</b> , GERMAN FEDERAL INSTITUTE FOR RISK ASSESSMENT, GERMANY		
2. 6 years (2010-2016) lag phage of ESBLA- to ESBLCarba in Enterobacteriaceae isolated from wild birds: Towards the start of the environmental spread of Carbapenamse producers in Bangladesh? <b>Mohammad Badrul Hasan</b> , UPPSALA UNIVERSITY, SWEDEN		
3. Alternative Approaches to Managing Demand for Antibiotic Treatment in Dairying <b>David Anthony Hennessy</b> , MICHIGAN STATE UNIVERSITY, US		
4. Longitudinal field study in evaluating the ecological spillover of antibiotic-resistant <i>Escherichia coli</i> from poultry to humans in rural Ecuador <b>Hayden Dana Hedman</b> , UNIVERSITY OF MICHIGAN, US		
5. Non-prescribed use of antibiotics in peri-urban small-holder dairy farms: A cross-sectional study of 510 farms across 5 cities in India <b>Manish Kakkar</b> , PUBLIC HEALTH FOUNDATION OF INDIA		
6. Population wide assessment of antimicrobial use in companion animals using a novel data source – a cohort study using pet insurance data <b>Laura Yvonne Hardefeldt</b> , UNIVERSITY OF MELBOURNE, AUSTRALIA		
13:45-14:00	<b>CLOSING CEREMONY</b>	SALON A-B
14:00-14:30	LUNCH	
14:30-15:30	<b>PRESS CONFERENCE - LIVE STREAM</b>	SALON C-D
<p>Prof. John Mackenzie, Prof. Ab Osterhaus and other key contributors to the congress will share the main outcomes on aspects of emerging and re-emerging infectious diseases and antimicrobial resistance. They will inform members of the press about the development of a “White Paper” - established during the congress. The White Paper will provide in-depth descriptions of the major One Health challenges and threats. It will openly state what is going wrong on a societal level, what is lacking and what the gaps are in order to make the world a safer place when it comes to One Health issues. The White Paper will come with a clear call for actions, a roadmap that describes what needs to be done - better and more. The press conference will be live streamed. The accompanying press statement will be distributed to members of the press globally.</p>		
<b>Innovative technologies and One Health – a Panel discussion</b> <b>vHive</b> ON INVITATION ONLY		
<b>How to Write and Publish a Great Scientific Paper</b> <b>Peter Daszak</b> , EDITOR-IN-CHIEF OF THE JOURNAL ECOHEALTH, AND PRESIDENT OF ECOHEALTH ALLIANCE ON INVITATION ONLY		
15:30-	<b>GUIDED EXCURSIONS</b>	
An extensive programme of guided excursions to a variety of natural, cultural and historical settings offered to congress participants.		

THE 5<sup>TH</sup> INTERNATIONAL


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# OHS ONE HEALTH SCIENCE 1

## OHS PATHOGEN DISCOVERY

### 1 OHS A01 - PATHOGEN DISCOVERY - SALON AB

#### Plagiorchis sp. in small mammals of Senegal: an emerging food-borne trematodiasis?

**Catalano, Stefano** (1); Léger, Elsa (1); Diouf, Nicolas D. (2,3); Nadler, Steven A. (4); Webster, Joanne P. (1)

- 1: Centre for Emerging, Endemic and Exotic Diseases (CEEED), Department of Pathobiology and Population Sciences, The Royal Veterinary College, University of London, Hatfield AL9 7TA, United Kingdom;
- 2: Unité de Formation et de Recherche (UFR) des Sciences Agronomiques, d'Aquaculture et de Technologies Alimentaires (S2ATA), Université Gaston Berger, Saint-Louis BP234, Senegal;
- 3: Institut Supérieur de Formation Agricole et Rurale (ISFAR), Université de Thiès, Bambey BP54, Senegal;
- 4: Department of Entomology and Nematology, University of California, One Shields Avenue, Davis, CA 95616-8668, USA

**BACKGROUND:** Trematodes of the genus *Plagiorchis* are cosmopolitan and characterized by low host specificity. *Plagiorchis* spp. infect lymnaeid freshwater snails as first intermediate hosts, a wide range of aquatic insects and freshwater fish as second intermediate hosts, and the intestinal tract of a variety of reptiles, birds and mammals, including humans, as definitive hosts. Whilst the zoonotic potential of *Plagiorchis* spp. has been documented across different countries of Asia, data on *Plagiorchis* spp. from Africa are insufficient and reports of this trematode remain anecdotal.

**METHODS:** Between May 2016 and November 2017, we trapped, humanely euthanized and necropsied 671 small mammals from sites in and around the town of Richard Toll and on the shores of Lake Guiers, Senegal. At post-mortem, organs were examined for helminths. DNA from individual worms was amplified for the complete internal transcribed spacer (ITS) region of the nuclear ribosomal DNA and for a segment of the cytochrome c oxidase subunit 1 (COI) gene of the mitochondrial DNA. Maximum Likelihood (ML) and Bayesian Inference (BI) were used to infer phylogenetic relationships and evolutionary lineages among *Plagiorchis* species.

**RESULTS:** *Plagiorchis* sp. was found in the liver and the proximal segment of the small intestine of 187/324 *Mastomys huberti* mice (57.7%), 7/22 *Crocidura* sp. shrews (31.8%), and 5/81 *Arvicanthis niloticus* rats (6.2%) from sampling locations around Lake Guiers. None of the 244 small mammal sampled from the Richard Toll area were found to be infected. Infection intensity was typically over-dispersed, with only 16.7% of the examined small mammals from Lake Guiers harbouring the majority of the parasites ( $\geq 60$  worms). ML and BI analyses of the ITS (1159 base pairs) and COI (396 base pairs) regions strongly supported monophyly of this West African *Plagiorchis* sp. and its inclusion within a clade composed by other *Plagiorchis* spp. infecting rodents, sister to a lineage represented by *Plagiorchis* spp. of bats.

**CONCLUSIONS:** This study provides substantial molecular data to resolve the phylogeny of this newly described *Plagiorchis* sp. from Senegal. Its wide host spectrum and high prevalence in the Lake Guiers region raise concern about the zoonotic potential of this parasite, particularly when considering phylogenetic relationships with other *Plagiorchis* spp. recognized as agents of human infections. The occurrence of two divergent lineages suggests that the genus *Plagiorchis* has a complex evolutionary history, which may be the result of ecological specialization in different habitats and/or intermediate hosts. Trematode diversity and food-borne parasite transmission is a neglected public health issue in developing countries of Africa. Understanding the life cycle and epidemiology of this *Plagiorchis* sp. could have potential implications on the health of communities inhabiting regions where the parasite circulates.

## 2 OHS A01 - PATHOGEN DISCOVERY - SALON AB

**Zika Virus Exposure In Malaysia; A Preliminary Study On Seroprevalence Among Local Population**

**Wan Ghazali, Wan Nabilatul Huda;** Azizan, Muhammad Afif; Savandarajan, Amritakumari; Thayan, Ravindran

INSTITUTE FOR MEDICAL RESEARCH, MALAYSIA, Malaysia

**INTRODUCTION:** Zika virus (ZIKV) is a zoonotic flavivirus transmitted via *Aedes* sp. mosquitoes and is known to cause mild disease. However, recent outbreaks linked ZIKV with congenital microcephaly and Guillain-Barré Syndrome alarming the public healthcare. In Malaysia, first isolation of ZIKV from mosquitoes was reported in 1969 while the first human case reported only in 2014. Subsequently, 8 cases of ZIKV were diagnosed using Real Time PCR (RT-PCR) during an outbreak in August 2016 where phylogenetic tree showed presence of both Micronesian and French–Polynesian strains. Meanwhile, a higher number of cases reported in the same year by the neighbouring countries; Thailand and Singapore, with 686 and 446 cases respectively. Infrequency in detection and diagnosis of ZIKV comparatively to flavivirus Dengue, provided limited information in assisting countries to tackle the disease. This study was conducted to measure the extent of ZIKV exposure in Malaysia by examining the seroprevalence of ZIKV among local population.

**METHODS:** A cross sectional study was conducted in Sabah, Malaysia and random sampling method was performed. All collected serum samples were tested for Anti-Zika IgG using the WHO approved commercial kit (Euro Immun Zika IgG ELISA) and for Anti-Zika IgM using the CDC Emergency Use Authorization (EUA) approved commercial kit (Inbios Zika IgM ELISA). Anti-Zika IgM reactive samples were then subjected to RT-PCR for detection of Zika viral RNA. All samples were subjected to Anti-Dengue IgG and IgM to eliminate cross-reactivity.

**RESULTS:** Out of 409 serum samples, 35.0% (143/409) were reactive for Zika IgG, and 4.9% (20/409) were reactive for Anti-Zika IgM. Following that, 10.0% (2/20) of Anti-Zika IgM reactive samples were detected for Zika viral RNA indicating an active ZIKV infection with viremia. Anti-Zika IgM reactive cases were detected from 9 different districts which were at least 30km apart. Analysis indicated that cases involved ranges from 12 to 80 years old, with the highest number of cases (30.0%) seen in above 50 year old age group. No significant gender and occupation groups showed inclination to ZIKV infection as the reactive cases were seen almost equally among farmers, students, housewife and other professions. All of them were asymptomatic. Seroprevalence of ZIKV in Sabah is estimated at 22.0% after correction for dengue cross-reactivity.

**CONCLUSIONS:** Approximately a quarter of Sabah's population have been exposed to ZIKV in their lifetime with a substantial number of active asymptomatic infection. Findings highlight the importance of ZIKV screening, especially among women of reproductive age due to risks of having foetal anomalies. A surveillance study on maternal ZIKV infections by monitoring foetal development is underway. This study also hints at the possibility of an existing large ZIKV natural reservoir among non-human primates triggering another research specifically targeting non-human primates.

## 3 OHS A01 - PATHOGEN DISCOVERY - SALON AB

**A new concept for de-novo detection of viral pathogens with adaptive diagnostics and integrated data analysis approaches results in the recent discovery of two novel viruses**

**Forth, Leonie** (1); Hoeper, Dirk (1); Lembcke, Robert (2); Peißert, Claudia (2); Holenya, Pavlo (3); Jenckel, Maria (1); Eckey, Maren (3); Reimer, Ulf (3); Noack, Karsten (2); Konrath, Andrea (4); Scholes, Sandra F.E. (5); Beer, Martin (1); Pohlmann, Anne (1)

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- 2: Scopeland Technology GmbH, Germany;
- 3: JPT Peptide Technologies GmbH, Germany;
- 4: Saxon State Laboratory of Health and Veterinary Affairs, Germany;
- 5: SAC Consulting Veterinary Services, Great Britain

**BACKGROUND:** New and reemerging viral infectious diseases cause frequent threats to both human and animal health. Diagnostic sequencing by unbiased next-generation sequencing is a key method for the identification of new pathogens. One major barrier for the use of this method in day-to-day diagnostics is often the lack of standardized workflows and data analysis tools in a user-friendly environment. The interdisciplinary project DetektiVir aims at closing this gap by deploying a new workflow which combines molecular nucleic acid-based virus detection by metagenomic sequencing with ad-hoc development of customized serological diagnostics, and integrates data in dynamic database applications.

**METHODS:** Central part of the new workflow is a novel diagnostic data hub application that combines raw sequence reads and metadata with the results from taxonomic classification software in a database environment. This core system offers flexible data interfaces and software algorithms in a user-friendly environment. The application was evaluated with samples from diseased animals infected with unidentified pathogens. Analyses comprised next-generation sequencing, data analysis and integration of data in the data hub. In case of sufficient data, full viral genomes were assembled and phylogenetically classified. Confirmation of the findings by RT-qPCR as well as attempts for virus isolation and electron microscopy were performed.

**RESULTS:** Applying the workflow, we were able to discover novel viruses. First, we identified a novel picornavirus, tentatively named ovine picornavirus, from 2-3 week old lambs in the UK, suffering with polioencephalomyelitis and ganglionitis. Phylogenetic analysis shows that the novel ovine picornavirus can be classified between the genera *Sapelovirus* and *Enterovirus* in the family *Picornaviridae*, and has 58 % overall pairwise sequence identity to a bovine picornavirus. Second, we identified a novel paramyxovirus, which was isolated from a diseased grizzled giant squirrel of Sri Lanka and is therefore preliminarily designated giant squirrel respirovirus. Interestingly, this novel virus has an overall pairwise sequence identity of 71 % with known murine respiroviruses and 68 % with human respiroviruses. Phylogenetic analysis suggests a novel branch between murine and human respiroviruses. The virus isolation was successful on primary porcine thyroid cells as well as electron micrographs of the virus particle.

**CONCLUSIONS:** The identification of the novel viruses proves the strength of the new workflow. By integrating the gathered information, including metadata, into the dynamic database the growing information will pave the way for earlier identification of associated outbreaks of a potential novel pathogen.

## 4 OHS A01 - PATHOGEN DISCOVERY - SALON AB

## Novel orthobunyavirus identified in an African child with severe encephalopathy

**Edridge, Arthur W.D.**(1,2); Namazzi, Ruth (3); Deijs, Martin (1); Jebbink, Maarten F. (1); Cristella, Cosimo (1); Kootstra, Neeltje A. (4); van Woensel, Job B.M. (2); de Jong, Menno D. (1); Idro, Richard (3); Boele van Hensbroek, Michael (2); van der Hoek, Lia (1)

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- 3: Department of Paediatrics and Child Health, Mulago Hospital, Makerere University College of Health Sciences, P.O Box 7072, Kampala, Uganda;
- 4: Laboratory of Viral Immune Pathogenesis, Department of Experimental Immunology, Academic Medical Center, Meibergdreef 9 1105 AZ Amsterdam, The Netherlands

**BACKGROUND:** Non-traumatic coma is common in children in sub-Saharan Africa and causes considerable morbidity and mortality. Most children present with a suspected central nervous system (CNS) infection, but the underlying cause remains unknown in a majority of cases resulting in inadequate prevention and treatment strategies. Novel pathogens are a likely explanation for the unexplained encephalopathies as Africa is regarded as a hotspot for vector borne emerging infectious diseases. Orthobunyaviruses are of particular interest as they commonly cause outbreaks in Africa, can be zoonotic, are vector borne and are known to cause human encephalitis.

**METHODS:** Viral metagenomics was performed on pooled plasma and cerebrospinal fluid (CSF) of a three year old African child with fever, non-traumatic coma and prolonged convulsion for whom diagnostics on a wide range of common viral and bacterial causes were negative. Eleven inflammatory biomarkers were measured to determine the likelihood of a CNS infection

**RESULTS:** A novel orthobunyavirus was discovered. Sequences from all three viral segments were found (936 nt of the L-segment; 178 nt of the M-segment; 282 nt of the S-segment) which showed high diversity to known viruses (>29% on amino acid level) and clustered consistently within a clade of Anopheles mosquito borne orthobunyaviruses (Figure). The viral load was  $3 \times 10^2$ /mL in CSF and the biomarker profile was typical of a CNS infection. Besides being present in CSF, the virus was also detected in plasma ( $5 \times 10^3$ /mL).

**CONCLUSIONS:** We present a novel orthobunyavirus, present in the CSF of a three year old patient who presented with severe encephalopathy. A viral encephalitis, elicited by the novel virus, was the most likely cause of disease. This virus is probably transmitted by Anopheles mosquitos, highlighting that human contact may be common. Further screening in the same geographic area of the index case needs to be performed to determine the prevalence of this virus.

## Seroprevalence of West Nile virus in wild birds in Bangladesh

**Islam, Ausraful** (1); Rahman, Md Asadur (1); Paul, Suman Kumer (1); Hannan, Minhaj A (1); Islam, Ariful (2); Hossain, Mohammad Enayet (1); Rahman, Mohammed Ziaur (1); Hosseini, Parviez Rana (2); Dey, Tapan Kumar (3); Zeidner, Nord (1,4)

1: icddr,b, Bangladesh, People's Republic of;

2: EcoHealth Alliance, New York, NY, USA;

3: Bangladesh Forest Department;

4: Centers for Disease Control and Prevention (CDC), Atlanta, Georgia, USA

**BACKGROUND:** West Nile virus (WNV) is the most widespread arbovirus in the world capable of causing epidemics in both humans and animals. It is transmitted by a wide range of mosquitoes and multiple species of birds can act as amplifying hosts. Migratory birds are considered to be the main vehicle for introducing WNV into new regions. In humans, the pathogenicity of WNV varies from mild, self limiting, non-fatal, febrile illness to severe encephalitis. The status of WNV in Bangladesh is currently unknown. We conducted this study to assess the prevalence of WNV among resident and migratory wild birds of Bangladesh.

**METHODS:** During the period of 2010 to 2012 birds were captured using mist nets and noose traps, and blood samples were taken from wild birds landing on the coastal sandbars of Cox's Bazar, Hakaluki haor (seasonal wetlands) of Sylhet and Moulvibazar, Tanguar haor of Sunamgonj and the rice paddy fields of Patuakhali, Netrokona and Guibandha. Recovered serum was tested at 50% dilution for detection of WNV antibodies using a commercially available competitive ELISA following the manufacturer's instructions (ID Screen® West Nile Competition, IDVet, Montpellier, France).

**RESULTS:** Blood samples were obtained from a total of 888 birds comprising 21 families and 80 species; 250 (28%) of them were resident and 638 (72%) were migratory. Forty eight birds (5.4%, CI 0.04-0.07) tested positive for WNV antibody. The positive birds consisted of 45 common coots (*Fulica atra*), one ferruginous pochard (*Aythya nyroca*), one fulvous whistling duck (*Dendrocygna bicolor*) and one great crested grebe (*Podiceps cristatus*). Among those birds, two common coots, one fulvous whistling duck and one great crested grebe were from the Hakaluki haor, and 43 common coots and one ferrogionous pochard were from Tanguar haor. Only one positive bird, a fulvous whistling duck, was a resident species.

**CONCLUSIONS:** Both resident and migratory wild birds of Bangladesh demonstrated exposure to WNV infection. Most of the WNV positive birds were migratory common coots, which is similar to previous reports from India and Iran. Future isolation and molecular characterization of the virus will allow us to better understand the epidemiology of this virus in Bangladesh.



## OHS DIAGNOSTICS

### 1 OHS A02 - DIAGNOSTIC - SALON AB

## Recombinant techniques to address the challenges in development of assays for diagnosis and surveillance of emerging zoonotic diseases

**Burt, Felicity Jane** (1,2); van Jaarsveld, Danelle (2); Damane, Deborah (2)

1: National Health Laboratory Service;

2: University of the Free State

**BACKGROUND:** Emerging zoonotic diseases include pathogens that are newly recognised, newly evolved or known pathogens with an increase in incidence and/or change in their geographic distribution. Many emerging pathogens are viruses that require high containment facilities for culturing, limiting the number of laboratories with capacity to handle these viruses. Serological assays are essential tools for diagnosis and surveillance. Commercial assays for many of these viruses are expensive and not readily available. Crimean-Congo haemorrhagic fever (CCHF) virus is considered an emerging zoonosis. Most reagents are developed in house within BSL4 laboratories, however recombinant antigens could play a role in development of safe reagents and increase diagnostic and surveillance capacity. To address the challenge of developing assays in the absence of high containment facilities, epitope prediction and recombinant technology were investigated for preparing reagents for detection of CCHF.

**METHODS:** In this study mammalian cells were transiently transfected with a plasmid expressing CCHF nucleoprotein (NP). In-house antigen slides were prepared using cells transfected with pcDNA<sup>TM</sup>3.1D/V5-His-TOPO.CCHFV.NP construct after confirmation that the construct could transiently express NP detectable in the cells by indirect immunofluorescent assays (IFA). A total of 14 serum samples from survivors of CCHF virus were screened for antibody. Negative samples were included to determine specificity. To confirm the in house assay results, the sera were tested using a commercial assay, CCHFV Mosaic 2 kit (EUROIMMUN AG). In addition, the samples were tested with an in house ELISA developed using bacterially expressed recombinant CCHF NP truncated to include epitopic regions identified using Bepipred Linear Epitope Prediction software.

**RESULTS:** Anti-CCHFV IgG antibody was detected in 14/14 serum samples using the commercial IFA and the in house IFA. Reactivity of sera with truncated NP antigens incorporating predicted epitopic regions identified an immunodominant region of the NP between amino acids 123 to 396. However there was limited reactivity of sera with a shorter truncated NP. A panel of CCHF IgG negative sera showed no reactivity.

**CONCLUSIONS:** The emergence in non-endemic regions and re-emergence in endemic areas that experienced long periods without CCHF cases emphasize the need for safe, validated, inexpensive assays. In house assays can also be readily modified for screening samples from other species. Prediction of potentially immunogenic epitopes in a given protein may reduce experimental efforts and cost for immunodiagnostics however functional assays are required to confirm the correlation between antigenic sites predicted using bioinformatics and biological activity. In summary recombinant proteins are a useful and safe alternative to native antigens and could have useful application in development of validated assays increasing capacity for diagnosis of medical and veterinary pathogens particularly in low resource environments.

## 2 OHS A02 - DIAGNOSTICS - SALON AB

**Comparison of two RdRp PCR assays for the detection of MERS related Coronaviruses**

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**BACKGROUND:** Coronaviruses (CoVs), specifically *Betacoronaviruses* (betaCoVs), are closely monitored in the context of emerging infectious diseases, as they are known to infect humans such as Severe Acute Respiratory Syndrome coronavirus (SARS-CoV), and Middle East Respiratory Syndrome-coronavirus (MERS-CoV). Bats are the suspected source of these viruses. Multiple surveillance studies in bats have been conducted on different continents. Sensitive methods for detection of known and novel viruses are important for accurate surveillance data. RT-PCR amplification of the RNA-dependent RNA polymerase gene (RdRp) has been widely adopted to detect and identify CoVs in bats and other animals. We compared the results of two RdRp RT-PCR assays detecting MERS-related CoVs.

**METHODS:** Bat rectal swabs were collected from 9 study sites in Thailand during 2013-2015 and tested using one step RT-PCR followed by hemi-nested PCR and the results were compared. Two PCR protocols were used, including Watanabe's protocol (440 bp amplified target) and Corman's protocol (242 bp amplified target). Five  $\mu$ L of RNA template was used for both methods. Positive PCR specimens were confirmed by nucleotide sequencing.

**RESULTS:** Of the 376 bat rectal swabs, 30 specimens were positively identified using both methods; 12 and 24 samples were positive by Watanabe method and by Corman method, respectively. There was total agreement in the results of the two methods in 352 specimens (346 negative, 6 positive). Eighteen of 24 specimens positive by Corman method were negative by Watanabe method, and 6 of 12 positive specimens by Watanabe method were negative by Corman method. Of the 12 Watanabe positive samples, sequencing of viral DNA identified 2 as AlphaCoV, 6 as lineage C betaCoVs or MERS-related CoV, and 4 as lineage D betaCoVs. From 24 positive viruses by Corman method, 2 were lineage B betaCoVs or SARS-related CoV, 7 were MERS-related CoV, 1 was lineage D betaCoV, and 13 were of unclassified lineage betaCoVs. Combining the results from both methods, eight MERS-related CoV positive specimens were found; five specimens were positive by both methods.

**CONCLUSIONS:** Using two PCR primer sets for detection of MERS-related CoVs positively identified more samples than either method alone. The Corman method showed higher sensitivity than Watanabe, but there were some discrepancies between these methods, since different assays showed different detectability for the virus. To avoid any false negative results, more than one PCR method should be conducted.

## 3 OHS A02 - DIAGNOSTICS - SALON AB

**The accuracy of pre-vaccination screening for Q fever and the extent of exposure – Bayesian latent class analysis**

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**BACKGROUND:** Q fever is an acute febrile illness caused by infection with *Coxiella burnetii* that is most prevalent in occupational groups directly and indirectly exposed to livestock. The main method of prevention in Australia is vaccination of high risk individuals with Q Vax® (CSL, Melbourne). Since the vaccine has more side effects in persons who have already had the disease Q fever, so testing is necessary before vaccination is given to avoid unwanted vaccine side effects. However, there is lack of data on the diagnostic accuracy of the pre-vaccination screening tests: serology and skin tests. According to the Australian immunisation handbook, there is no information available on the accuracy of pre-vaccination Q fever screening tests.

**OBJECTIVE:** Therefore, the aim of this study was to assess the accuracy of pre-vaccination screening tests for Q fever. Methods: Bayesian latent class analysis (BLCA) used to determine the accuracy of the screening tests assuming that none of the serological tests is gold standard. Cohen's kappa used to assess the test agreement. We used data on the outcome of screening 79,414 individuals from Queensland, Australia tested between 1991 and 2016 obtained from the Q fever vaccination registry. We analysed the data using R Statistical Package: R-3.4.2 for Windows.

**RESULTS:** The posterior means of the sensitivity of blood and skin test, respectively, were found to be 67.3% and 77.0%. The posterior means of the specificity of blood and skin test, respectively, were found to be 99.0% and 95.6%. The mean posterior predictive positive values for blood and skin tests were, respectively, 85.0% and 59.7%. The mean posterior predictive negative values for blood and skin tests were, respectively, 97.2% and 98.0%. The posterior mean of the extent of the true latent Q fever exposure prevalence was found to be 7.9%. Agreement between serology and skin tests was only moderate (46%). The almost perfect agreement between the skin test and the health workers interpretation suggests they rely on this test for the overall decision.

**CONCLUSIONS:** The study confirmed previous findings of moderate agreement between screening tests (46%) and predictive value of history of vaccination/ exposure (immunity). In addition, the false negative rate was high (33% for blood test and 23% for skin test). The positive predictive value of the skin test found to be very low (59.7%) showing lower benefit of the skin test for ruling out previous immunity for Q fever. Moreover, up to 92% of new entrants in high-risk workplaces will be susceptible to Q fever and require vaccination. We recommend using serological tests for pre-vaccination screening in this high-risk population (i.e., phase out skin test). Further, follow up research in order to strength the current finding implicated.

## 4 OHS A02 - DIAGNOSTIC - SALON AB

## Reproducibility of results and performance of TB diagnostics in East Africa Public Health Laboratory Networking Project sites in Kenya: Implication on Policy Resolution for Strategic TB Diagnosis

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 3: KEMRI-Centre for Microbiology Research;  
 4: South Eastern Kenya University

**BACKGROUND:** Reproducibility of laboratory results and performance of diagnostic tools form major part of quality assurance in diagnosis, which is key to patient care. There no documented comparison of reproducibility of results and performance of TB diagnostics in different geographical settings.

**METHODS:** People presumed to have TB, aged 18 years and above were enrolled in a cross-sectional study between 2013 and 2016 at nine selected public health facilities in Kenya. Spot and morning sputum specimens collected from participants on two consecutive days with a total of 5715 specimens. At study site, a proportion of each specimen was processed for ZN, FM and GeneXpert MTB/RIF. The remaining portion was shipped to the Kenya Medical Research Institute (KEMRI) laboratory, Nairobi. ZN, FM, GeneXpert and Lowensen Jensen (LJ) culture were done according to standard procedures. KEMRI laboratory personnel were blinded of the study site results. Data processed with MySQL and IBM SPSS version 24 software. Reproducibility determined by Kappa values using specimen as unit of analysis and performance by diagnostic values (sensitivity, specificity, positive/negative predictive values) using the patient as unit of analysis. LJ culture used as gold standard. Results at the study sites were compared with those from KEMRI.

**RESULTS:** GeneXpert had excellent Kappa value (0.855(95% CI:0.834-0.876) and was significantly higher than ZN microscopy (0.721(95% CI:0.708-0.734), FM Kappa value (0.749(95% CI:0.736-0.762), indicated substantial agreement. Specific results for the three diagnostic tools varied across the sites for microscopy but were not significantly different for GeneXpert. Marginal significant incremental sensitivity of microscopy at study sites for ZN (69.9% (95%CI:64.3-75.5); and FM (76.7% (95% CI:71.1-82.3); compared to KEMRI ZN (68.7% (95% CI:63.1-74.4); and FM (70.8% (95%CI:64.8-76.8). Sensitivity of GeneXpert at study sites (81.4%(95%CI:71.4-91.3); was not significantly different from that at KEMRI (81.4%(95%CI:71.4-91.3). Specificity of GeneXpert at site was not significantly different from KEMRI but significantly lower than microscopy both at site and KEMRI. Microscopy results varied across study sites but not significantly different for GeneXpert. Similar pattern was observed for positive/ negative predictive values.

**CONCLUSIONS:** GeneXpert indicated excellent reproducibility of results but not significantly difference in performance in study sites in Kenya suggesting that under ideal conditions GeneXpert is reliable irrespective of site setting. However, with higher specificity and positive predictive values, microscopy could compliment GeneXpert in strategic detection of mycobacteria especially in settings with inadequate capacity including infrastructure, human resource and high workload. The concept was adopted as a policy resolution in the East, Central and Southern Africa health Community – ECSA-HC 10th best practices Forum and 26th Directors Joint Consultative Committee Meeting April 2017 in Arusha, Tanzania.

## 5 OHS A02 - DIAGNOSTICS - SALON AB

**Development of lateral flow immunochromatographic test for multiple detection of *Salmonella* Species in poultry food product****Sayed, Rafik**

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**BACKGROUND:** *Salmonella* bacteria are facultative intracellular pathogens causing localized or systemic infections, in addition to a chronic asymptomatic carrier state. They have worldwide economic and public health significance. The largest number of food born illness cases attributed to poultry and poultry products are caused by the paratyphoid serotypes of *Salmonella*, namely *S. enteritidis* (group D) and *S. typhimurium* group (B). In Egypt, diagnosis and control of avian salmonellosis depend upon the use direct bacteriological isolation and PCR. This approach, however, is expensive, time consuming and require specialized laboratory and experienced personnel. Therefore, the need of a simple, sensitive, rapid and reliable test for detection of *Salmonella* Sp. sufficient to be applied on large scale of poultry is essentially required. Among the test candidates nominated to achieve this goal are the lateral flow immunochromatographic test (LFIT).

**MATERIAL AND METHOD:** The LFIT test for detection of SE and ST bacteria antigen in poultry and table poultry egg for human consumption. This work was planned to develop a simple rapid field test of high sensitivity, specificity, and accuracy that can improve and facilitates rapid field surveillance of salmonellosis. A rapid LFIT has been developed, in which rabbit antibodies against SE (somatic D) and ST (Somatic B) labeled with the gold chloride molecules laid on the conjugate pad. *Guinea pigs antibodies against SE and Guinea pigs antibodies against ST* were used as capture antibody at the test line 1 and test line 2 respectively of a nitrocellulose (NC) membrane and anti-rabbit antibodies were used as capture antibody at the control line (C) of the NC strip in the lateral flow layout.

**RESULTS:** The minimal microbial counts to be give positive of LFIT was 100CFU/100µl. The sensitivity, specificity and accuracy of LFIT as compared to PCR were calculated and was found to be 82.6%, 94.2 % and 90.6% respectively, The pretesting treatment of the test sample associated with pre-incubation in Tryptic soya broth for 4hr at 37°C increased significantly the sensitivity results and can detect 1CFU/100µl sample.

**CONCLUSIONS:** The developed test is a simple field rapid test of high sensitivity, specificity, and accuracy that control these pathogens from entering the food chain with subsequent reduction of the incidence of human salmonellosis transmitted through chicken and chicken food products

**OHS SOCIAL SCIENCE AND POLITICS****1 OHS A03 - SOCIAL SCIENCE AND POLITICS - SALON AB****Antimicrobials In Society: A One Health Approach in Kampala, Uganda**

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**BACKGROUND:** The rise of antimicrobial resistance is a major challenge. A One Health framework has been adopted by WHO, FAO and OIE, articulating connections between humans, animals and the environment through the movement of antimicrobials and microbes. One Health approaches also emphasise wider social and political contexts. In this research, we explore and contextualise reasons for high levels of antimicrobial use in humans and their animals amongst vulnerable populations, with a specific focus in Kampala, Uganda.

**METHODS:** This research focuses on informal urban settlements and peri-rurban pig and poultry farms in Kampala, Uganda. Using ethnographic methods including direct observations and interviews, we explore the roles played by antimicrobials in everyday lives and livelihoods. Analysis is informed by anthropological theory including medicalisation and pharmaceuticalisation.

**RESULTS:** We find that antimicrobials – particularly antibiotics – perform important roles in productivity and protection in our setting. In a context of socioeconomic precarity, antimicrobials allow day wage labourers to continue to work, and farmers to maximise meat production. Antimicrobials provide protection against inadequate water and sanitation infrastructure, for people and their animals, and against infection risks posed by socio-economic structures that create high rates of transactional sex.

**CONCLUSIONS:** Antimicrobials are an important part of care. Rather than being used indiscriminately, our informants use them carefully to provide care to their children, animals and themselves. The context in which this care is required is one of poor infrastructure and acute precarity, rendering people's lives and livelihoods vulnerable. Antibiotics are one of a few tools available to respond within this context. Efforts to scale back use of antibiotics must therefore consider ways to support peoples' lives and livelihoods such that reliance on antibiotics is reduced.

## 2 OHS A03 - SOCIAL SCIENCE AND POLITICS - SALON AB

**(Re)Claiming Water Stewardship in a Changing Climate – Learning from the Margins**

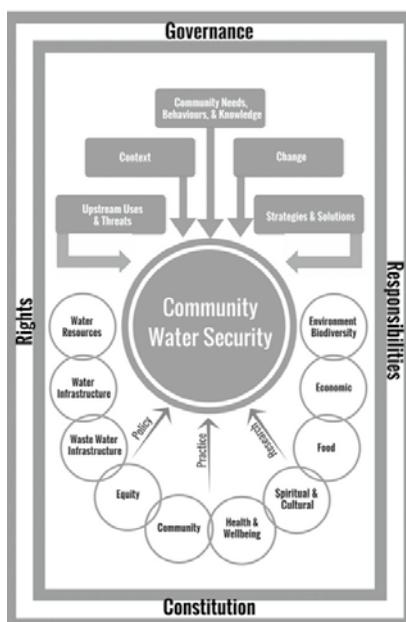
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**BACKGROUND:** As millions of people in low- and middle-income countries (LMICs) and recent experiences in South Africa and California can attest, access to sustainable, reliable water resources of suitable quality is not a sure thing. Resources are under threat from poor wastewater treatment, poor governance, competing uses for food, energy, and industry, and climate change impacts. But other dimensions to local water security are often overlooked – social, cultural, economic – that shape knowledge, attitudes, and practices around water and contribute to inequities. Given that local water security is essential to enable everyone to lead healthy, dignified, productive lives, we argue for a more nuanced framing of local water security and the development of tools that support comprehensive assessment and engagement at the community level. With a focus on health and wellbeing, systems, and feedback, the ecohealth and one health approaches lend themselves to this reframing of local water security considering both direct (e.g., water-related diseases) and indirect (e.g., nutrition and livelihoods) impacts on health.

**METHODS:** Mixed methods community-based assessments in East Africa and Canada have provided insight into the multiple facets of local water security. Focus groups, PhotoVoice, key informant interviews, community questionnaires, georeferencing, water point assessments, and water quality analyses have been employed to assess and understand knowledge, attitudes, and practices around local water resources and challenges.

**RESULTS:** A framework for local water security has been developed collaboratively with local community partners (Figure 1), to identify appropriate variables and develop, modify, and use local assessment tools that combine knowledge, human, and physical systems. Specific tools under development include the Community Water-Health Assessment Tool (C-WHAT) and WELLness, a tool for private well owners. The framing has also been applied to identifying and understanding the different water-related risks facing pregnant women.



**CONCLUSIONS:** Many communities have resources that can be brought to bear on local water security issues. This includes local knowledge and traditional interventions developed over time in response to challenges faced. Access to mechanisms for these communities to find a voice to share their stories and experiences enables them to (re) claim water stewardship and prepare for the uncertainties of a changing climate. The vulnerability and resilience of individuals, the cohesion and fragmentation of communities, and the capacity of governments to set standards, upscale successful development projects, sustain innovative approaches, and reinforce impacts of positive local strategies all require more flexible and responsive measurement strategies and tools. An age-old challenge for scientists is to find innovative and appropriate mechanisms to engage with communities to bridge research, policy, and practice for cohesive, reinforcing, sustainable difference on the ground. Reconceptualising and reframing complex systems using multiple knowledge systems in an era of big data and computational sophistication is not only possible, but essential.

## 3 OHS A03 - SOCIAL SCIENCE AND POLITICS - SALON AB

**MAN-IMAL: An experimental One Health degree program around animal-man-food**

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In 2011, the French government began a vast experiment on pedagogical innovation by funding 37 projects experimenting creative, collective, and cross-disciplinary approaches to teaching.<sup>1</sup> One of these projects, MAN-IMAL, is the first France-based international higher education degree program exclusively founded on the "One World, One Health" initiative. MAN-IMAL experiments: i) the use of ICTE<sup>2</sup>; ii) a multidisciplinary approach by its study content conceived by academics from Agricultural, Medical, and Veterinary Sciences; iii) as well as the interest of mixing students from various backgrounds (medical and veterinary studies, agricultural engineering, biological, and pharmacy studies). The created training courses include several Bachelor-level modules and an international One Health post-graduate degree taught entirely in English, the latter experimenting a multicultural approach. The teachers participating in the MAN-IMAL experiment have at their disposal a full-time support staff of 10 persons for 7 years, including pedagogical engineers, graphic designers, an audiovisual manager, education and studies assistants as well as a program coordinator. Today, almost 6 years after the beginning of the program, we are able to show results from multiple aspects of the project. Firstly, we present a successful multi-disciplinary cooperation between academics from different fields, secondly the particularities of coordinating a cross-disciplinary and multicultural class of students, and finally the importance of the close cooperation between the support staff and academics.

1. <http://www.enseignementsup-recherche.gouv.fr/cid59599/37-projets-de-formation-labellises-idefi.html>, <http://www.man-imal.fr/en/home/introduction>

2. *Information and Communication Technology in Education*



## 4 OHS A03 - SOCIAL SCIENCE AND POLITICS - SALON AB

**Human Behavioural Research at the Animal-Human Interface: Hunting and Trading of Bushmeat in Lao PDR**

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**BACKGROUND:** Lao PDR is a major source of, and transit route for, wildlife that is hunted and traded for consumption or medicinal purposes. The livelihood of most Lao people in rural areas is based on non-timber forest products and bushmeat is an especially important source of their protein. However, hunting and trading of wild animals carries a risk of viral spillover from animals to humans.

**METHODS:** As part of USAID's PREDICT-2 program, quantitative questionnaires and qualitative interviews and focus groups which focused on human interactions with wild animals were conducted in Champasack province, which borders Cambodia, in southern Lao PDR. Interviews and questionnaires took place in the same location as ongoing viral surveillance of humans, wildlife, and livestock, in an effort to connect viral findings with human behaviours.

**RESULTS:** In Na Pa Kieb village, 34 quantitative questionnaires, 11 in-depth quantitative interviews, and 1 focus group with 9 individuals were conducted. The data collected indicated that villagers often cross the Lao PDR border to Cambodia to hunt animals like squirrels, giant flying squirrels, and bats, for household consumption and/or to sell to wildlife markets. As well, Khmer people from Cambodian villages near the border bring their bushmeat to sell to Lao people. Furthermore, quantitative interviews were conducted with a wildlife market vendor and a market supervisor, in order to gain knowledge on where animals originate, wildlife consumption habits, and hygiene or personal protective equipment used in the capture or slaughter of animals.

**CONCLUSIONS:** Data collection is ongoing and all behavioural information will be combined with biological and virological findings to produce a greater understanding of how viruses are shared between animals and humans, and what precautionary measures could be taken to reduce risk. With the government of Lao PDR as an integral partner in this research, the aim is to increase the awareness of locals of the potential for viral disease emergence and decrease the risk posed to people who rely on bushmeat as vital sources of protein.

## 5 OHS A03 - SOCIAL SCIENCE AND POLITICS - SALON AB

**Evaluation of one health-ness: insights into interdisciplinary and cross-sectoral integration**

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**BACKGROUND:** One Health (OH) is promoted as an approach for many current health challenges, particularly those arising from the intertwined spheres of humans, animals and the ecosystems constituting their environment. Adequate responses to these so-called wicked problems are achieved through interdisciplinary and cross-sectoral integration and participation, which must consider features of complex adaptive systems. The EU COST funded “Network for Evaluation of One Health (NEOH)” has identified characteristic features of OH initiatives and developed an evaluation framework to systematically assess the degree of OH integration associated with their outcomes.

**METHODS:** The NEOH framework hypothesises that, by definition, each OH initiative tackles complex problems at the animal, human, environmental interface. Therefore, OH initiatives require adaptive leadership to apply systems thinking, transdisciplinary working, and flexible planning to enable an appropriate response to unexpected outcomes. In addition, infrastructure providing opportunities for learning at individual, team and organisational levels is essential, which in turn requires sharing of data, information and experiences. The NEOH evaluation framework provides tools and metrics to assess these aspects systematically in a semi-quantitative way and summarizes them in a OH-index and OH-ratio. We illustrate its application in eight case studies and discuss the information it provides.

**RESULTS:** The assessment tools systematically identify areas in the six dimensions that are working well, and gaps that may hamper the progress or success of a OH initiative. Because the scoring is based on professional judgment by the evaluators, the summarizing OH-index currently only provides a rough indication of the degree of integration achieved by an initiative. In contrast, the OH-ratio illustrates quite clearly how intentions to tackle the complexity of a challenge are matched with infrastructure for learning and sharing, as well as adequate leadership.

**CONCLUSIONS:** The framework is useful to assess OH integration in initiatives that aim to tackle complex health challenges. The concept of the OH-index and OH-ratio produce insights into the comprehensiveness of a given OH initiative. Further implementation of the framework will provide benchmarking and best practices to minimize subjectiveness inherent in many evaluations.

## OHS DRIVERS FOR EMERGING DISEASES 1

### 1 OHS A04 - DRIVERS FOR EMERGING DISEASES 1 - SALON AB

## Quantifying the health, economic, and ecosystem impacts of land-use change as a driver of disease emergence in Southeast Asia

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**BACKGROUND:** Deforestation and land use change are occurring at an unprecedented rate in tropical countries. This activity has significant private benefits (e.g. industry profits) and social benefits (e.g. economic development, job creation) but also long-term negative effects on ecosystem services (e.g. loss of biodiversity, increased pollution, reduced capacity for disease regulation) that can impact social welfare. Our previous work shows that land use change is one of the most important drivers of disease emergence (31.5% of total emergence), and is involved in increased public health impacts from zoonotic diseases. Our research aims to: 1) describe the relationship between land use change and infectious diseases; 2) quantify an ecosystem's disease regulating value; and 3) build models of land-use change and economics of disease emergence that can be used by local and regional policy makers.

**METHODS:** We collated data on the conversion and production costs from the oil palm industry, on health impacts on society (i.e. malaria cases, mosquito control expenditure), and on land cover and land use change. We used this information to construct a spatially explicit model to estimate the effects of land conversion on the disease regulation capacity of forests in Sabah Malaysia, particularly the burden of malaria due to land use change. We combined these results with data on ecosystem services values, revenues from palm oil, and conversion costs to create a dynamic optimization model that seeks to optimize social welfare by accounting for private benefits and social costs (e.g. disease treatment) of oil palm development, allowing us to determine the economically optimal rate of palm oil development for each year after disease risk and ecosystem services cost are considered.

**RESULTS:** Our results showed that land use change, particularly deforestation and forest fragmentation, is associated with the increase of malaria cases in Sabah Malaysia. Our dynamic optimization model showed that since 1993, once the health and ecosystem services costs are considered, the pace of land clearing for timber and subsequent conversion to oil palm has outpaced what would be optimal, resulting in public costs for society and reduced profits for the plantations involved in land conversion.

**CONCLUSIONS:** Land use change is an important driver of disease and the failure to consider the disease regulation as another ecosystem service can lead to a reduction in both private and social welfare. Quantifying the impact of land use change on disease and the resulting economic benefits and costs allows for the development of targeted control strategies. We are using this approach to work with stakeholders in government, industry, and local communities to enhance planning approaches and develop more sustainable strategies for land use that benefit public health as well as economic development and conservation.

## 2 OHS A04 - DRIVERS FOR EMERGING DISEASES 1 - SALON AB

## Impacts of urbanization and conversion of rainforests into large industrial oil palm plantations on the ecology of *Aedes* vectors in arbovirus foci, Côte d'Ivoire

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- 3: Centre for Neglected Tropical Diseases, Liverpool School of Tropical Medicine, Liverpool, United Kingdom;
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- 5: Swiss Tropical and Public Health Institute, Basel, Switzerland;
- 6: University of Basel, Basel, Switzerland;
- 7: Innovative Vector Control Consortium, Liverpool School of Tropical Medicine, Liverpool, United Kingdom

**BACKGROUND:** Arboviruses are zoonotic pathogens that have (re-)emerged from their enzootic reservoirs in Africa and the Americas, and caused many infections and diseases among humans worldwide, partly due to filtering effects of landscape anthropization forces on the ecology of *Aedes* vectors. We explored the effects of anthropogenic ecosystem disturbances such as urbanization and conversion of rainforests into large industrial oil palm plantations on the ecology of *Aedes* mosquitoes within yellow fever and dengue foci in Côte d'Ivoire.

**METHODS:** From January 2013 to December 2014, *Aedes* mosquitoes were sampled along an urbanization gradient (rural, suburban, and urban), and among four land-covers (rainforests, polycultures, oil palm monocultures, and rural-housing areas) using ovitraps, larval surveys, and human-baited double-net traps, coupled with socio-ecological surveys.

**RESULTS:** A total of 51,439 specimens of *Aedes* mosquitoes belonging to 20 species (*Ae. aegypti*, *Ae. africanus*, *Ae. albopictus*, *Ae. angustus*, *Ae. apicoargenteus*, *Ae. argenteopunctatus*, *Ae. dendrophilus*, *Ae. fraseri*, *Ae. furcifer*, *Ae. haworthi*, *Ae. lillii*, *Ae. longipalpis*, *Ae. luteocephalus*, *Ae. metallicus*, *Ae. opok*, *Ae. palpalis*, *Ae. stokesi*, *Ae. unilineatus*, *Ae. usambara* and *Ae. vittatus*) were collected. *Aedes* species richness was higher in rural (18 species), followed by suburban (7 species) and urban (3 species) areas. Conversely, the highest *Aedes* abundance was found in urban (n= 51,439; 50.7%), followed by suburban (32.6%) and rural (16.7%) areas. *Ae. aegypti* was the predominant species, and displayed higher abundance in urban areas (n= 26,072; 99.4%). *Aedes*-positive breeding site proportions were higher in urban (2,136/3,374; 63.3%), followed by suburban (1,428/3,069; 46.5%) and rural (738/2,423; 30.5%) areas. Rural areas exhibited a larger array of *Aedes* breeding sites ranging from natural containers (tree-holes...) to traditional containers (claypots...), and industrial containers (cans, tires, water receptacles...), while urban areas showed mainly industrial containers (2,129/2,136; 99.7%). Only four specimens of *Ae. aegypti* were collected in oil palm monocultures, whereas *Aedes* vectors showed higher abundance in polyculture (n= 28,276; 60.9%) and higher species richness (11 species) in rainforests. The anthropophilic *Ae. aegypti* and zoophilic *Ae. dendrophilus* and *Ae. africanus* vectors exhibited unexpectedly variable human blood-feeding behaviors according to human-disturbed land-covers, with high biting rates in polycultures (21.48 bites/human/day) and rural-housing (4.48 bites/human/day), and low biting rates in rainforests (0.62 bites/human/day).

**CONCLUSIONS:** In Côte d'Ivoire, anthropogenic ecosystem disturbances resulting from urbanization and conversion of rainforests into industrial oil palm plantations modify the ecology of anthropophilic and zoophilic *Aedes* arbovirus vectors. This suggests the coexistence of several arbovirus transmission cycles (enzootic: animal-to-animal; epizootic: animal-to-human; epidemic: human-to-human), with higher exposure of humans (citizens, villagers and farmers) to *Aedes* bites and yellow fever and dengue virus transmission risks in urban, rural-housing and polyculture areas. Arboviral disease control strategy should encompass integrated vector management (IVM), including landscape epidemiology, ecotope-based vector control, forestry, urbanism, water management, waste management and agricultural practices.

## 3 OHS A04 - DRIVERS FOR EMERGING DISEASES 1 - SALON AB

## The use of a nationwide pig movement network to predict the spatial risk of Nipah virus outbreaks in Thailand

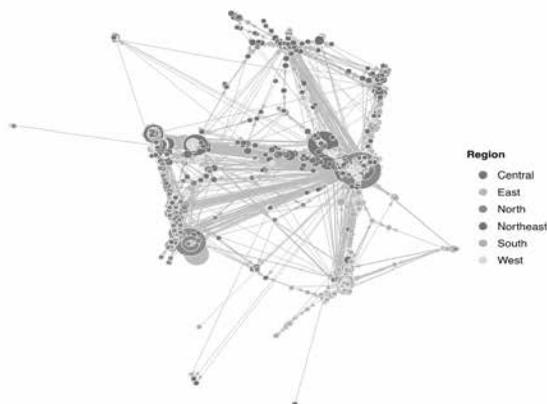
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**BACKGROUND:** Nipah virus (NiV) was first notified in pig populations in Malaysia in 1998. A total of 105 out of 265 infected human individuals died during the outbreaks and millions of pigs were culled to control the spread of the virus. NiV has never been reported in pigs in Thailand. However, the genetic evidence of the virus was detected in the flying foxes (*Pteropus* spp.) in the central plain of the country. High density of pig production as well as multiple colonies of flying foxes in the plain may drive the emergence of the disease. The present study therefore aimed to quantify the risk of NiV spread from the central plain to different regions of Thailand via the pig movement network.

**METHODS:** The national animal movement database was used in this study. We analyzed the pig movement data in May 2016. The month was previously identified as the highest recovery of NiV RNA viruses in bats. A directed one-mode network was constructed for the pig movement in the subdistrict level. The strongly and weakly connected component were examined. A Potential Surface Analysis (PSA) was applied to map the high-risk areas for bat-to-pig transmission. The map was then overlapped with subdistricts identified in the pig trade network to model the pig-to-pig transmission. The province with the highest number of high-risk subdistricts was chosen for further simulations. The NiV infection was mathematically seed into each subdistrict. The final epidemic size was observed and the infected probability was calculated. The programming language R was employed throughout analyzes.

**RESULTS:** The pig movement was identified in 1,627 subdistricts with 22,374 trade activities. A giant weakly connected component composing of 1,554 subdistricts (95.5% of the total nodes) was observed (Fig. 1). Based on our risk-based selection criteria, Chon Buri province was chosen. After simulations, 407 subdistricts across the country were identified as the NiV destinations. The highest risk was observed in Thai Ban Mai subdistrict, Mueang district, Samut Prakan province (Geocode: 110116) with the infection probability of 41.8%.



**CONCLUSIONS:** We suggested that the nationwide pig movement network in Thailand was vulnerable to the spread of NiV and other infectious diseases. Once the NiV emerges, it may spread to different regions of the country. The related authorities should strengthen the surveillance program on the network.

*Fig. 1. A giant weakly connected component found in the nationwide pig movement network at subdistrict level (#node: 1,554, #tie: 3,424). The arrowhead indicates the direction of animal movements.*

## 4 OHS A04 - DRIVERS FOR EMERGING DISEASES 1 - SALON AB

**Ecosystem Change and Zoonoses Emergence**

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**BACKGROUND:** Changes in land use change, animal populations and climate, primarily due to increasing human populations, drive the emergence of zoonoses. Force of infection (FOI), which for zoonoses is a measure of the ease with which a pathogen reaches the human population, can change with specific zoonoses and context.

**METHODS:** Here we outline three habitat classifications - domestic, peridomestic and sylvatic, where disease ecology alters the FOI of specific zoonoses namely *E. coli* O157, leptospirosis and *Echinococcus multilocularis*. In addition, we examine how the relationship between the vector, pathogens, reservoirs hosts, habitats and the potential for Lyme borreliosis in humans alters with different habitat contexts.

**RESULTS:** Human intervention has an overriding effect in the emergence of zoonoses therefore we need to understand the disease ecology, evolutionary capacity, virulence, resistance, stability, infectivity etc. of pathogens that are likely to interact differently within dynamic landscapes and the context is hugely significant. Biodiversity is just one factor of many that impacts the FOI.

**CONCLUSIONS:** Interdisciplinary collaboration, incorporating One Health land use planning, must appreciate that comparable empirical studies with powerful inference are difficult because of differences in local context. Further integration of additional explanatory variables that influence FOI such as human behaviour, economics and social dimensions will facilitate risk analyses to predict, manage and respond to zoonotic outbreaks.

## 5 OHS A04 - DRIVERS FOR EMERGING DISEASES 1 - SALON AB

**Identification of molecular determinants of aquatic and terrestrial morbillivirus cross-species infections**

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**BACKGROUND:** Members of the genus *Morbillivirus* are capable of infecting a wide variety of mammalian species, including humans, canines, felines, ruminants, and cetaceans. Cetacean morbillivirus (CeMV), canine distemper (CDV) and phocine distemper viruses (PDV) have in recent decades caused mass mortality events in both aquatic and terrestrial mammals. CDV is characterized by a broad host range, infecting not only carnivore and omnivore species, but also non-human primates, indicating that CDV may pose a zoonotic threat upon eradication of the closely related measles virus from the human population. In this study our primary aim was to identify molecular determinants important for intra- and inter-species transmission of aquatic and terrestrial morbilliviruses.

**METHODS:** CDV- and CeMV-infected wildlife tissue samples from terrestrial and marine mammals and cell culture adapted CeMV strains were processed and prepared for deep sequencing on an Illumina MiSeq system. The morbillivirus receptor CD150 from different phocid species was amplified, sequenced and cloned into an expression vector. New reverse genetics systems were generated for dog and Caspian seal CDV strains. Furthermore, the fusion (F) and hemagglutinin (H) glycoproteins from various morbillivirus strains were cloned for use in virus fusion and entry assays (pseudotyped-VSV) using cells expressing heterologous CD150 receptors.

**RESULTS:***Aquatic morbillivirus*

The CeMV strain, dolphin morbillivirus, infects a wide range of cetacean host species with minimal genetic adaptation. However, CeMV adaptation to growth in African green monkey (Vero) cells appears to require changes in the matrix protein.

*Terrestrial morbillivirus*

Phylogenetic analysis of the full genome of the CDV strain responsible for the mass mortality in Caspian seals in 2000 showed that this strain is a member of a novel lineage most closely related to the 'oldest' lineage: American I. Host molecular determinants regulating virus transmission were investigated by comparing CD150 receptors of different phocid and other terrestrial CDV host species. New reverse genetics systems based on viral sequences amplified from CDV-infected tissues from a dog and Caspian seal were used to assess the role of specific mutations in species tropism.

**CONCLUSIONS:** The combination of rapid full genome sequencing and *de novo* generation of recombinant morbilliviruses directly from wildlife tissue samples will enable more comprehensive analyses and risk assessment of future disease outbreaks caused by morbillivirus cross-species infections.

## OHS DRIVERS FOR EMERGING DISEASES 2

### 1 OHS A05 - DRIVERS FOR EMERGING DISEASES 2 - SALON AB

#### **Leveraging viral phylodynamics to inform spatiotemporal transmission of viral infectious diseases in Africa: 2009 Influenza A/H1N1 in Africa**

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**BACKGROUND:** Emerging and re-emerging viral pathogens pose serious health threats to both humans and livestock. Although all global regions are at risk of viral infectious disease outbreaks, the African continent is disproportionately disadvantaged due to its weak health systems to mitigate, manage and prevent further spread of the pathogens in an outbreak situation. Molecular sequence data in combination with ecological, economic and demographic factors have proven to robustly describe phylodynamics of viral infectious diseases. Human mobility plays a central role in infectious disease transmission and due to economic constraints probably road transport networks are the key drivers of infectious disease spread in Africa rather than air travel, railway networks or Euclidean distances between sampling locations

**AIMS AND OBJECTIVES:** This study sought to unravel the introduction, the spatial dispersal pattern and to evaluate the contribution of genetic, ecological, and economic predictors of viral infectious transmission patterns using the case of 2009 Influenza A/H1N1 pandemic virus on the African continent.

**MATERIALS AND METHODS:** In this study, we combined ecological, economic and demographic data Bayesian phylogenetics to unravel the introduction, dispersal and test predictors of viral infectious diseases transmission patterns using the case of 2009 Influenza A/H1N1 pandemic virus on the African continent.

**RESULTS, DISCUSSION AND CONCLUSIONS:** Our study suggested that there were multiple simultaneous introductions of the 2009 H1N1 pandemic virus into the African continent and the phylogenetically inferred probable source populations existed in North America and Asia. Transmission predictor analysis suggested that proximity (geographical distance), air travel, and sampling location latitude might have contributed significantly to the spread of the 2009 Influenza A/H1N1 pandemic virus in Africa.



## 2 OHS A05 - DRIVERS FOR EMERGING DISEASES 2 - SALON AB

**Risk of pneumonia among residents living near goat and poultry farms**

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- 3: Wageningen University, Animal Production Systems group, The Netherlands;
- 4: NIVEL, Netherlands Institute for Health Services Research, The Netherlands

**BACKGROUND:** The human health risks associated with industrial livestock production become increasingly clear. Recent research in the Netherlands suggests an increased risk of pneumonia among residents living close to goat and poultry farms, but the causes of this increased risk are unknown. For goat farms, specific analyses make it unlikely that the Dutch Q-fever epidemic of 2007-2009 is still responsible for the elevated pneumonia incidence reported over the years 2010-2013. Around poultry farms, the increased risk may be caused by the high particulate matter emissions from these farms, but additional evidence is required to support this hypothesis. Besides these uncertainties, there are some inconsistencies in results of previous analyses, which are hard to interpret because of the different measures of exposure and statistical methods used in different studies. More evidence and certainty is urgently needed since the risk of pneumonia would add to several other environmental and public health impacts of livestock production, such as chronic respiratory effects, odor annoyance, zoonotic disease transmission, eutrophication and greenhouse gas emissions. This multitude of effects influences political decisions, for example regarding the expansion of goat farms. More evidence may be obtained from analyses over more recent years than the 2007-2013 period on which previous analyses were based. In this study, such new analyses are performed to investigate whether the relation between general practitioner-diagnosed pneumonia and living close to goat and poultry farms can be confirmed for more recent years. In addition, the influence of more specific farm characteristics is studied, i.e. to distinguish between farms housing broilers or laying hens, thereby potentially providing more information regarding the causes of an increased pneumonia incidence.

**METHODS:** A cross-sectional analysis was performed, including about 100,000 patients registered in 23 general practices in a livestock-dense area in the south-east of the Netherlands, with on average about 35 goats, 130 cattle, 1,400 pigs and 8,000 chickens per km<sup>2</sup>. Analyses are based on diagnoses of pneumonia from 2014-2016, as registered in electronic medical records. The association between pneumonia and farm proximity was analyzed using logistic regression models, which included several measures of distance of resident homes to goat and poultry farms as exposure variables, as well as variables to account for differences in sex, age and the presence of other farms.

**RESULTS:** Associations between pneumonia incidence and residential proximity to goat and poultry farms will be presented at the conference. This update over the years 2014-2016 should indicate whether the previously found associations (over the years 2007-2013) can be confirmed.

**CONCLUSIONS:** Previous studies show an increased risk of pneumonia among residents living within 1-1.5 km from poultry farms and 1-2 km from goat farms. The ongoing research will establish whether this association is still present in more recent years.

## 3 OHS A05 - DRIVERS FOR EMERGING DISEASES 2 - SALON AB

## Effect of Habitat Modification on Risk of Scrub Typhus, An Emerging Infectious Disease in Bhutan

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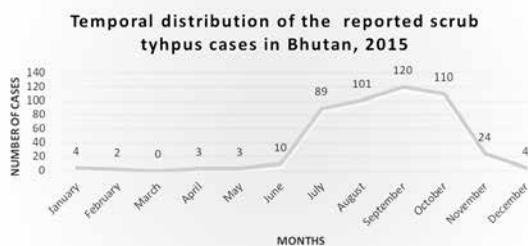
- 1: Khesar Gyalpo University of Medical Sciences of Bhutan;  
 2: Massey University, New Zealand;  
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**BACKGROUND:** Scrub typhus or tsutsugamushi disease is an emerging zoonotic infection causing acute febrile illness in humans. The annual incidence of diagnosed scrub typhus in Bhutan has been increasing since first detected in 2008, reflecting significant public health impact. We conducted a nation-wide prospective observational study and a case-control study to measure the impact of this re-emerging disease in Bhutan and understand major environmental drivers.

**METHODS:** Three sources were used to recruit as many incident cases as possible occurring throughout Bhutan in the year 2015: (1) patients diagnosed in hospitals throughout Bhutan (Rapid diagnostic test RDT+ve); (2) notified cases to the Royal Centre Disease Control in Thimphu (RCDC) through national sero-surveillance (ELISA+ve); and (3) patients enrolled in the matched case-control study (78 cases and 205 controls from 11 districts, mainly located in southern Bhutan, between October and December 2015). In the case-control study, for each case, two controls were matched by village/location and a third was randomly selected from people visiting the same hospital. Interviews conducted using a standard questionnaire collected data on environmental and occupational exposures in the previous month.

**RESULTS:** The prospective study identified a total of 470 scrub typhus cases in Bhutan during January-December 2015, a 10-fold increase compared to cases identified through passive surveillance in previous years. The annual cumulative incidence was 60.5 new cases per 100,000. There was a clear seasonal pattern, with an epidemic peak between August and October, and a higher incidence in southern districts of Bhutan. In the case-control study, major risk factors identified for clinical scrub typhus included: harvesting cardamom (OR 10.6 to 18.7); clearing bush (OR 4.9); and sitting or sleeping on grass (OR 4.1).

**CONCLUSIONS:** Our study confirmed scrub typhus as an emerging disease in Bhutan. The seasonal pattern and increased risk associated with clearing bush and harvesting cardamom indicate an effect of habitat modification on the occurrence of disease emergence, and suggest scrub typhus may be an occupational hazard of this type of farming. Cardamom farming has recently been introduced to Bhutan and is becoming increasingly common. This study highlights the role of a change in agricultural practice as a potential driver for emergence of scrub typhus in Bhutan.



## 4 OHS A05 - DRIVERS FOR EMERGING DISEASES 2 - SALON AB

## A One Health Understanding of the Rodent Meat Value Chain in the Mekong Delta, Vietnam: Implications for Zoonotic Disease Risk Mitigation (Wellcome Trust VIZIONS)

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2: Metabiota, United States of America;

3: Oxford University Clinical Research Unit in Vietnam

**BACKGROUND:** The Mekong Delta is a large floodplain in southern Vietnam and is one of the world's most productive rice and aquaculture zones. Agriculture expanded rapidly in the late 1980s and, as rice production increased, rodent populations expanded to fill a growing ecologic niche. By the late 1990s, the severity of rodent outbreaks prompted national policies aimed at controlling rodent populations through synchronized planting and live capture. In the last two decades, as a byproduct of increased live capture, the region has seen a booming market for rodent meat, estimated at 3,500 tons annually.

Rodents are of particular importance in the emergence of zoonotic diseases and have been associated with nearly 20% of new human pathogens since 1980. Given the intensity and scale of this rodent meat value chain, further research on human-rodent interactions may help better characterize the risk of zoonotic spillover and support the development of mitigation strategies.

**METHODS:** As part of the Wellcome Trust VIZIONS project, we conducted 92 in-depth interviews between 2014 and 2017 throughout An Giang and Dong Thap provinces, Vietnam with individuals involved in the rodent value chain. Interviews were recorded using digital audio recorders and then translated and transcribed into English by native speakers familiar with the value chain. Transcripts were analyzed in Dedoose using a grounded theory approach.

**RESULTS:** The rodent value chain involves distinct roles, with individuals often fulfilling one or more different activities. Common roles include: rodent hunting/trapping, transporting, small- to large-scale accumulation, slaughtering, and market sale. Rodents are mostly collected live in small metal cages along the perimeter of rice fields. Transporters typically shuttle stacks of cages between collection points and regional markets by motorbike for small loads and by truck or van for large loads. Rats are generally kept live until sold, at which point slaughterers will kill, skin, and butcher the rodent for consumers. In larger settings, rodents are butchered in mass and transported on ice to urban centers.

Throughout the value chain, rodent workers rarely utilize personal protective equipment, explaining that it makes the slaughtering too difficult or diminishes their dexterity at grabbing and manipulating live rodents. Rodent workers note frequent bites and slaughterers, in particular, are in constant contact with rodent blood and viscera. While some workers wear face masks, exposure to rodent hair and aerosolized urine and feces is ever-present. Despite the pervasive exposure, the population generally perceives field rodents to be "clean" and "healthy," contrasting them to "city rats" or farmed livestock.

**CONCLUSIONS:** Rodent workers have an inadequate understanding of the health risks that rodents can pose; there is a poor understanding of how rodent-borne diseases can be transmitted to humans. Greater public health messaging innovative strategies to mitigate exposure risk are required.

## Climate variability and infectious diseases nexus: Evidence from Sweden

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2: Uppsala University, Sweden

**BACKGROUND:** Many studies on the link between climate variability and infectious diseases are based on biophysical experiments, do not account for socio-economic factors and with little focus on developed countries.

**METHODS:** This study examines the effect of climate variability and socio-economic variables on infectious diseases using data from all 21 Swedish counties. Employing static and dynamic modelling frameworks, we observe that temperature has a linear negative effect on the number of patients. The relationship between winter temperature and the number of patients is non-linear and "U" shaped in the static model. Conversely, a positive effect of precipitation on the number of patients is found, with modest heterogeneity in the effect of climate variables on the number of patients across disease classifications observed. The effect of education and number of health personnel explain the number of patients in a similar direction (negative), while population density and immigration drive up reported cases. Income explains this phenomenon non-linearly. In the dynamic setting, we found significant persistence in the number of infectious and parasitic-diseased patients, with temperature and income observed as the only significant drivers.

## HS VACCINES 1

### 1 OHS A06 - VACCINES 1 - SALON AB

## Portfolio Approach, Development and Stockpile of MERS-CoV Vaccines: A Case Study

**Blayer, Simone;** Saville, Melanie; Norheim, Gunnstein; Gouglas, Dimitrios

CEPI, United Kingdom

**BACKGROUND:** CEPI was launched at Davos 2017 as a response to the emerging consensus following the Ebola and Zika outbreaks that a coordinated, international and intergovernmental plan was needed to develop and deploy new vaccines to prevent future epidemics. As such, CEPI's mission is to stimulate, finance and co-ordinate vaccine development against diseases with epidemic potential where market incentives fail. There is broad agreement that CEPI should avoid duplication and focus funding on the critical gap - the lack of capability to move vaccine candidates quickly from the preclinical stage through to proof of principle.

**METHODS:** This vaccine development requires funding the preclinical and clinical development required for proof of principle, facilitating early and frequent interactions between vaccine developers and regulators, and ensuring that a vaccine candidate can be successfully deployed in the event of an outbreak by working closely with clinical investigators, public health officials, and national regulatory authorities in at-risk countries. In addition to directly funding the development of specific vaccine candidates and platforms, CEPI will also fill gaps in developing biological standards, assays, animal models and other aspects of regulatory science for its funded projects and will coordinate with other institutional stakeholders to set priorities, develop pathogen specific road maps, and plan for accelerated clinical testing and regulatory review of products in epidemic situations. Finally, CEPI will coordinate with major institutional stakeholders such as Gavi and UNICEF on vaccine stockpiling and distribution.

**RESULTS:** In this paper, we will introduce the CEPI portfolio of MERS CoV vaccine candidates as an example of our work and discuss the technologies behind the vaccine programmes. We will also review manufacturing, stockpile, preclinical and clinical strategies deployed in emergency settings vs conventional vaccine development. We will present progress made on filling gaps on aspects of critical regulatory science and mechanisms of engagements of regulatory authorities for the enhancement of use of experimental vaccine candidates in emergency settings for efficacy trials in at-risk countries.

**CONCLUSIONS:** The CEPI portfolio approach for MERS CoV vaccine is an example for a coordinated, rapid development and deployment of vaccine candidates in emergency settings.

## 2 OHS A06 - VACCINES 1 - SALON AB

**Protective non-specific effect of rabies vaccine in humans, dogs and cattle: One Health implications**

**Conan, Anne:** Knobel, Darryn

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Non-specific effects of vaccines are defined as effects on recipient's health beyond those resulting from the vaccine's effect on its specific target agent. It has been proposed that the type of vaccine determines the nature of the effect, with live vaccines having beneficial non-specific effects and non-live vaccines having deleterious ones. To date, these effects have only been reported in human populations. We present the results of three separate studies (two published and one new study) reporting non-specific effects of rabies vaccine in humans, dogs and cattle, and discuss their implications.

The first study was a Phase 3 trial of RTS,S malaria vaccine in children in two age categories. Rabies vaccine was used as a comparator vaccine in the control group in the older age category. The low incidence of meningitis and cerebral malaria in this group relative to other study arms in both age categories is most parsimoniously explained by a protective non-specific effect of rabies vaccine. The second study was a population-based cohort study in free-roaming dogs in a high-mortality setting. During quarterly visits, heads of households were asked about owned dogs, including data on entry and exit events, demographics (sex and age) as well as rabies vaccination. Survival analyses using a piecewise exponential survival model by age group was performed, accounting for clustering within household. The study showed a reduced risk of death for vaccinated dogs (from 16 to 56%) in all age groups. The final study was a quasi-randomised controlled trial of non-specific effects of rabies vaccine on the incidence of bovine respiratory disease (BRD) in feedlot cattle. Following their arrival at the feedlot facility, 5,126 cattle from high-risk lots were allocated to receive a single intramuscular injection of rabies vaccine in addition to routine prophylactics, or to a control group that received routine prophylactics only. The risk of BRD within the first 60 days of arrival was reduced by 9% (95% confidence intervals 0% - 18%) in the rabies-vaccinated group, relative to the control group.

The three studies are consistent with the hypothesis of a protective non-specific effect of rabies vaccine, a non-live vaccine. This casts doubt on the proposition that non-specific effects of non-live vaccines are necessarily deleterious. Although rabies vaccine is known to be a safe and efficacious vaccine, its routine use as pre-exposure prophylaxis in children is not recommended as it is not cost-effective in most situations. A substantial non-specific protective effect against other infections would improve the cost-comparability of routine pre-exposure prophylaxis vs. post-exposure prophylaxis in areas where canine rabies is endemic. We therefore recommend further studies in animals and people to quantify this effect and understand the biological mechanism through which it arises.

**3 OHS A06 - VACCINES 1 - SALON AB****Brucellosis in the changing peri-urban dairy systems of West Africa**

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1: RVC, United Kingdom;

2: Ecole Inter-Etats des Sciences et Médecine Vétérinaires de Dakar, Senegal

The dairy sector in West and Central Africa is evolving as demand for dairy products is growing and consumer preferences and behaviours are changing. High rates of urbanisation alter purchasing patterns and taste for value added and convenient products. The growth of the dairy industry in the region is undoubtedly positive in terms of increased nutrition and diversity in the diets of consumers, as a driving force for poverty alleviation amongst farmers and as an avenue for national and regional economic growth. However, this burgeoning demand is not without inherent risks in terms of the spread of zoonotic diseases and exposure to food borne pathogens. Of these risks, brucellosis is perhaps one of the most significant threats due to the potential impact on both human health and animal health and productivity.

In order to characterise this emerging sector and estimate the impact of brucellosis in West and Central Africa, a multi method approach was applied in six countries (Senegal, Cameroon, Togo, Mali, Burkina Faso and Ivory Coast). A cross sectional seroprevalence survey was carried out on bulk milk samples alongside a knowledge, attitudes and practices questionnaire administered to cattle keepers. Following this, focus group discussions with farmers and milk processors aimed to investigate opinions on barriers within dairy farming and attitudes regarding animal health care and vaccines. In general, those participating in focus groups had little knowledge about or access to vaccines for their livestock and felt that adequate healthcare as well as financial and land issues were the biggest barriers facing dairy farming at the present time.

This work lays the foundations for the next stages in estimating the farm level economic impact of the disease in this setting and assessing potential intervention strategies to inform policy within the region.

## 4 OHS A06 - VACCINES 1 - SALON AB

## Evaluation of Rabies Post-exposure Prophylaxis Procurement and Delivery System in Vietnam

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**BACKGROUND:** Vietnam has made monumental progress towards reducing canine-mediated human rabies deaths. Within a 22 year time frame, cases have dropped 82%, from 505 cases in 1994 to 91 cases in 2016. This reduction was largely due to the expanded access to rabies biologics throughout the country. While an average of 400,000 vaccine doses are administered and 32,000 people receive equine immunoglobulin (eRIG) each year, limited data exists regarding the procurement, distribution, storage, and administration of rabies biologics at the provincial and district level medical centers.

**METHODS:** Between February through June 2017, Vietnam's National Rabies Control Program surveyed 191 medical centers that order biologics directly from vaccine manufactures in 2016. Questionnaires were emailed or mailed to all 63 provincial medical centers (PMC) and 130 district medical centers (DMC).

**RESULTS:** There was a 68.59% (63 PMCs and 69 DMCs, N=132 medical centers) response rate. 100% (131) medical facilities provided vaccine and 53.4% (70/131) provided eRIG. 43.5% (57) medical centers experienced delays in receiving vaccine or eRIG and 77 (58.8%) medical centers experienced a vaccine or eRIG shortage within the past year. Approximately 90% (118) medical centers used their internal funds to pay for biologics. Nineteen (15%) facilities depended on refrigerated space for other vaccines to store rabies biologics. Eight-seven medical facilities (66.4%) responded that lack of knowledge was the primary barrier for wound treatment after an animal exposure. Medical centers reported that financial cost (55%) to the patient, lack of vaccine/eRIG and the distance from health facilities (31%) were reported barriers to getting rabies biologics. 65% of prediction demand of rabies vaccine and immunoglobulin depended on amount of patients monthly.

**CONCLUSION:** Vietnam rabies system is inadequate VPs in district level. Provincial level did not have a VPs providing eRIG due to many problems, including population in that areas did not receive eRIG timely. The demand of VX/eRIG increase but not enough supply. The price of VX is still high. VP delays and shortages are from VX manufactures, solving policy and resource obstacles among VX manufactories to promote them producing more rabies vaccine. Integrated interventions between governments and vaccination companies that minimize administrative procedures and encourage pharmaceutical companies to subsidize vaccine/RIG cost could further reduce the price and increase VPs.



## 5 OHS A06 - VACCINES 1 - SALON AB

## A systematic review of strategies for reducing missed opportunities for vaccination

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2: Centre for Evidence Based Health Care, Stellenbosch University

**BACKGROUND:** Missed opportunities for vaccination (MOVs) occur when persons eligible for vaccination visit a health facility and do not get the vaccines they need. We conducted a systematic review to assess the effects of interventions for reducing MOVs.

**METHODS:** We conducted a literature search in PubMed, Scopus, and the Cochrane Library. Three authors independently screened search outputs, reviewed full texts of potentially eligible papers, assessed risk of bias, and extracted data; resolving disagreements by consensus. We expressed study results as risk ratios (RR) with their 95% confidence intervals (CI) and assessed the certainty of the evidence using the Grading of Recommendations Assessment, Development and Evaluation (GRADE) tool.

**RESULTS:** Six studies (five trials and one cohort study) met our inclusion criteria, all conducted in the United States of America. All six studies had various limitations and were classified as having a high risk of bias. We found moderate certainty evidence the following interventions aimed at reducing MOVs probably improve vaccination coverage: patient education (RR 1.92, 95% CI 1.38 to 2.68), patient tracking and outreach sessions (RR 1.18, 95% CI 1.11 to 1.25), and patient tracking, outreach, and prompting (RR 1.24, 95% CI 1.18 to 1.31). In addition, we found low certainty evidence that education targeted at clinic and family settings concurrently may increase vaccination coverage (RR 1.25, 95% CI 1.08 to 1.46).

**CONCLUSIONS:** The currently available evidence supports the use of provider education; patient education; and patient tracking, outreach, and prompting as interventions to opportunities for vaccination and improve vaccination coverage. Rigorous trials are required to confirm these findings and increase the certainty of the current evidence base.

**OHS VACCINES 2****1 OHS A07 - VACCINES - SALONS AB****Development of a highly pathogenic avian H7N9 influenza disease model in mouse**

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H7N9 influenza virus is a threat to public health because it has caused 1557 human laboratory-confirmed cases as of 25 July 2017, with 605 of them resulting in death. Although the avian origin H7N9 virus is currently unable to effectively transmit between humans, the potential of acquiring this trait through adaptation poses an imminent pandemic threat to society. To better understand the pathogenesis of H7N9 virus and to ultimately develop and evaluate novel vaccine protection, we established a mouse disease model infected by the highly pathogenic avian influenza A/British Columbia/2015 (H7N9) virus. For this model, four groups of 12 mice each were infected intranasally with either different doses of the virus ( $10^3$  pfu/mouse, 104 pfu/mouse and 105 pfu/mouse) or PBS which served as the mock control. Both body weight and survival rate were monitored daily for 12 days. Mice were sacrificed and organs collected when they fell below 20% of their total body weight. On day 2 and 5 post-infection, 3 mice from each group were sacrificed and the lung, spleen and brain were collected.

In the  $10^3$  pfu/mouse group, 50% of the mice fell below the body-weight cut-off by day 7 and were sacrificed, whereas the rest of the mice fell below the cut-off on day 8 and were also sacrificed. Similarly, in the 104 pfu/mouse group, 100% of the mice fell below the cut-off weight by day six and were sacrificed. In the 105 pfu/mouse group, 50% of the mice were sacrificed by day four, and the rest sacrificed at day five. On the last day (day eight) whereby the last mice of virus groups were sacrificed, the PBS mock group was also sacrificed and the trial was finished. Currently, cytokine and chemokine profiles as well as viral titres in the collected samples are being analyzed. For future studies 103 pfu/mouse will be chosen. This model will allow identification of viral virulent factors and evaluation of antiviral interventions.

## 2 OHS A07 - VACCINES - SALONS AB

**A trial to assess the thermotolerance of an inactivated rabies vaccine**

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- 2: MSD Animal Health, Netherlands;
- 3: Global Animal Health Tanzania;
- 4: University of Glasgow, UK;
- 5: MSD Animal Health, UK

**BACKGROUND:** Canine mediated human rabies is a neglected tropical zoonotic disease responsible for approximately 59,000 deaths and 8.6 billion USD in losses annually. The highest incidence is in rural Africa. Where annual mass dog vaccination (MDV) is implemented coverage of 70% will eliminate rabies. Teams in vehicles usually deliver campaigns, however this is expensive and, due to the requirement to refrigerate vaccines, reach is limited to areas in proximity to facilities with refrigeration units. Thermotolerant vaccines, storable at ambient temperatures for extended periods, could alleviate these constraints. The study's aim was to investigate the thermotolerance of the Nobivac® Rabies vaccine, commonly used in MDV around the world. Our objective was to determine whether the immunological response following non-cold-chain storage was not inferior to the response elicited by doses of the same vaccine following cold-chain storage (4°C).

**METHODS:** A controlled and randomized non-inferiority trial was carried out comparing the serological response at four weeks post vaccination in Tanzanian dogs inoculated with vaccine stored at elevated temperatures for different periods of time, with the response in dogs vaccinated with vaccine stored at 4°C.

**RESULTS:** The effectiveness of the vaccine at stimulating rabies neutralizing antibody was not inferior to cold-chain stored vaccine when it was stored for up to six months at 25°C or for three months at 30°C.

**CONCLUSIONS:** The neutralising antibody titre (a surrogate of protection) stimulated by the vaccine following extended storage at high temperatures is not inferior to cold-chain stored vaccines. These findings enable consideration of novel delivery strategies. For example vaccines could be stored in remote communities for extended periods allowing dogs to be vaccinated throughout the year, rather than annually. This could result in more consistent coverage (Figure 1) with less risk of herd immunity dropping below the critical threshold, below which rabies transmission is sustained. As with the successful smallpox and rinderpest eradication programs, a thermotolerant rabies vaccine that enables communities to manage their own campaigns could have a transformative impact on global rabies elimination plans ('Zero by 30').

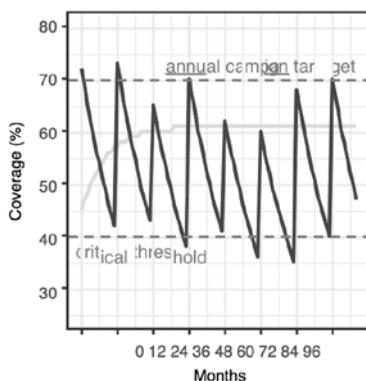


Figure 1: Blue line is hypothetical vaccination coverage, with peaks representing levels immediately after annual campaigns. Subsequent decline results from birth of susceptible pups and natural mortality of vaccinated dogs. Coverage is expected to remain above the critical threshold (lower red line) if the target of 70% (upper red line) is reached. The green line shows hypothetical coverage following community-managed delivery using vaccines stored locally and used throughout the year.

## 3 OHS A07 - VACCINES - SALONS AB

**ACCEPTANCE OF HETEROLOGOUS PRIME-BOOST VACCINATION REGIMENS – AN ASSESSMENT**

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**BACKGROUND:** Heterologous prime-boost regimens involve delivering antigens through different vaccine types, administered in a defined sequence. The approach is used to develop vaccines inducing both humoral and cellular immune responses as considered necessary against some major infectious diseases for which no efficacious vaccines are available, such as tuberculosis, HIV and Ebola virus disease. Additionally, the approach might become relevant for anti-cancer vaccines. Several vaccine candidates are in the development pipeline but none have reached licensure yet. An assessment has been performed to explore the potential future acceptance and uptake of the heterologous prime-boost vaccination concept.

**METHODS:** Following a literature review, 62 semi-structured key informant interviews were conducted with representatives of global and national stakeholders including National Medicines Regulatory Authorities, vaccination programs, health workers, academics and non-governmental organizations in 6 countries across 4 continents. Additionally, a quantitative online survey was answered by 50 respondents. It presented different scenarios in which the regimen might be introduced and asked respondents to indicate the expected benefits and challenges.

**RESULTS:** The majority of the respondents were unfamiliar with the heterologous prime-boost approach, despite belonging to the vaccine and public health community. Regional differences in knowledge and implementation considerations about the heterologous prime-boost vaccination approach were noted amongst respondents. While the overall first reaction to the approach was cautiously positive, familiarity and excitement grew the closer to research the key informant worked. Particularly appealing was the prospect of developing vaccinations against major public health threats. Respondents working on vaccine delivery and logistics expressed stronger reservations, mainly linked to the challenge of ensuring complete vaccination as per recommended schedule. A scenario in which a heterologous prime-boost vaccine was offered to adults to protect them against a disease for which currently no vaccine is available was considered the most likely, followed by a scenario in which such a vaccine, or an alternative to an existing vaccine requiring more than 2 appointments, was offered to children as part of the EPI schedule. Deploying heterologous prime-boost vaccines in anticipation of, or in response to, a disease epidemic was seen less favourably. With regard to licensure and uptake at country level, it was highlighted that such a product needed to be assessed holistically, taking safety, potential impact, delivery concepts, as well as communications into account.

**CONCLUSIONS:** Respondents were generally excited about a vaccination technology offering the prospect of controlling major diseases, but were conscious about the potential logistical challenges associated with its delivery. There is a need to prepare the public health community via proactive, transparent and scientifically solid communication.

## 4 OHS A07 - VACCINES - SALONS AB

**Identifying Genomic Predictors of Vaccine Response in Swine**

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Vaccination is recognized among the most effective tools for the control of infectious diseases, and is a widely-used disease-prevention strategy in the pig industry. However, response to vaccination can be highly variable between individuals, and the molecular events that lead to, or anticipate protective immunity are not well understood. We investigated gene expression patterns in whole blood and microbiome signatures in the gut as potential predictors of a protective immune response. The effect of raising pigs with or without antibiotics on these traits was also investigated.

*Mycoplasma hyopneumoniae* (*M.hyo*) vaccine was chosen as an exemplifier, because it elicits both humoral and cell-mediated immune responses. Healthy *M.hyo* infection free piglets (n=120) were used at the University of Alberta, Canada, swine research facility. At processing, 80 piglets received 0.5 ml Oxytetracycline, whereas the remaining were raised antibiotic free. Blood samples for RNA-Seq analysis were collected on experimental Day 0 (D0; 28 days of age) just prior to vaccination, D2, and D6 post-vaccination. A vaccine booster was given at D24. Fecal samples for microbial DNA sequencing were collected at 7 days of age, and on experimental D0 and D35. At D35, blood samples were collected, and *M. hyo*-specific antibodies in serum were quantified, and the results were used to classify pigs based on antibody titer levels, and groups of 'high' and 'low' responder pigs (n=15 each) were identified.

Biological activities including: leukocyte migration, recruitment, activation and migration of immune cells, adhesion of phagocytes, proliferation of T lymphocytes, inflammatory response, and movement of antigen presenting cells, increased in the 'high' group at D2. In contrast, cytotoxicity of T lymphocytes, synthesis of reactive oxygen species, and immune response of cells, decreased in 'low' compared to 'high' pigs. At D6, the 'low' group was associated with a decrease in migration of cells, phagocytosis, immune response of T lymphocytes, inflammatory response, proliferation of immune cells, and delayed hypersensitivity reaction. No significant changes were observed on D0. Secreted phosphoprotein 1 (SPP1), C-C Motif Chemokine Receptor 2 (CCR2), C-X-C Motif Chemokine Ligand 8 (CXCL8), were among the genes associated with these changes. Several genes that could be potential vaccine response biomarkers or predictors were also identified. Fecal bacterial profile revealed significant differences between the high and low responder pigs, and between pigs raised with or without antibiotics at different time points, suggesting a role of microbiota in vaccine response.

The results suggest that, the 'high' pigs had immunologically competent cells prior to vaccination, hence, were able to mount an effective and specific immune response following the vaccination, compared to the 'low' ones. Therefore, gene expression biomarkers and microbiota profile could be potential predictors of vaccine response, and thus, improve cost-effectiveness of vaccination, an important industry consideration.

## 5 OHS A07 - VACCINES 2 - SALONS AB

**Q fever vaccine failure rate, duration of longevity of immunity and associated demographic factors in Australia**

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**BACKGROUND:** Since its commercial availability in Australia in 1989, the Q fever vaccine (Q-Vax) vaccine is considered highly effective in adults and proven to be a complete and long lasting vaccine. Though there were studies and meta-analysis that reported 83% - 100% efficacy rate of the Q fever vaccine, there is limited understanding of the efficacy as a result of lack of well-designed follow up studies which utilize multiple source of data on Q fever. In this study, we presented a novel approach considering linked data from Q fever vaccination registry, Q fever notification and admission data reported between 1991 and 2016.

**OBJECTIVE:** The main aim of the study was to estimate the Q fever vaccine failure rate, determine the duration of vaccine immunity and identify demographic factors associated with duration of immunity of the Q fever vaccine.

**METHODS:** Retrospective cohort study with record review based on a linked and de-identified data from three large databases containing information on Q fever from 1991 to 2016 was conducted. Vaccine failure rate was computed as the number of Q fever cases per 100,000 person years of follow-ups. Multivariable Cox Proportional Hazard (CoxPH) model was fitted to estimate the duration of immunity of Q-VAX accounting for potential confounding demographic factors: age, sex, and job as covariates.

**RESULTS:** Lack of adherence to vaccination protocol was observed since 158 individual sought vaccination services after their notification/admission and 532 individuals with negative screening tests did not receive the vaccine. The incidence in vaccinated and unvaccinated individuals, respectively, were 5.40 [95% CI: 3.65, 7.72] and 89.50 [95% CI: 70.50, 112.00] per 100,000 person years of follow up. The duration of immunity of the Q fever vaccine found to be at least 20 years in vaccinated individuals. The hazard rate of Q fever infection was 0.07 (95% CI: 0.04, 0.10) in vaccinated individuals compared to unvaccinated individuals, i.e., vaccinated individuals were 93% less likely to be infected. The hazard was the highest from 25-54 years of age, i.e., 2.06 (95% CI: 1.18, 3.58) in 25-34 years, 2.21 (95% CI: 1.22, 4.01) in 35-44 years and 2.20 (95% CI: 1.11, 4.35) in 45-54 years. The hazard was 2.76 (95% CI: 1.11, 6.85] times higher among workers in a meat processing plant compared to other workers.

**CONCLUSIONS:** The vaccine is highly effective in protecting from Q fever infection. However, higher incidence was observed in unvaccinated individuals considered immune during the pre-vaccination screening. In addition, lack of adherence to vaccination protocol was observed. We pose questions on the effective implementations the Q fever vaccination program, especially, the pre-vaccination screening tests. How accurate the pre vaccination screening/or diagnostic tests in confirming prior exposure to Q fever? How adherent to vaccination protocol?

# HS ONE HEALTH SCIENCE 2

## HS SURVEILLANCE AND EARLY DETECTION

### 1 OHS B01 - SURVEILLANCE AND EARLY DETECTION - SALONS CD

#### **One Health-oriented outbreak response in Cameroon: A case study of the 2016 Monkeypox outbreak response in Cameroon.**

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1: Mosaic, Cameroon;

2: Metabiota Inc

**BACKGROUND:** Monkeypox virus (MPXV) is an *Orthopoxvirus* that causes clinical disease in monkeys and appears to be hosted in either rodents and an unidentified host. It can infect humans, causing disease with potential secondary transmission. On August 14, 2016, a chimpanzee in a primate sanctuary at Mfou National Park, Cameroon, stopped eating and died the next day. Lesions consistent with Monkeypox infection (MPXV) were noted at the time of death. Government technical staff from the Ministry of Livestock (MINEPIA), Ministry of Defense, Ministry of Forestry and Wildlife (MINFOF) and Ministry of Health (MINSANTE) established a multi-sectorial team to manage the outbreak using a One Health (OH) approach to implement surveillance and control measures.

**METHODS:** MINFOF and MINEPIA staff collected specimens from the dead chimpanzee, additional animals with suspected MPXV infections, and took environmental swab samples from the enclosure housing the infected chimpanzees. Monkeypox reservoir surveillance was initiated by collecting samples from rodents captured around the enclosures of the chimpanzees infected with MPXV. All samples were sent to the Military Health Research Centre (CRESAR) in Yaoundé for analysis using a real-time PCR assay.

**RESULTS:** The outbreak occurred in a group of 23 healthy chimpanzees at a sanctuary that housed approximately 300 primates in 18 enclosures. The outbreak killed two chimpanzees, 19 additional chimpanzees had clinical signs consistent with MPXV infection, and 22 humans were exposed to the infected animals and enclosures. Within 24 hours of the first chimpanzee's death, MPXV was confirmed at CRESAR with support from the USAID PREDICT project and the results were reported to MINEPIA. An official report was sent to OIE 10 days after first symptoms were detected, in contrast to the 16 day reporting lag during the 2014 MPXV outbreak. Rodents sampled during the active surveillance were all negative. Control measures were put into place one day after lab confirmation of the first case; these included closing the sanctuary to the public, limiting access to the affected group, enhanced disinfection procedures, training of staff in the use of PPE, reduced animal contact, and temperature checks for exposed workers. The rapid mobilization of the multisectorial team allowed for rapid identification of the virus, deployment of response protocols, no spread of the virus beyond the one enclosure, and no human infection.

**CONCLUSIONS:** A OH multi-sectorial approach greatly improved the investigation and response capabilities which, in turn, enabled Cameroon to quickly detect, confirm, and report on MPXV. It also allowed Cameroon to implement successful control measures which resulted in containment of the outbreak. This decreased the risk of human exposure and the potential economic impact of this zoonotic virus.

## 2 OHS B01 - SURVEILLANCE AND EARLY DETECTION - SALONS CD

**Zoonotic Enteric Parasites in Humans, Animals, and Drinking Water in Mongolian Households and Their Associated Risk Factors**

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- 1: D43 One Health Team of the Institute of Veterinary Medicine, Ulaanbaatar, Mongolia;
- 2: Duke University, Durham, North Carolina, United States;
- 3: The National Center for Communicable Diseases, MOH, Ulaanbaatar, Mongolia, Mongolia;
- 4: The National Center for Zoonotic Diseases, MOH, Ulaanbaatar, Mongolia

**BACKGROUND:** Mongolians live in close harmony with their domestic animals through harsh weather and among rough, expansive terrain. But this contact puts herders and their families at risk for zoonotic disease. As part of a larger study on zoonotic enteric parasites, the current research aimed to determine of presence of *Cryptosporidium* spp., *Giardia lamblia*, and *Entamoeba histolytica* in humans, animals, and drinking water from rural, peri-urban, and urban Mongolian households and to identify risk factors for zoonoses based on household survey data.

**METHODS:** A total of 250 households were enrolled from the rural provinces of Selenge, Zavkhan, and Dundgovi and from the capital city Ulaanbaatar, within Tov province. This cross-sectional study was carried out between April and October 2017 using a One Health framework. Following a survey on topics related to animal contact, water, sanitation and hygiene behaviors, diarrheal disease, and animal care practices, stool samples from household members and domestic animals were collected as well as a sample of the household drinking water. Multiplex real-time PCR was used to simultaneously detect the 18S ribosomal RNA gene for *Giardia lamblia* and *Entamoeba histolytica* and the COWP (*Cryptosporidium* oocyst wall protein) for *Cryptosporidium* spp. from all samples. Multivariate logistic regression was utilized to assess the association between the presence of zoonotic enteric parasites and household risk factors.

**RESULTS:** Initial analysis of household survey data shows that unimproved drinking water sources are common and adherence to drinking water treatment methods is inadequate. Self-reported hand washing is widespread after animal contact but does not often occur before preparing food, eating a meal or after visiting the toilet. Open defecation is the primary sanitation option for many rural and peri-urban households. All rural households report animal contact and cohabitation with livestock inside gers is not uncommon, especially during the winter or if an animal is sick. Many households reported diarrheal disease among their livestock in the past year with some describing a resulting herd die-off. Close contact during home slaughtering, butchering, milking, and birthing presents distinct exposure risks for rural Mongolian households. Laboratory analysis is forthcoming.

**CONCLUSIONS:** Our study uses a multidisciplinary One Health approach to study sectors of food, environment, animal and human health. It aims to study neglected enteric parasites in a holistic manner that will provide a more comprehensive description of the exposures and transmission pathways associated with human and animal infection from zoonotic enteric parasites. Resulting information on risk factors and the presence of pathogens in household members and the household environment will aid in developing unique messages for healthier human-animal interactions and the prevention of zoonotic diseases within Mongolia.



## 3 OHS B01 - SURVEILLANCE AND EARLY DETECTION - SALONS CD

## Evidence of silent infection of domestic pigs with Highly Pathogenic Avian Influenza H5N1 and H1N1pdm09 in 'hot spot' Nigeria: Is a pandemic virus already in the pipeline?

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2: Institute of Epidemiology, Friedrich-Loeffler-Institut, Isle of Riems, Germany;

3: Institute of Virus Diagnostics, Friedrich-Loeffler-Institut, Isle of Riems, Germany

**BACKGROUND:** Avian influenza viruses (AIV) potentially transmit to swine. Further reassortment in swine may contribute to the generation of pandemic strains. Associated risks of AIV inter-species transmission are greater in countries like Nigeria with recurrent epidemics of highly pathogenic AI (HPAI) in poultry and significant pig population.

**METHODS:** In a central slaughter house in Jos, Plateau state Nigeria, 129 tracheal swab specimens were collected from apparently healthy pigs in December 2015 to February 2016 during presence of HPAI virus H5N1 outbreaks in poultry. In addition, a total of 500 swine sera were collected as follows: 100 in 2013 when there were no cases of AIV; 300 in 2016 during AIV cases from the same slaughter house. Also, another 100 sera were obtained from another slaughter house in south west Nigeria in 2013. Swabs were analyzed by Reverse Transcriptase-Polymerase Chain Reaction (RT-PCR) and gene sequencing by Sanger methods. Sera were first screened for antibodies using competition Enzyme Linked Immunosorbent Assays (ELISAs) against influenza A virus nucleoprotein and subsequently H5 HA and thereafter subtyped by Hemagglutination Inhibition (HI) tests according to procedures described by kit manufacturer and the World Organization for Animal Health (OIE) manual.

**RESULTS:** Assay for influenza A by RT-qPCR yielded 43 positive samples. Twenty-two could be determined by clade specific RT-qPCR as belonging to the H5N1 clade 2.3.2.1c which was confirmed by partial hemagglutinin (HA) sequence analysis. Serologically, 222 (44.4%) and 42 (8.4%) sera were positive for influenza A virus NP and H5 antibodies, respectively. Selected sera reacted differently to H5N1 and A/H1N1pdm09 strains by HI.

**CONCLUSIONS:** We report for the first time in Nigeria of natural exposure of domestic pigs to H5N1 and H1N1pdm09 in the same population. This has implication for co-infection and gene reassortment in the mixing vessel and may result in the emergence of a novel, zoonotic or pandemic virus. The potential public health and pandemic risk requires further investigation and monitoring.

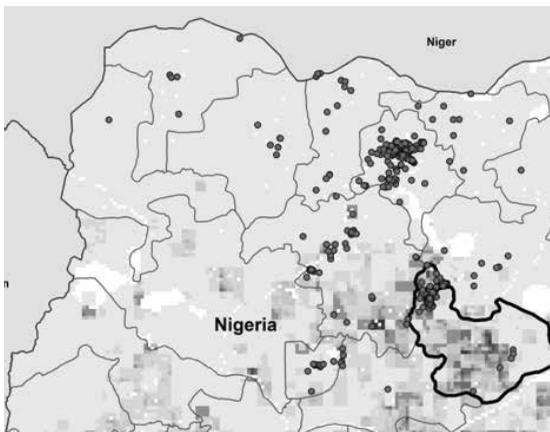


Figure 1. Map of Nigeria, Plateau state, source of pigs to the slaughterhouse. Color bar shows density of pigs in the state while dots indicate spatial distribution of HPAI H5N1 outbreaks in poultry in 2015-2016. Map generated with ArcGIS (Software: ArcGIS 10.3 by ESRI- <https://www.esri.de/support-de/produkte/arcgis-for-desktop-10-3>). Data source: Global Administrative Areas (<http://www.gadm.org/>) and Global Pig Density (2005) – GeoNetwork by FAO (<http://www.fao.org/geonetwork/srv/en/main.home>).

Table 1. Summary of NP (Nucleoprotein) and H5 influenza ELISA serology on three categories of sera collected from Jos (2013 and 2016) and Enugu (2013).

Sera collection	ELISA serology					
	NP			H5 ELISA		
	total	Pos	%	total	pos	%
Jos abattoir, 2016	300	183	61	183	42	22.9 (14)
Jos abattoir, 2013	100	15	15	15	0	0
Enugu slaughter slab, 2013	100	24	24	24	0	0
<b>Total</b>	<b>500</b>	<b>222</b>	<b>44.4</b>	<b>222</b>	<b>42</b>	<b>18.9 (8.4)</b>

Table 2. Sero-reactivity of swine influenza strains H1avN1av, H1huN2, H1N1pdm and H3N2 on selected NP-positive sera

Antigens		Field sera ID (titre)													
Sub-type	Virus strain	353	186	30	24	100	202	15	56	286	72	48	129	204	293
H1avN1av	A/sw/Germany/R1738/2011	80	40	160	20	80	40	20	20	160	40	160	160	40	40
H1huN2	A/sw/Germany/R2107/2010	40	20	640	40	80	10	20	80	40	40	80	20	20	20
H1N1pdm	A/sw/Germany/R26/2011	1280	1280	640	320	320	320	320	320	1280	640	1280	640	640	640
H3N2	A/sw/Germany/R96/2011	10	10	80	10	10	20	10	10	10	20	10	10	10	10

Table 3. Sero-reactivity of H5 strains to H5N1 2.3.2.1c, H5N8 2.3.4.4, H5N1 2.2. and H5N3 on selected NP positive sera

Subtype/clade	Virus strain	Sera ID					
		106	192	229	294	232	242
H5N1 2.3.2.1c	A/Dubai/AR/3435/14	640	640	1280	160	320	320
H5N8 2.3.4.4.b	A/Tufted duck/AR/8444/16	10	10	10	10	10	10
H5N1 2.2.	A/Whooper swan/Germany/R65/2006	40	10	10	160	20	80
H5N3	A/Common teal/England/7894/2006	80	80	640	320	160	320

## 4 OHS B01 - SURVEILLANCE AND EARLY DETECTION - SALONS CD

## Phylogenetic analysis of viruses detected in mosquitoes, horses and humans supports epidemiological data indicating two different geographical origins for epidemics of encephalitis due to Murray Valley encephalitis virus

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**BACKGROUND:** Murray Valley encephalitis virus (MVEV) is a member of the Japanese encephalitis serogroup of flaviviruses. It is maintained primarily in a mosquito-water bird cycle. Human illness varies from a nonspecific febrile illness to severe encephalitis, with a mortality of 20-25%, and persisting neurological deficits in 50% of survivors. Initial outbreaks occurred on the Australian east coast but, since 1975, activity has been almost completely confined to north-western (NW) Australia. An enzootic mosquito-water bird focus there leads to MVEV activity every wet season, and usually less than five human cases. Occasional larger outbreaks that spread beyond these areas, including uncommon instances of MVEV activity in central and south-eastern Australia, have been thought to represent spread from this enzootic focus. In 2011, extensive rainfall and flooding occurred over much of Australia, followed by the largest outbreak of MVEV encephalitis in humans and animals since 1974.

**METHODS:** Mosquitoes were collected from multiple sites within the Kimberley region at the end of the 2011 wet season using standard EVS-CO2 light traps. They were stored and transported on dry ice for speciation and virus culture, followed by sequencing of the E-gene of isolates.

**RESULTS:** Between March and May 2011, 16 confirmed cases of MVEV encephalitis occurred: 13 in NW Australia and three in south-eastern (SE) Australia. Cases were also reported in horses and ducks in SE Australia, and there were extensive MVEV seroconversions in sentinel chickens. We obtained partial or full E gene sequences for 17 MVEV isolates from mosquitoes collected in the Kimberley region. Phylogenetically, all the 2011 NW mosquito MVEV sequences plus a human isolate in GenBank formed a group within sub-lineage 1A of genotype 1 (G1-1A), which has been confined to NW Australia and Papua-New Guinea since 1951. In contrast the isolate from a Victorian (SE Australia) horse belonged to sub-lineage 1B (G1-1B), which has been widely spread across Australia since the 1960s.

**CONCLUSIONS:** The phylogenetic data combined with the epidemiology strongly suggest two simultaneous but separate epidemics: one due to G1-1A arising in NW Australia, the other due to G1-1B and having a separate origin which, as G1-1B is widespread in northern Australia, we could not determine where. However, the pattern of cases and historical records of outbreaks and sporadic cases of MVEV encephalitis suggest a reservoir within eastern Australia as well. Confirming this is important in better understanding how and when epidemics may occur, and how interventions should be directed. Ongoing human, insect and animal surveillance, with collective analysis of data, will be of great ongoing value.

## 5 OHS B01 - SURVEILLANCE AND EARLY DETECTION - SALONS CD

**Prevalence and characterization of *Brucella* spp. in slaughter animals in Gauteng Province abattoirs and assessment of zoonotic risk factors posed to abattoir workers**

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2: Department of Production Animal Studies, University of Pretoria, South Africa;

3: Gauteng Department of Agriculture and Rural Development, South Africa

**BACKGROUND:** Brucellosis is a neglected zoonotic disease that affects humans, and domestic animals; a One Health concern. Globally, abattoirs are used for passive and active surveillance of diseases of both economic and public health significance. Surveys by serological assays of slaughter animals can detect newly introduced disease agents and monitor disease control and eradication programmes. This research goal was to determine the prevalence and characterize *Brucella* spp. in slaughter livestock in abattoirs in Gauteng Province, South Africa and to assess the zoonotic risk factors posed to abattoir workers.

**METHODS:** Fourteen abattoirs in the Gauteng province were visited and unclotted blood and lymph node samples were collected from 256 animals (199 cattle and 57 sheep). Rose Bengal test (RBT), complement fixation test (CFT) and indirect enzyme linked immunosorbent assay (iELISA), were used to determine the sero-prevalence of brucellosis in the slaughter animals. Lymph node samples were cultured for *Brucella* spp. using standard methods. AMOS PCR was used for molecular characterization; isolates were biotyped using standard methods. A structured questionnaire in Microsoft office was used to interview 143 abattoir workers to assess perceptions and risk factors that could predispose the workers to zoonoses. A 'One Health' approach was applied to produce educational materials such as brochures, mugs and posters, which were used to sensitize the abattoir workers and managers. Data collected were managed using Microsoft access, EpiData for questionnaires, and R CRAN was used for descriptive analysis.

**RESULTS:** The RBT screening revealed a sero-prevalence of 11.1% (22 of 199) for brucellosis. The CFT confirmed 2.5% (5 of the 22) as sero-positives and iELISA confirmed 5.5% (11 of 199) cattle as sero-positive for brucellosis. AMOS PCR characterized DNA of seven isolates from lymphatic tissues of the cattle as three *B.abortus* and four *B.melitensis*, of which five (5 of 7) were biotyped as two *B. abortus* biovars 1 and four as *B.melitensis*, of which one was biovar 2 and two were biovars 3. *Brucella ovis* iELISA revealed a sero-prevalence rate of 1.8% (1 of 57) in the sheep tested and AMOS PCR detected *B. ovis* DNA in the lymphatic tissues of the sero-positive sheep. Of the 143 abattoir workers interviewed, 78% were males and 22% were females. Of these workers, 37.1% believed they cannot contract zoonoses from working at the abattoir, 83.9% had hand cut injuries while on duty, 32.9% experienced fever and flu-like symptoms on duty and 88.1% do not seek medical attention when sick.

**CONCLUSIONS:** The combination of RBT and iELISA was more specific than RBT and CFT in this study. *Brucella* isolates were recovered from the cattle sampled. Brucellosis poses a potential zoonotic risk to abattoir workers. We recommend abattoir workers be tested to obtain baseline data to brucellosis exposure.

## OHS INTERVENTION STRATEGIES

### 1 OHS B02 - INTERVENTION STRATEGIES - SALONS CD

## **Adapting the determinants of health perspectives to developing and implementing integrated priorities to address social and ecological expectations for fisheries and community health**

**Stephen, Craig:** Wittrock, Julie

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**BACKGROUND:** We hypothesized that a unified salmon health definition based on the determinants of health model from human population health could account for the socially and ecologically complex and cumulative nature of health in order to integrate information across scientific, social and management perspectives. Our objective was to adapt the determinants of health model to salmon and assess if that model could be used to foster dialogue to find common priorities between government and Indigenous fisheries management groups to meet community, fisheries and ecological needs.

**METHODS:** A systematic, thematic literature analysis was used to develop a draft socio-ecological model of salmon health. Themes were based on the human determinants of health. An expert opinion method determined if the draft model reflected expert perceptions, if the model could be used to detect shared priorities, and where human-animal and environmental interactions drove health. Experts from Fisheries and Oceans Canada and the First Nations Fisheries Council were identified using peer-referential techniques. A diagrammatic approach to network analysis using open-source network visualization and analysis software and the Fruchterman Reingold algorithm were used to visualize the relationships between the determinants. The Eigenvector centrality statistic was used to describe determinants' interconnections. The most negatively and positively important relationships identified by either group was determined by multiplying the mean score of the relationships by the number of times that experts mentioned relationships.

**RESULTS:** Both literature and expert opinion supported the validity of adapting the determinants of health model to describe salmon health as a cumulative effect of interaction abiotic, biotic and social determinants. The draft model was agreeable and understandable to both expert groups. These resource managers and researchers emphasized abiotic environmental determinants over pathogens, however, fish health policy emphasized pathogens as critical determinants of health. Human dimensions of salmon health were absent from expert opinion. The network analysis allowed visualization of critical relationships and comparison between groups; finding common ground between the regulators and fishing rights holders.

**CONCLUSIONS:** The One Health philosophy of integrating concepts of human and animal health lead to a useful approach to re-defining how to characterize and manage salmon health. The resulting conceptual model served as a useful tool to help regulators see how their various programs influenced health. It also was an understandable tool to visualize common priorities between a government and First Nations fisheries management agency. Further work to define and validate critical determinants and develop consensus on socially and biologically meaningful thresholds is needed to move the model from a planning and dialogue tool to a measuring and managing tool.

## 2 OHS B02 - INTERVENTION STRATEGIES - SALONS CD

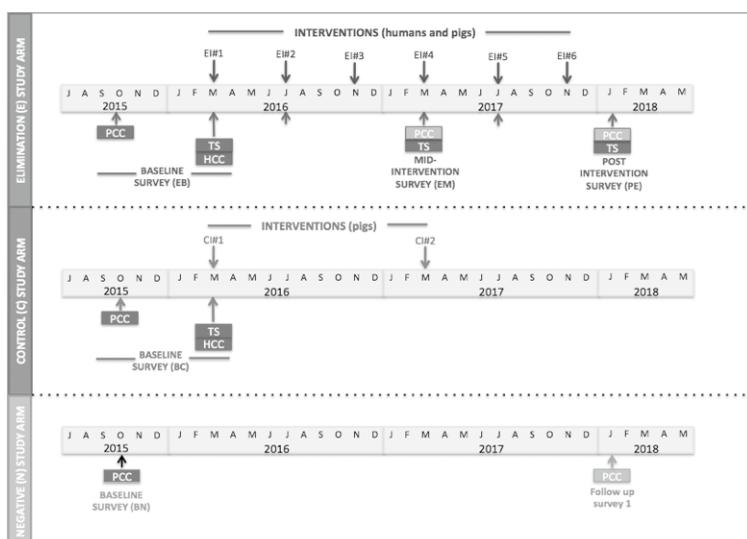
## Control versus elimination of *Taenia solium* in eastern Zambia: Preliminary assessment of a two-year interventional program in the Katete and Sinda districts in the Eastern Province of Zambia

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**BACKGROUND:** The zoonotic tapeworm *Taenia solium* causes significant health and economic burdens worldwide. A large-scale interventional study is currently underway in Zambia, to evaluate and compare the effectiveness of an integrated human- and pig-based *T. solium* elimination program versus a lower-intensity pig-only control strategy.

**METHODS:** A two-year intervention period was conducted in the Nyembe (Katete district), and Chimvira and Herode (Sinda district) communities in the highly endemic Eastern Province of Zambia, from March 2016 to November 2017. Integrated 'elimination' interventions were conducted in Nyembe on all eligible humans (praziquantel 10mg/kg PO or niclosamide 2g PO) and pigs (oxfendazole 30mg/kg PO and TSOL18 vaccine, 1mL intramuscular) at four-monthly intervals for six iterations (see Fig. 1.) In Chimvira, the 'control' study arm, eligible pigs were given oxfendazole (30mg/kg PO) once yearly for two iterations ('control' interventions). Herode was the 'negative control' study arm, in which no chemotherapeutic interventions were conducted. Health education was implemented in all three study arms. Monitoring and treatment will continue in the intervention study areas for another three years.



Sampling surveys determined porcine cysticercosis (PCC), taeniasis (TS) and/or human cysticercosis (HCC) prevalence in the various study arms at baseline (0 months), mid-intervention (+12 months) and post-intervention (+24 months) as outlined in Fig. 1.

*Figure 1: Timeline of project activities during the intervention period. EI#1-6 represent Elimination interventions; CI#1-2 represent Control interventions. The baseline, mid- and post-intervention surveys indicate which diseases are tested for at each time point (PCC, TS and/or HCC).*

	HUMANS				PIGS			
	Stool tested	TS pos (AgELISA)	Blood tested	CC pos (AgELISA)	Blood tested	CC pos (AgELISA)	Carcasses dissected	Cyst positive (dissection)
E study arm	251	39 (16%)	345	94 (27%)	102	42 (41%)	37	16 (43%)
C study arm	373	43 (12%)	484	102 (21%)	72	26 (36%)	15	9 (60%)
NC study arm	-	-	-	-	66	29 (44%)	16	11 (69%)
OVERALL	624	82 (13.1%)	829	196 (23.6%)	240	97 (40.4%)	68	36 (52.9%)

Preliminary results and **CONCLUSIONS:** Average baseline prevalence of TS was 13% (copro AgELISA), and of human CC was 24% (serum AgELISA). Average baseline PCC prevalence was 40% (serum AgELISA) to 53% (carcass dissection) (see Table 1.)

Table 1: Results from Baseline survey conducted in

study arms in October 2015 (pigs) and March 2016 (humans).

At mid-intervention (March 2017), TS prevalence was 6.8%, compared to 16% at baseline (E arm). This substantial reduction in prevalence is expected to continue throughout the remainder of the intervention period. (Mid-intervention PCC prevalence could not be determined due to low pig numbers following an African swine fever outbreak.)

Results of the post-intervention survey (to be conducted in January 2018) will be presented and discussed.

## 3 OHS B02 - INTERVENTION STRATEGIES - SALONS CD

## An integrated human-animal health approach to reduce the disease burden of psittacosis

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**BACKGROUND:** Psittacosis is a highly underdiagnosed zoonotic disease linked to birds. Notified infections in humans mainly present as community-acquired pneumonia (CAP). For a timely response in zoonotic outbreaks such as psittacosis, a prompt exchange of epidemiological, clinical and laboratory data between the human and animal health chains is vital. The aim of this study is to reduce the disease burden of psittacosis via the establishment of a 'One Health' data exchange platform for psittacosis and to add essential information on *C. psittaci* in humans and animals.

**METHODS:** The research is organised in a five-year project with seven work packages: 1) develop an integrated human-veterinary information platform, 2) implement a 'One Health' typing method for *C. psittaci*, 3) determine the occurrence of *C. psittaci* in selected animal populations, including the poultry sector, 4) reduce the human diagnostic deficit, 5) determine disease burden in humans and identify the main animal reservoirs for zoonotic transmission, 6) perform improved source finding of reported human and animal cases, and 7) realise legally backed interdisciplinary cooperation. Nine Dutch partners and one Belgian partner are participating in the project.

**RESULTS:** An integrated, web-based information platform has been established in which human and animal case information, including OmpA genotyping information, can be uploaded and exchanged between the medical and veterinary domain. A digital source finding tool was developed and is now in use by the human and veterinary public health authorities. Disease burden from psittacosis in humans in the Netherlands was estimated at 222 (95% CI 172–280) Disability-Adjusted Life Years (DALYs) per year, highlighting the public health importance of psittacosis. Essential input for the burden estimate was provided by a meta-analysis of published CAP aetiological studies that indicated *C. psittaci* was the cause in 1.03% (95% CI 0.79–1.30) of CAP cases. To reduce the diagnostic deficit in humans, a PCR starter's kit was developed and offered to labs. To assess the presence of *Chlamydia spp.* on poultry farms, pooled faecal samples were collected from 151 layer hen farms, all testing negative for *C. psittaci* DNA. But, *C. gallinacea* DNA was detected on 47% of these farms. Exploratory spatial analysis of notified human psittacosis cases showed a large cluster that covered a highly poultry-dense area, and several smaller clusters. In multivariable analysis, the presence of chicken-processing plants and slaughter duck farms in a municipality were associated with a higher rate of human psittacosis notifications.

**CONCLUSIONS:** We show the three-year results of an integrated human-animal health project to reduce the disease burden of psittacosis. Research highlights include a relation between human psittacosis notifications and poultry density, and *C. gallinacea* but not *C. psittaci* detection on layer farms. Legal aspects of human-veterinary collaboration require further attention.



## 4 OHS B02 - INTERVENTION STRATEGIES- SALONS CD

**Factors associated with improved uptake of Johne's Disease control mechanisms on Australian dairy farms: Regulatory insights from evolving control strategies**

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**BACKGROUND:** Johne's Disease (JD), caused by *Mycobacterium avium ssp. paratuberculosis* (MAP), is a debilitating disease affecting dairy cattle in most countries with established dairy industries. Australia has a relatively low herd prevalence of infection (1.8%) yet a well-established livestock export industry relies on certification of freedom from numerous diseases including MAP. The convergence of animal welfare, farmer, industry, and government objectives for JD control presents an issue which has responded variably to different control policies globally. Over the last decade, there has been debate over the link between MAP and human gastrointestinal disease. Although recent evidence refutes this link, this perception contributes to the challenges of a complex One Health dynamic. Producer frustration with previous control programs implemented over the years, including various quarantine measures as well as subsidized and unsubsidized testing and culling, yielded unsatisfactory adoption of programs, prompting a review. As of 2017, JD in Australia remains a notifiable disease, though farms certify disease freedom through a voluntary, producer driven, risk assessment-based control program as part of integrated biosecurity planning intent on fostering increased participation for more successful JD control. We report on a study underway that aims to identify factors associated with choice of a JD control strategy on Australian dairy farms under the current regulatory climate and interpret these findings relative to JD control progress in other countries tackling this problem.

**METHODS:** Dairy farms in six Australian states are being surveyed proportionately using an online questionnaire capturing demographics, perceptions of JD control strategies, and control mechanisms in place. Assuming a 15% response, we are targeting > 2500 farms to obtain data from approximately 400 farms (6-7% of all Australian dairy farms), their veterinarians, milk processors, and state governments. The questionnaire covers knowledge of JD, attitudes and perceptions to JD control, and farm demographics. Choice variable regression methods will be used to identify associations between independent variables and choice of a control strategy. Tree and node diagrams coupled with joint probability functions and Bayesian statistics will be applied to estimate the likelihood of using a control mechanism under various scenarios of farm demographics, perceived benefits, and perceived barriers.

**RESULTS:** The relationship between demographics, knowledge, perceptions, attitudes to JD control policy, and choice of a control strategy will be described. We expect to identify key factors of a successful regulatory environment supporting JD control.

**CONCLUSIONS:** Considering the moderate success of Australian JD control programs admixed with some pitfalls over time, this evolution presents a valuable learning opportunity for understanding better the regulatory policy opportunities for all stakeholders to improve JD control. Identifying the factors influencing a successful participatory approach through integrated biosecurity may lead to healthier, more productive animals thereby improving sustainability and reducing the public health risk of MAP.

## 5 OHS B02 - INTERVENTION STRATEGIES - SALONS CD

**Harm reduction: A strategy for One Health action in the face of uncertainty and conflict**

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2: Ross University School of Veterinary Medicine. St. Kitts and Nevis

**BACKGROUND:** We hypothesized that harm reduction, effectively used in public health against complex, persistent problems such as addiction and homelessness, could promote collaboration and cooperation in cases where scientific uncertainty and social conflict stagnate action at the wildlife-society-environment interface.

**METHODS:** A scoping literature was supplemented with two qualitative case studies; (1) conflicts between community well-being and wild monkeys in St. Kitts and (2) aquaculture conflicts with marine conservation in Canada.

**RESULTS:** There is little evidence that harm reduction and its allied field of health promotion have guided risk management at the human-animal interface. The health belief model, theory of planned behaviour and other health promotion and harm reduction theories are rarely in the animal health lexicon. Case study #1 - Recommendations for Fraser River sockeye salmon recovery were consistent with harm reduction principles, but the current management approach focussed solely on hazard elimination. Debate over the attributable fractions of harm from specific hazards predominated the policy and science dialogue. It was no one's responsibility to integrate and coordinate the social and ecological dimensions of harms to identify opportunities for collaborative governance or action. Diverging values, scientific uncertainty, and multiple ideologies resulted salmon farming remaining a subject of public debate and source of social conflict that prevented harm reduction actions. The harm reduction approach was incorporated into recommendations by a multi-stakeholder government advisory panel as a new mechanism to motivate collaborative action. Case study #2 - Introduced vervets are impeding progress on three important areas of climate change adaptability in St. Kitts; (i) agriculture and food security; (ii) human health; and (iii) community livelihoods. There were strong divergent views on how to manage this issue. Lacking resources, only irregular attempts have been made to control this socio-ecological conflict, most often looking to biological controls. Harm reduction was seen as a viable approach to strategic collaboration to reduce social conflicts and climate vulnerabilities created by the vervets while protecting the cultural and economic benefits they bring.

**CONCLUSIONS:** A lack of awareness of the scope and uncertainty about the purpose of harm reduction impedes the animal health community's engagement with the human dimensions of community health and environmental risk management. There is little scholarship on how to enable people to increase control over and to improve their resilience to socio-ecological shocks by managing their relationships with animal health. Harm reduction approaches helped two intractable problems prioritizes issue(s) for which the group can agree progress can feasibly be made. It was seen as a means to reduce conflict by reorienting to collaborative governance and promoting a shared understanding of issues.

## OHS PATHOGENESIS 1

### 1 OHS B03 - PATHOGENESIS 1 - SALONS CD

## Cytokine patterns in Hemorrhagic Fever with Renal syndrome and Crimean-Congo Hemorrhagic Fever

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**BACKGROUND:** Two viral hemorrhagic fevers are present in the Balkans, hemorrhagic fever with renal syndrome (HFRS) caused by hantaviruses (mainly by Dobrava-Belgrade virus, DOBV) and Crimean-Congo hemorrhagic fever (CCHF) caused by CCHF virus (CCHFV). Even though the pathogenesis of these diseases is not fully understood, the activation of immune response system and the secretion of cytokines is thought to play a major role. Aim of the present study is to evaluate and compare the cytokine patterns in patients with HFRS and CCHF.

**METHODS:** The study included 6 serum samples from 5 HFRS patients (5 male) aged 25-68 years (median 35) and 6 serum samples from 6 CCHF patients (2 male) aged 25-62 years (median 44.5). One HFRS and two CCHF cases were fatal. All samples were collected 3-7 (mean 5.9) days after onset of the symptoms. Patients' samples were divided into groups according to the outcome of the disease. Serum samples from 16 apparently healthy individuals (9 males) aged 18-65 years (median age 45 years) were included in the study as control group. The quantification of 27 cytokine and chemokine serum levels was done using the kit Human Grp I cytokine 27-Plex-Panel in Bio-Plex™ Suspension Array system (Bio-Rad Laboratories, CA). The statistical analysis was performed using the software package IBM SPSS Statistics version 22 (SPSS Inc). Mann-Whitney U-test or Kruskal-Wallis test was used to evaluate the differences between groups. The significance level was set at p-value of < 0.05.

**RESULTS:** Compared to the control group, mean level of RANTES was decreased in both HFRS and CCHF patients ( $p < 0.05$ ). Similarly, in fatal HFRS and CCHF cases IP-10 was increased and IL-4 was decreased ( $p < 0.05$ ). Levels of IL-10 were increased only in fatal HFRS cases ( $p < 0.05$ ), while in fatal CCHF cases, MCP-1 and TNF- $\alpha$  were significantly increased and IL-12 was decreased ( $p < 0.05$ ). Mean levels of IL-6 and IL-8 were increased in all HFRS cases and in fatal CCHF cases ( $p < 0.05$ ). VEGF was increased only in HFRS survivors ( $p < 0.05$ ). No significant differences were found among fatal cases, while among survivors, mean levels of IL-8, IL-9, IL-10 and eotaxin were higher in HFRS patients ( $p < 0.05$ ).

**CONCLUSIONS:** Even though HFRS and CCHF are both hemorrhagic fevers, several similarities and differences were noticed in their cytokine patterns. The released cytokines may affect the course and the outcome of the disease. Understanding the role of cytokines may help to decipher the pathogenesis of viral hemorrhagic fevers, identify potential biomarkers and facilitate the development of new therapeutic approaches for these patients in the future.

## 2 OHS B03 - PATHOGENESIS 1 - SALONS CD

**Replication of naturally occurring MERS-CoV protein 4a deletion variants in vitro and in vivo**

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**BACKGROUND:** Middle East respiratory syndrome coronavirus originates from dromedary camels and ultimately from bats. Zoonotic infection of humans can cause a severe lower respiratory tract infection. Despite sequencing efforts, there is no substantial evidence for viral genome changes associated with human adaptation. However, viruses that contained a 48-nucleotide deletion in ORF4a were detected in humans in Jordan in 2015 (Lamers et al., 2015). Overexpression studies suggest that the protein encoded by ORF4a (p4a) is a dsRNA-binding protein that acts as an interferon suppressor by shielding viral dsRNA from recognition by either MDA5 or PACT (Sui et al., 2014; Niemeyer et al., 2013). Here, we aimed to assess the *in vitro* and *in vivo* replication of clinical isolates containing a naturally occurring deletion in p4a.

**METHODS:** Two viruses containing a deletion in p4a were isolated from clinical specimens obtained from the Jordan 2015 outbreak. Virus growth curves, comparing these novel isolates with the EMC strain (which contains an intact p4a), were performed on Vero, Huh-7, Calu-3 and primary normal human bronchial epithelial (NHBE) cells to assess *in vitro* differences in growth kinetics between isolates. Furthermore, *in vivo* differences in replication were assessed in the rabbit model.

**RESULTS:** *In vitro* replication kinetics of the p4a deletion viruses were similar to the EMC strain in Vero, Huh-7, Calu-3 and NHBE cells. *In vivo*, the deletion viruses replicated to similar levels as EMC until 2 days post inoculation. At day 3 and 4 post inoculation, deletion variants showed ~1 log lower titers in tracheal and nose swabs, respectively. This was in agreement with fewer infected cells in the nose of animals inoculated with the deletion variant as shown by immunohistochemistry.

**CONCLUSIONS:** The deletion in p4a appeared to have no effect on MERS-CoV replication *in vitro* in human and monkey cells, while only limited differences were observed in the rabbit model. Although we cannot not exclude the existence of compensatory mutations in the deletion viruses that may mask the effect of the p4a deletion, our data suggests that p4a is dispensable for replication in humans and may only be required in camels or bats. This hypothesis is currently under investigation.

## 3 OHS B03 - PATHOGENESIS 1 - SALONS CD

## The effect of antiretroviral naïve HIV-1 infection on the ability of Natural Killer cells to produce IFN- $\gamma$ upon exposure to *Plasmodium falciparum*-infected Erythrocytes.

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**BACKGROUND:** In sub-saharan Africa intense perennial *Plasmodium species* transmission coincides with areas of high prevalence of human immunodeficiency virus type 1 (HIV) infection. This implies that antiretroviral naïve HIV infected people living within these regions are repeatedly exposed to *Plasmodium species* infection and consequent malaria. NK cells are known to contribute to malaria immunity through the production of IFN- $\gamma$  after exposure to *Plasmodium falciparum*-infected erythrocytes (iRBC). However in antiretroviral naïve HIV-1 infection these functions could be impaired. In this study we assess the ability of NK cells from antiretroviral naïve HIV-1 infected people to respond to iRBC.

**METHODS:** This study was approved by the National ethical committee of Cameroon with administrative authorization number 2015/08/631/CE/CNERSH/SP. Participant's enrolment was voluntary and each participant signed an informed consent. Twenty three (23) ARV naïve HIV-1 infected participants and eighteen (18) HIV-uninfected negative controls aged between 21 to 65 years were recruited to be part of this study. After venous blood drawing, Peripheral Blood Mononuclear Cells (PBMC) were isolated from the whole blood by density gradient centrifugation (using ficoll-hypaque). Magnetically sorted NK cells from anti-retroviral naïve HIV-1 infected people were tested for their ability to respond to iRBC following in vitro co-culture. NK cell IFN- $\gamma$  production after coculture was measured through multiparametric flowcytometry analysis.

**RESULTS:** Our data show a significant reduction ( $p=0.03$ ) in IFN- $\gamma$  production by NK cells from antiretroviral naïve HIV-1 infected people after co-culture with iRBCs. This was in contrast to NK cells response from healthy controls which demonstrated elevated IFN- $\gamma$  production. NK cells IFN- $\gamma$  production from untreated HIV-1 infected participants correlated inversely with the viral load ( $r = -0.5$ ,  $p = 0.02$ ) and positively with total helper CD4+ T cells count ( $r=0.4$ ,  $p = 0.04$ ).

**CONCLUSIONS:** The reduction of NK cells IFN- $\gamma$  production observed in ARV naïve HIV-1 infected people was closely related to HIV disease progression, as we observed an inverse correlation between IFN- $\gamma$  production and plasmatic viral loads. This is probably linked with an effective immune system as lower plasmatic viral load ( $<2$  Log<sub>10</sub>) usually correlate with the ability of individuals to control the virus. This clearly indicates that anti-retroviral naïve HIV-1 infection impairs the ability of NK cells to respond to iRBC. In malaria intense regions there is need to consider people living with HIV as highly vulnerable to malaria and should therefore be offered prophylactic malaria treatment like in pregnant women and children.

## 4 OHS B03 - PATHOGENESIS 1 - SALONS CD

**Inflammatory effects of glyphosate and endotoxin exposure on human alveolar epithelial cells**

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**BACKGROUND:** Pesticides are commonly applied in both occupational or non-occupational settings. Exposure to pesticides at low concentrations has shown an ability to induce lung inflammation. Glyphosate is the most common active ingredient in herbicides and pesticides containing glyphosate are the most commonly applied worldwide. Despite the benefits for food production, exposure to glyphosate has been linked to health effects including respiratory symptoms in exposed workers. However, there is little information on lung inflammation related to glyphosate exposure. Moreover, endotoxin (LPS) exposure is common for agricultural workers and is a well-known stimulant for lung inflammation. Thus, we hypothesized that glyphosate can induce lung inflammation and that co-exposure to glyphosate and LPS can further enhance the inflammatory response.

**METHODOLOGY:** We studied the inflammatory effects of LPS and glyphosate exposure by using a human alveolar epithelial cell line (A549). Cells were treated for 24 hours with different concentrations of LPS and glyphosate individually and in combination. Supernatants were harvested and assessed for cytokines (interleukin-8 (IL-8)) using ELISA. RNA was isolated from treated cells and tested for expression of A20 (also known as tumor necrosis factor alpha-induced protein 3, TNFAIP3) with Real Time PCR to assess the potential for gene expression inhibition of NF- $\kappa$ B.

**RESULTS:** Glyphosate alone had no effect on IL-8 release at all concentrations (0.1 mM, 1 mM, 10 mM). However, there was a significant reduction in IL-8 in cells co-treated with LPS (100  $\mu$ g/ml) and glyphosate (10 mM). Further, we found an increase in expression of A20 in cells co-treated with glyphosate and LPS, with no significant reduction in cell viability.

**CONCLUSION:** Taken together, our results suggest that glyphosate co-exposure may inhibit the LPS mediated lung inflammation, and A20 may be an important regulator. Future experiments include evaluation of the inflammatory effects of glyphosate and LPS coexposure in an animal model.

## 5 OHS B03 - PATHOGENESIS 1 - SALONS CD

## Dynamic interaction of rabies virus with endosomes and end binding partners (EB3 and p140cap) of Cytoskeleton

**Ahmad, Waqas** (1,2); Yinying, Li (2); Maolin, Zhang (2); Liu, Zengshan (2); Khan, lahtasham (1); Awais, Muhammad (1)

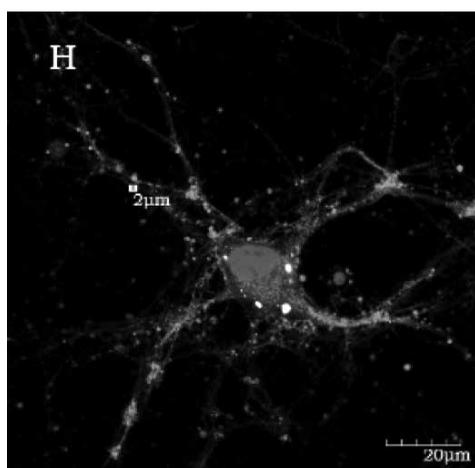
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**BACKGROUND:** The objective of the present study was to investigate the interaction of rabies virus (RABV) with proteins of early endosome (Rab5, EEA1) and late endosomes (Rab7 and LAMP1) in order to understand the earlier events of rabies virus (RABV) right after internalization in neuronal and SH-SY5Y cell lines. The fixed and street strains of RABV were used to see their effects on the localisation and quantifications of EB3 and p140cap genes which essentially regulate postsynaptic density, shapes of dendrites and overall neuronal morphology. It was hypothesized that RABV depend on endosomal proteins or engorge itself into vesicles through early and late endosomes for hijacking neuronal cell machinery. Furthermore, it was also hypothesized that RABV produces degenerative changes in the neurons by down-regulating EB3 and p140cap proteins which are essential end binding proteins of microtubule and actin.

**METHODS:** The study was carried out in the key laboratory of zoonosis, Jilin University, China. Fixed strain was used to observe the intracellular kinetic interaction of RABV with respect to endosomes using immunofluorescence, western blotting, electron microscopy and RNA interference. On the other hands, both fixed and street strains were used to screen and quantify the gene expression using real time PCR and western blotting respectively, while immunofluorescence was also performed to see the localisation of EB3 in infected and fixed nerve cells at different time periods.

**RESULTS:** The findings propose validity to our hypothesis by showing that RABV colocalized with markers for early and late endosomes during different time intervals of fluorescence staining. The down-regulation of Rab5 and Rab7 hampered the normal trafficking of RABV inside the cells. Both strain of RABV significantly down-regulated the gene expression of EB3 and p140cap. Furthermore, both strains also demonstrated disfigured localisation of EB3 in different time intervals of staining.



**CONCLUSIONS:** RABV transport follows clathrin mediated endocytosis, in a favourable intracellular environment of low pH, via early and late endomes as transport vehicles. Rab5 and Rab7 are fundamental bioelements located on endosomes that regulate a sprawled network of endosomal trafficking with other organelles. The disfigured position of EB3 might predict the degenerative changes in the form of deformed dendrites and misshaped neuronal morphology.

*Fig: Localisation of EB3 in RABV infected neurons at 48 hours of post-infection (Green, blue and thick red spots indicate RABV, nucleus, and EB3).*

# OHS ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

## 1 OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES - SALONS CD

### Molecular detection and characterization of *Anaplasma phagocytophilum* strains associated with different hosts in Bushbuckridge, Mpumalanga, South Africa

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- 4: Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA.;
- 5: Hans Hoheisen Wildlife Research Station, University of Pretoria, Pretoria, South Africa

**BACKGROUND:** *Anaplasma phagocytophilum* is a zoonotic, tick-borne, obligate intracellular bacterium capable of causing disease in diverse hosts, including humans, dogs, cattle and horses. It has not often been detected in Africa but recent research suggests its presence in the Mnisi community, a rural community nestled in the heart of a human/livestock/wildlife interface in Bushbuckridge Municipality, Mpumalanga Province, South Africa. The aim of this study was to explore the genetic diversity of *A. phagocytophilum* in different hosts in order to better understand its circulation in the study community.

**METHODS:** To achieve this, DNA extracted from blood samples from 282 wild rodents from five different habitat areas, 74 humans diagnosed with non-malarial undifferentiated acute febrile illness at the community clinics, 100 cattle and 56 domestic dogs, and 20 pools of *Rhipicephalus sanguineus* ticks collected from domestic dogs (1 pool=8 adult male ticks), were screened for *A. phagocytophilum* using a quantitative real-time polymerase chain reaction (qPCR) assay that targets the *msp2* gene.

**RESULTS:** Results revealed that 59% of wild rodents, 11% of humans, 10% of cattle, 82.9% dogs, and 85% *R. sanguineus* ticks were positive for *A. phagocytophilum*. Characterization of different strains by targeted sequencing of the 16S rRNA, *msp4* and *ankA* genes from positive samples revealed the presence of different variants of *A. phagocytophilum* circulating within the community.

**CONCLUSIONS:** Sequence analyses confirmed the presence of *A. phagocytophilum* DNA in different hosts. *A. phagocytophilum* sequences identical to the *A. phagocytophilum* type strain Webster were obtained from a human patient, as well as from rodents, dogs and *R. sanguineus* ticks in the Mnisi Community. This serves as the first detailed report of the detection of *A. phagocytophilum* in humans as well as in other hosts in South Africa and highlights its importance as a possible cause of non-malarial AFI in South Africa.

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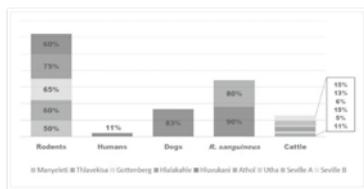


FIGURE 1: Percentage of samples from the different localities positive for *A. phagocytophilum* DNA using the *msp2* gene qPCR assay.

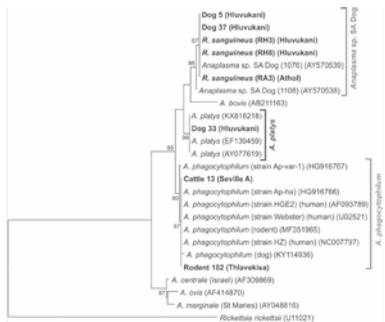


FIGURE 2: A neighbour-joining tree based on 16S rRNA nucleotide sequences showing phylogenetic relationships between the *Anaplasma* spp. The evolutionary distances were computed using the Kimura 2-parameter method and are in the units of the number of base substitutions per site. All positions containing gaps and missing data were eliminated. There were a total of 566 positions in the final dataset.

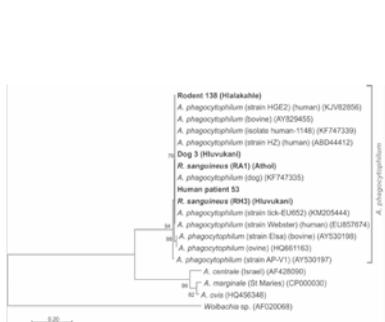


FIGURE 3: Maximum likelihood tree based on *msp2* deduced amino acid sequences showing the phylogenetic relationships between the *Anaplasma* spp. The evolutionary history was inferred by using the Maximum Likelihood method based on the JTT matrix-based model. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. All positions containing gaps and missing data were eliminated. There were a total of 166 positions in the final dataset.



## 2 OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES - SALONS CD

## Assessment of aerosolization of Avian Influenza A associated with market hygiene and practices and potential occupational exposure of live bird market workers in Bangladesh

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- 3: Chittagong Veterinary and Animal Sciences University (CVASU), Bangladesh;
- 4: Bangladesh Livestock Research Institute (BLRI), Bangladesh;
- 5: FAO, Bangladesh;
- 6: City University of Hong Kong;
- 7: London School of Hygiene and Tropical Medicine, UK

**BACKGROUND:** Zoonotic avian influenza A virus subtypes H5N1 and H9N2 are endemic in Bangladesh where poultry consumption via live bird markets (LBM) is usual and popular. We aimed to assess the presence of aerosolized AIVs at LBMs and to evaluate association of AIV contamination with biosecurity practices and personal hygiene of LBM workers.

**METHODS:** A cross-sectional survey of 702 workers in 42 LBMs, with sampling probability proportional to market size, was carried out, collecting nasal and throat swabs and information on high risk practices. In each market, air samples were collected together with market-level hygiene assessments. A longitudinal study was also initiated in August 2017 to collect air samples and market level data every monthly from 10 LBMs for one year.

**RESULTS:** Most of the LBMs were retail markets (76.2%). While 61.9% had official weekly market closure day, all but one sold poultry every day. Birds not sold at the end of the day were kept in the same original stall. In 57.1% LBMs, wild birds were seen roaming freely. Only 3 LBMs had separate central slaughter house. All but 2 LBMs had daily market cleaning option. Less than two thirds of LBMs had systems in place for disposal of carcasses and offal. All but 3 markets had a hand washing station, and almost all (97.6%) had running water facility within the market. More than half (54.8%) had open drains. Dead birds were observed on the ground of 11.9 % markets. Laboratory testing of air samples is ongoing but initial findings from 23 LBMs suggested 39.1% of them were contaminated with Avian Influenza A. There was no obvious evidence of an association with market level hygiene on a preliminary analysis of 23 of the 42 markets and further analyses are being conducted.

Provisional results suggested 93.4% stalls were used for slaughtering or butchering of birds and 41.5 % used defeathering machines. At the individual level, most workers (93.3%) were involved in slaughtering and 79.9% in defeathering activities. Less than a quarter used masks during their work, only 0.7% used gloves, none used aprons, gowns or boots. Most of them (95.0%) reported they touched sick or dead poultry with bare hands. Only 21.8% washed their hand with soap after touching dead poultry and 17.3% washed their hand after touching sick poultry. With one step rRT-PCR, 14.4% LBM workers were tested Influenza A positive with nasal and/or throat swab.

**CONCLUSIONS:** The study provides evidence of aerosolization of AIVs in LBMs and its presence in respiratory passages of workers, thus risk of spillover infections. Longitudinal sampling will further inform periods of higher risk and relationship to changes in biosecurity over time. These findings support moving from emergency response to prevention of spillover.

## Transformation within Indigenous Lived Experiences and the Journey from a Pedagogy of Oppression to a Pedagogy of Hope and Freedom

### Poelina, Anne

Madjulla Association, Australia

**BACKGROUND:** My career has focused on Indigenous Health and Wellbeing development using cultural, administrative and clinical actions; human and Indigenous rights; and environmental justice in the protection of environmental and public health. As an Indigenous researcher exploring and analysing within the Indigenous context, it is important that this research honours Indigenous science (knowledge making and adaptation) and culture from the beginning of time to modernity.

#### *Description of the problem*

A critical outcome of this research proposal is the imperative to frame Indigenous health and wellbeing as a set of practices within Aboriginal society that are complementary with, and act as a vehicle for reconciliation with, the Western deterministic view of health and its approach to research. Additionally what is the connection between the cultural, physical and emotional wellbeing of the individual and the health of the nation of which we are citizens.

#### *Purpose and objective of the research*

The purpose and objective of my research proposal is to emphasize and advocate a justice lens which explores the claim that Kimberly Aboriginal people in Australia continue to experience colonisation and its impact at different times and in different locations. This research is specifically aimed more generally into the emerging scholarship of 'cultural as well as the socio-economic determinants of Indigenous health and wellbeing'.

**METHODS:** The context encompasses multiple methods and a trans-disciplinary approach through a critical research approach that champions both Indigenous methods and participatory action. The research approach and position embraces the convergence of Western and Indigenous science. Through this approach I plan to forge an 'insiders' understanding of contemporary context of colonization and its continuing aftermath.

**CONCLUSIONS:** This research frames the characteristics of colonisation not as an artefact of history rather it continues to be the lived experience of contemporary Indigenous Australian people acted out as personal, family and community and systemic violence. Freire theories apply to the construction of oppression from the viewpoint of its anti-dialogic actions regarding oppressive government policies towards Indigenous Australians. The Freire framework is based on mutual respect involving open and honest dialogue. This heightened sense of cooperation, has instruments known as 'unity, organisation, [and] cultural synthesis' which if undertaken leads to a process for a truly more positive life which enshrines the principles of human rights (Paulo Freire 1968).

The alternative put forward is a 'strength based' approach which is somewhat analogous to Freire's dialogic action. It rejects narratives that promulgate inferiority. Strengths based education has a greater focus on innate ability, the advantages of Indigenous culture (rather than framing it as disadvantageous), dialogue, and 'hopes and aspirations' for 'how we want to be'. A strengths based research approach to 'reframe' research: how problems are defined and how they should be solved.

## 4 OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES - SALONS CD

## Tackling the second deadliest Neglected Tropical Disease: Predicting and reducing the impact of snakebite on human and animal health through One Health analyses of hotspots and access to care

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4: MSF

**BACKGROUND:** Snakebite is the second neglected tropical killer being responsible for over 100,000 human deaths and 400,000 victims of disability globally every year. It affects poor and rural communities in developing countries (e.g. farmers and agricultural workers), where snakebite is more frequent and access to healthcare is limited. Snakebite also affects livestock animals intensifying its burden on these communities through an indirect impact on livelihood. However, snakebite is dramatically under-reported and the snakebite crisis is first of all a crisis of data. Following the inclusion of snakebite in WHO NTDs list in June 2017 and the subsequent political and scientific momentum, we advocate for an innovative One Health approach to snakebite and we aim to quantify for the first time its double human-animal burden in snakebite hyper-endemic areas.

**METHODS:** To address this question, the *Swiss National Science Foundation* will support during the next four years our Swiss and international team of experts in tropical medicine, One Health, herpetology, and spatial analysis. We plan an unprecedented collection of data from 24'000 households through a regional and national human-animal health survey in Nepal and Cameroon. This survey will feed an analysis of the impact of snakebite on livelihoods and will be complemented with geo-spatial information on national infrastructures (e.g., roads), demography, environment, etc., to set the basis to map local and regional human and animal snakebite hotspots and develop predictive models of access to healthcare.

**RESULTS:** Using a One Health approach to snakebite, this project will first contribute to tackling the data gap on snakebite in human and animals, and provide a systemic understanding of its burden in rural communities, including an indirect impact through a loss of livelihood. Second, this project will predict and map local and regional snakebite hotspots and accessibility to life- saving healthcare, serving as an evidence-based tool to support local and national health policies.

**CONCLUSIONS:** This project will raise scientific, political and public awareness on snakebite in Cameroon and Nepal, and at the regional level in Sub-Saharan Africa and South Asia due to the potential for extrapolation of our results, tools and recommendations. The results of this project will reinforce the global political momentum on snakebite (e.g. January 2018, WHO's Executive Board recommends the resolution of snakebite to the WHA).

This project will promote the recognition of lay knowledge and its integration in epidemiological investigations while giving political voice to neglected communities. The project will not only improve our understanding of the impact of snakebite, but also on other NTDs associated with poverty, opening an opportunity to tackle them in an integrated and locally adapted manner.

## What will it take to eliminate rabies in Africa?

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3: Directorate of Veterinary Services, Zoonotic Disease Unit, Kenya;

4: Ministry of Health, Zoonotic Disease Unit, Kenya

**BACKGROUND:** Every year approximately 59,000 people die from dog-mediated rabies globally. Each rabies death is vaccine-preventable and a global target for elimination of human rabies deaths has been set for 2030. The feasibility of this goal is supported by the existence of effective rabies vaccines for dogs and humans, epidemiological characteristics of the disease that support elimination, and evidence of elimination success across regions in developed and developing economies. Over a third of human rabies deaths occur in Africa.

**METHODS:** Using data from running contact-tracing programs to enhance surveillance for human and dog rabies, mass-dog vaccination programs reaching up to 30,000 dogs per single 10-day campaign, and working with the government to finance mass dog vaccinations and provision of post-exposure prophylaxis in Kenya, we address the question of what it will take to eliminate rabies.

**RESULTS/CONCLUSIONS:** We argue it will take five critical actions to catalyze progress towards attaining freedom from dog-mediated rabies by 2030; prioritization of rabies elimination in each endemic country, development and adoption of rabies elimination plans, domestic ownership and commitment to implementing the plans, innovations in the delivery of rabies interventions and integration of rabies elimination programs into national health systems.

## OHS PATHOGENESIS 2

### 1 OHS B05 - PATHOGENESIS 2 - SALONS CD

## Species specific binding of the MERS-coronavirus S1<sup>A</sup> protein.

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2: Virology Division, Department of Infectious Diseases & Immunology, Faculty of Veterinary Medicine, Utrecht University, 3584 CL Utrecht, The Netherlands.

**BACKGROUND:** MERS-coronavirus uses its spike protein to enter target cells. One part of this spike protein, the S1<sup>B</sup> domain, attaches to dipeptidyl peptidase-4 (DPP4) to mediate entry during infection. Recently, using a nanoparticle-based approach, we found that another part of the spike protein, the S1<sup>A</sup> domain, binds to  $\alpha$ 2,3-sialic acid. We showed that these glycotopes are involved in mediating MERS-CoV infection when expressed together with DPP4. The *in-vivo* relevance of this finding is currently unclear. In this study we tested the binding of the A domain to tissues of susceptible animal species.

**METHODS:** We obtained respiratory tract tissues from human, camel, llama, pig, and rabbit from previous experiments as well as intestinal tissues of Pipistrelle bat, Serotine bat, Gambian and Egyptian fruit bat. We performed DPP4 immunohistochemistry and nanoparticle displaying multivalent S1<sup>A</sup> protein (np-S1<sup>A</sup>) histochemistry on all these tissues. Additionally, we also performed lectin histochemistry and MERS-coronavirus nucleoprotein immunohistochemistry on camel, llama, pig, and rabbit tissues. To further evaluate the importance of MERS-coronavirus S1<sup>A</sup> binding in human lungs, we used primary normal human bronchial epithelial (NHBE) cell culture as a model.

**RESULTS:** Consistent with our findings that MERS-coronavirus replicates better in the nasal epithelium of camel in comparison to llama, pig, and rabbit – the nasal epithelium of dromedary camels expressed DPP4 and exhibited S1<sup>A</sup> binding. In humans, S1<sup>A</sup> bound to type II pneumocytes in the lungs, which also expressed DPP4. In NHBE cells, we found that neuraminidase treatment could significantly reduce MERS-coronavirus infection. In bats, on the other hand, DPP4 is expressed in the intestinal epithelium of the four bat species included in this study, but S1<sup>A</sup> only bound to that of Pipistrelle bat.

**CONCLUSIONS:** MERS-coronavirus S1<sup>A</sup> protein binds specifically to camel nasal epithelium, human type II pneumocytes, and Pipistrelle bat intestinal epithelium, but not to similar tissues of other susceptible animals. Our results support dromedary camel and human as the host for MERS-coronavirus. Additionally, these data also support Pipistrelle bat as a potential host for MERS-coronavirus-like-viruses.

## 2 HS B05 - PATHOGENESIS 2 - SALONS CD

**Using Bioluminescent Salmonella Strains to Study Host - Pathogen Interaction in Chicken will Allow One-Health-Approach**

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Chickens (*Gallus gallus domesticus*) are asymptomatic carriers of *Salmonella enterica* serovar Enteritidis (SE), one of the main *Salmonella* serovars responsible for human salmonellosis globally. Here we have characterized putative virulence genes of SE using a bioluminescent imaging (BLI) model to investigate the role of each gene in colonization & infection in chickens. We hypothesized that BLI would provide insight into host-pathogen interactions between SE and the chicken and further our understanding of *Salmonella* infection, colonization and transmission within the avian host. To allow for continuous monitoring of SE during *in vivo* infection, the *lux* operon (*luxCDABE*) from *Photobacterium luminescens* was integrated into the SE wildtype and mutant strains, and expressed under a constitutive promoter to generate a continuous light signal. Virulence genes of interest included: *Salmonella* Pathogenicity Island 1 (SPI-1), SPI-2, ferric uptake regulator (*fur*), *pagN* (i.e., PhoP/Q regulated genes) and *tonB* (which encodes the energy transducer to facilitate  $Fe^{3+}$  uptake). Using cell enumeration, we compared virulence-defective mutant strains of SE compared to wildtype cells for differences in their ability to colonize day-old birds following oral challenge. We did not see a significant difference in cecal colonization from either virulence-defective mutant strain compared to wildtype at day 4, 5 post challenge. This was confirmed by ex-vivo imaging where strong signals came through cecum from each reporter strain during the time frame. The cecum is thought to be the primary colonization site for SE in chicken and our finding is contrast to role of SPI-1, *pagN* in mammalian models which play an important role in gastrointestinal colonization. SPI-2 plays a major role in systemic infection in mammals, and similarly we observed a dramatic reduction in the bacterial load in spleen and liver. However, performing enrichment cultures at day 4, 5 post challenge showed that 100% of the birds were systemically infected (most of them at a very low level). Iron is thought to be critical for bacterial survival and TonB facilitates uptake of  $Fe^{3+}$  from host tissue. Our data show evidence that  $Fe^{3+}$  uptake may not be critical for colonization in the cecum of chicken during early life. *Fur* acts as a global regulator in regulating iron homeostasis in Gram negative bacteria. Here we provide evidence that disruption of *fur* didn't affect colonization in the cecum. Overall our approach using BLI has revealed new insights into the interactions between SE and chickens. The development of a live imaging model using bioluminescent *Salmonella* strains is a first step in a true one-health approach as it will provide a powerful tool to understand host-pathogen interaction, and to investigate the effect of therapeutic strategies (e.g., vaccination) with benefits for human health and the environment.

## 3 OHS B05 - PATHOGENESIS 2 - SALONS CD

**Influenza A viruses activate host PI3K/Akt survival pathway for pro-viral advantage in chicken but not in duck cells**

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3: Pennsylvania state university, USA

Avian influenza viruses (AIVs) are a major threat to millions of poultry farmers. Highly pathogenic avian influenza viruses (HPAIVs e.g. H5N1) metamorphose from its progenitors in poultry flocks causing high mortality and pose a significant human health risk. On the contrary, ducks are mostly refractory and reservoirs. Disparate disease outcome between AIV infected chicken and ducks suggest potential species differences in mounting an antiviral response. Mammalian studies indicate that AIV non-structural protein 1 (NS1) interacts with vital host proteins, to interfere and hijack cellular functions for replication advantage. NS1 has been shown to bind to PI3K/Akt (phosphatidylinositol-3-kinase) p85beta subunit resulting in pathway activation. The PI3K/Akt pathway regulates cellular differentiation, proliferation and survival through inhibition of pro-apoptotic factors. However, the regulation of PI3K/Akt signalling and its implications on AIV replication in avian hosts is yet unknown. Understanding host cellular response to AIV infections is key to develop control measures. Therefore, the present study investigated the regulation of PI3K/Akt and its implications on virus replication. Chicken or duck embryo fibroblast (CEF/DEF) cells were infected with wildtype (WT) LPAI H2N3/H6N1 or recombinant H5N1 (rH5N1) or H9N2 (6:2 system 6 genes from H5N1 (50-92 or Tky05 or H9N2 with PR8 HA, NA). Activation of PI3K/Akt in infected cells was determined by western blotting. Virus titration from infected CEFs or DEFs was performed by foci forming assay (FFA). Inhibition of PI3K/Akt was done using LY294002 or Wortmannin. Cell metabolic activity and caspase 3/7 activity was measured using commercial kits as per manufacturer's instructions.

The results demonstrated that AIV infected CEFs produced significantly ( $P \leq 0.0001$ ) higher infectious virus compared to DEF cells at 9 and 24hrs post infection (hpi). Activation of PI3K/Akt only in infected chicken but not in duck cells. Post-infection PI3K/Akt inhibition significantly reduced virus titres at 6 ( $P \leq 0.05$ ), 9 ( $P \leq 0.0001$ ) and 24 ( $P \leq 0.0001$ ) hrs post infection in CEFs. Differential PI3K/Akt activation was observed between LPAI and rH5N1 viruses. All three LPAI H2N3, H6N1 and H9N2 viruses activated PI3K/Akt at 6 and 9 hpi only. Whilst a prolonged PI3K/Akt activation was observed even at 24hpi in both rH5N1 virus infected CEF cells. Inhibition of PI3K/Akt in WT H2N3 virus infected CEF cells resulted in significantly ( $P \leq 0.0001$ ) higher apoptosis induction compared to controls at 24 and 48 hpi. Counterintuitively, although duck cells exhibited potent apoptosis induction than CEFs, the level of induction was comparable (non-significant) across treatment groups at 24 and 48 hpi. Results imply novel differences in the activation of PI3K/Akt survival mechanism in AIV infected chicken and duck cells are responsible for underlying host differences. The study signifies host-specific viral replication strategy that may find potential use in disease control interventions in the future.

## 4 OHS B05 - PATHOGENESIS 2 - SALONS CD

**Environmental CO<sub>2</sub> Modification of Innate Immune responses to LPS and Organic Dust**

**Schneberger, David;** Thompson, Brooke; Singh, Upkardeep; Kirychuk, Shelley

University of Saskatchewan, Canada

**BACKGROUND:** Exposure to immune stimulants in the lung potentially act in the context of environmental dusts and accumulated gases. Carbon dioxide is a commonly elevated gas in work and home environments that at extremely high levels (hypercapnia) has been shown to cause changes in immune responses. Little to no work has concentrated on possible immune system effects at levels seen in poorly ventilated home and work environments. Exposure to organic dusts in concentrated animal feed operations have been shown to cause chronic inflammation in the lungs of workers, leading to increased incidences of asthma, COPD, chronic bronchitis, and a general reduction in lung function over time. As these facilities also experience elevated CO<sub>2</sub>, we investigated if CO<sub>2</sub> exposure altered immune responses to these dusts. We hypothesized that increased CO<sub>2</sub> could modify innate immune responses to organic barn dust extract (BDE).

**METHODS:** Mice were intranasally instilled with either LPS or BDE then exposed for six hours at 5000, 2500, or 1000ppm CO<sub>2</sub> gas levels before lung lavage and lung tissue sampling. Lung lavage was centrifuged for cells that were counted and identified, and fluid which was used for ELISAs. Lung tissue was used to extract mRNA for RT-PCR.

**RESULTS:** Few changes were detectable in animals given saline or saline with CO<sub>2</sub>. Conversely, LPS and BDE treated animals showed signs of inflammation by measures of cytokines (IL-8, MIP-2, MCP-1) and lavage cell counts. BDE exposed animals showed increases in these measures over saline, with 5000ppm CO<sub>2</sub> co-exposure increasing these measures over BDE alone. LPS conversely showed a trend to increased lavage cells, but a significant decrease in the same measured cytokines at all CO<sub>2</sub> co-exposure levels.

**CONCLUSIONS:** Exposure of mice to CO<sub>2</sub> with saline alone at workplace relevant levels had no apparent effect on immune responses in mouse lungs. When CO<sub>2</sub> exposure was combined with LPS or BDE challenge however there was an increase in lung lavage cells and inflammatory cytokines with BDE at 5000ppm CO<sub>2</sub>, and a decrease in cytokine levels down to 1000ppm in LPS treatment alone. This suggests that increased CO<sub>2</sub>, as low as 1000ppm may modify inflammatory responses in the lung to innate immune challenge. These changes due to CO<sub>2</sub> differed depending on the immune stimulus. Overall these results suggest that the local environment, in the form of gas buildup, may combine with innate immune stimuli to directly modify immune responses.



## 5 OHS B05 - PATHOGENESIS 2 - SALONS CD

## Rabies virus interrupts cofilin pathway and induces depolymerization of actin in hippocampal region

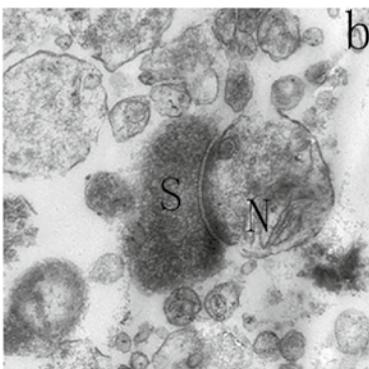
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**BACKGROUND:** Rabies virus (RABV) is a neurotropic pathogen that produces severe encephalitis and terrifying neurological symptoms in humans and animals. The pathological mechanism of RABV is poorly understood, but the current studies show that the virus preferably causes neuronal dysfunction instead of cell death or necrosis. Proteins involved in synapse and postsynaptic density are integral sub-cellular components that maintain neuronal cell shape in multiple aspects. For example, p21-activated kinases (PAKs) regulate the phosphorylation of cofilin in neuronal cytoskeleton; Rac1 is a G signaling protein belonging to Rho family of GTPases and controls orientation of cytoskeleton and growth of neuronal cell; cell division control protein 42 homolog (Cdc42) also regulates cell cycle and related signaling events. The present study speculates the hypothesis that RABV hampers the cofilin pathway and depolymerizes the filamentous actin in hippocampal region of brain tissue.

**METHODS:** The study was carried out in the key laboratory of zoonosis, Jilin University, China. Western blotting, immunohistochemistry and real time PCR were carried out to determine the interaction of street and fixed strains of RABV with associated mediators and binding partners of cofilin mediated pathway.

**RESULTS:** Results showed that RABV inhibits the gene expression of PAK, phosphorylated cofilin and total cofilin that ultimately interferes with interacting partners such as Cdc42 and Rac1. These changes perhaps cause depolymerization of filamentous actin in neuronal cytoskeleton of hippocampus. Moreover, the street RABV infection also hampers the binding of GTP Rac1 and Cdc42 with PAKs. Street RABV also causes significant reduction in the content of active Rac1 (GTP binding form), while total Rac1 contents remain unchanged after 1 hour of infection. It can also inhibit the transformation of inactive Rac1 to active Rac1 without affecting the expression of total Rac1.



**CONCLUSIONS:** These findings suggest that the RABV may alter the structural and physiological architecture of dendritic spine as well as postsynaptic density by reducing the amounts of specific proteins involved in maintaining the shape of dendritic spines. The present study also helps us to interpret network of pathways involving PAKs and Cdc42.

*Fig: Close up view of a complete synaptoneurosome (10000X) showing Synaptosome(S) and neurosome*

**OHS INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 1****1 OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 1 - SALONS CD****Integrating Ecosystem Approaches to Health: A One Health Investigation of Rift Valley Fever Virus**

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**BACKGROUND:** Outbreaks of Rift Valley fever (RVF) can be devastating to livestock production sectors and have severe human health and high socio-economic impacts. The life cycle of RVF virus's presumptive primary vector, floodwater *Aedes* mosquitoes, is influenced by environmental factors, and outbreaks have been associated with high levels of precipitation and subsequent rapid vegetation growth as measured by normalized difference vegetation index. Despite knowledge of these associations, the prediction of RVF outbreaks remains elusive. These factors necessitate a One Health approach to understanding and managing RVF, incorporating human, livestock, and environmental factors.

**METHODS:** We describe a case study in One Health research and the benefits of One Health study design, based on work conducted in South Africa on RVF. Our approach includes integrating experts in climate, soil science and vegetation ecology into our team of veterinary and public health epidemiologists, enabling us to study relationships among weather and climate, vegetation, the vector and the circulation of RVF virus in human and animal hosts.

**RESULTS:** We demonstrate how this integrated team used an ecosystems approach to conduct research on an infectious disease. We show the benefits of this approach and the importance of designing One Health studies *a priori* so as to assess and present the benefits of disease monitoring and investigations to policy makers and funders.

**CONCLUSIONS:** This RVFV example demonstrates a functional program design for One Health investigations as well as the scientific advantages in coordinated, *a priori* One Health investigations as compared to siloed investigations and *post-hoc* analyses.

## 2 OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 1 - SALONS CD

**The Other Side of One Health: A Brucellosis story**

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**BACKGROUND:** Reflections on zoonotic pathogens and associated diseases often focus more on the disease burden, pathogenesis, treatment, and control. In the analysis of the disease in a One Health perspective, however, it is essential to analyse indirect impacts of infectious diseases on the animal industry, particularly the affected farmers. A farmer may not be directly infected with a zoonotic pathogen, but the effects of losing a herd and the impact of the challenges faced post an outbreak on the farmers health, investments and psyche need to be explored and understood, bringing to fore the essence of One Health and the need to explore it on an interdisciplinary platform

**METHODS:** This research focused on *Brucellosis* in selected wildlife in South Africa, analysing data from farmers, veterinarians, researchers and other stakeholders. Using veterinary reports, farm records, and interviews, the indirect effects of *Brucellosis* on farmers were explored and analysed. A systemic review of published data on economic losses resulting from *Brucellosis* in Africa is also conducted. The diagnosis of *Brucellosis*, focusing on challenges in the system are further explored

**RESULTS:** A total of 42 research papers on the economic impacts of *Brucellosis* were retrieved after a comprehensive search and critical appraisal of published literature using search terms “*Brucellosis*” AND “Economic Impact”. Unpublished reports, including farm records, veterinary reports and interviews with farmers were also analysed. Initial reports on *Brucellosis* in one wildlife farm perked losses at approximately 1 million rands (approx. \$80,000), where the prices of Sable antelope have fluctuated between R 178 000 (Matetsi/ Southern Sables) and R 485 000 (Zambian Hybrids). Farm records documented the trauma of the farmer’s loss of revenue and investments with records of depression and fatigue. The research built on that to discuss losses experienced by other farmers in the industry and this is being analysed. It was identified that gaining a “clean herd” reputation in the industry is a major hurdle farmers have to overcome, post-quarantine and outbreak and the strategies to ensure these are identified and discussed. The analysis also points to need for evidence- based research in diagnostics of pathogens as evasive as *Brucella*.

**CONCLUSIONS:** Within One Health, there is the need to look at indirect effects of disease outbreaks on human and animal populations, as well as systems and societal structures. A constant research- based control system is also important in addressing challenges posed by infectious diseases such as *Brucellosis*.

## 3 OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 1 - SALONS CD

**One ring to rule them all: Uniting human, animal, and environmental data using the Checklist for One Health Epidemiological Reporting of Evidence (COHERE)**

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**WHY:** Harmonizing and integrating the human, animal, and environmental data from One Health studies is complex and has not been adequately addressed by existing guidelines for scientific reporting. Improvement of the quality of reporting One Health literature is critical to demonstrate the value and integrity of this rapidly growing field.

**WHAT:** We created a Checklist for One Health Epidemiological Reporting of Evidence (COHERE) to assist authors to advance the quality of reporting interventional or observational epidemiological investigations that integrate data from multiple sectors and/or disciplines.

COHERE was developed by a core writing team, with guidance from an external, international and multidisciplinary panel of One Health experts.

**WHAT:** We present the peer-reviewed checklist that was developed and published, and demonstrate the checklist in action, using real-world examples to illustrate how COHERE is applied to One Health studies. We also show how COHERE helps to incorporate the Ecohealth perspective into One Health reporting. We aim to promote the idea that One Health studies should include all three domains (humans, animals and environment).

**WHAT:** This checklist can aid investigators at multiple points of a study, including study design, data analysis, and data reporting, and should facilitate the future generation of One Health meta-data that will allow higher level analyses.

## 4 OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 1 - SALONS CD

## Ecohealth Project at the community level: Disease Research and development at the human-domestic animal and wildlife interface, Uganda

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**BACKGROUND:** Community capacity to manage health challenges at the human-domestic animal and environment interface has been limited due to lack of home grown solutions. Most of the research conducted in Africa does not go back to the community nor are there interventions to address some of the challenges the communities are facing. The purpose of the Ecohealth Chair project was to conduct research on human and animal disease at the human-animal and wildlife interface in and around a biosphere reserve.

**METHODS:** Using an Ecohealth approach, communities in and around Queen Elizabeth National Park, Western Uganda, participated in identifying, ranking and prioritizing health and environmental challenges in their population(s). Samples were collected from animals and analyzed using basic and molecular typing methods. In addition, surveys were conducted to understand knowledge and practices of community and health workers on animal and human diseases. Each community selected an intervention based on results. More than 900 animal samples have been analyzed for Trypanosomiasis, Q-fever, and brucellosis and antihelminthic resistance.

**RESULTS:** Domestic animals had a prevalence of 13.6% for *Coxiella burnette*. Nearly 9% of the cattle were positive for *Trypanosoma brucei*. Farmers using communal livestock management system were more than 9 times at risk of helminth infection than those on paddocks system (OR=9.4, CI: 3.3-21.6, P = 0.001). The cattle that were sharing water points with wildlife were 14.7 times more likely to get helminth infection than those that were not (OR=14.7, CI: 3.6-23.5, P = 0.001). The cattle that feed on pastureland where wild animals visit daily were 6.1 times more likely to get helminths than those where wild animals never visited (OR=6.1, CI: 1.4-13.2, P = 0.031). Based on these results up to 5 communities selected interventions. These included training on zoonotic diseases, construction of spray race and provision of water for animals and cattle

**CONCLUSION:** This is the first study in the study area to report *T. brucei* and *C. burnette*. It also the first project to conduct research and development in the study area.

## “Whenever I see a fruit bat, I think Hendra” – Attitudes and risk perception of Australian horse owners towards flying foxes in relation to Hendra virus

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**BACKGROUND:** Hendra virus (HeV) is a zoonotic paramyxovirus that has threatened both equine and human health in Australia. It sporadically spills over from flying foxes (*Pteropus* spp.) to horses to humans causing neurological and respiratory disease with high mortality in horses (75%) and humans (57%). Prevention strategies, such as vaccination of horses and property management measures, are widely publicized, but hinge on initiative and action taken by horse owners as they mediate management and care of their animals. While outbreaks significantly impact the equine industry, they also propagate fear and misinformation amongst horse owners about flying foxes, leading to calls for more radical flying fox management approaches, including dispersal and culling. This study investigated knowledge and risk perception of horse owners towards flying foxes as reservoirs of HeV to identify common attitudes, knowledge gaps and misconceptions.

**METHODS:** Using a mixed method approach, data presented are derived from a two-year, online longitudinal survey as well as semi-structured face-to-face interviews with horse owners in Australia. Questionnaires comprised horse owner demographics, property management and mitigation measures, HeV risk awareness and knowledge, and attitudes towards flying foxes and their management. Uni- and multivariable analyses were performed to evaluate association of demographic, management and behavioral variables with perception of flying foxes as a direct threat to the health of horses. Interviews covered previous experience with HeV, HeV information-seeking behaviour, and risk perception and mitigation. All interviews were recorded, transcribed verbatim and analyzed with NVivo using thematic analysis.

**RESULTS:** Attitudes towards flying foxes and their management differed among the participants. Descriptive analyses revealed that the majority (73%) of respondents to the latest survey (N= 577) acknowledged the important role flying foxes play in the environment, yet 40% supported their culling if roosting in areas where they are causing a nuisance. Dispersal was not seen as an effective method of flying fox management because it just moves the problem somewhere else (73%). Interestingly, 59% considered flying foxes as a significant health threat to horses. Horse owners who saw flying foxes or believed that a HeV case was likely to occur in their area were more likely to perceive flying foxes as a threat.

**CONCLUSIONS:** The important ecological role of flying foxes in pollinating and dispersing seeds of native Australian flora was well recognized by the majority of horse owners as well as the need for them and support for their protection. However, there also was considerable support for their culling, potentially reflecting increasing human-wildlife interfaces and conflicts in urban and peri-urban areas due to anthropogenic changes. These findings facilitate a better understanding of horse owner perspectives and help to inform effective communication strategies.

## OHS INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 2

### 1 OHS B07 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 2 - SALONS CD

## The role of mainland-island bat movement in the dissemination of viruses of public health concern in the Caribbean

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**BACKGROUND:** The Caribbean island of Trinidad, which lies just 7 miles off the northeastern coast of South America, has the highest bat species diversity of the Caribbean islands, with 69 bat species documented. Bats are recognized as reservoirs for many important zoonoses, including rabies, and are implicated in cross-species transmission of viruses to human and animal populations. Bat-transmitted rabies was first reported from Trinidad in the 1930s when the virus was transmitted from vampire bats (*Desmodus rotundus*) to humans and animals causing mass mortalities. Vampire bat rabies continues to cause sporadic outbreaks in livestock on the island, but it is unclear whether outbreaks reflect enzootic cycles or re-introductions of the virus from mainland South America and if so, the geographic origin of introductions. Therefore, the aim of this study was to assess the role of *D. rotundus* bats in the spread of rabies virus from the South American mainland to the island of Trinidad, as well as to identify other viruses of public health concern that these bats may transmit.

**METHODS:** Nucleic acid amplification and sequencing of the N gene was carried out for 37 rabies viruses isolated in Trinidad from 1997-2010. These N gene sequences were compared phylogenetically with pre-existing sequences from South America, to investigate viral evolutionary dynamics and geographic source. Microsatellite (DNA) analysis was performed to investigate genetic diversity and gene flow between *D. rotundus* bat populations from Trinidad, Guyana, French Guiana, Venezuela and Suriname (1910-2017) to determine mainland-island bat movement. Polymerase Chain Reaction (PCR) followed by Sanger and next generation sequencing (NGS) was also conducted on 83 bat fecal swab samples from seven species of bats sampled on the island of Trinidad during the period 2012 to 2016.

**RESULTS:** Trinidad rabies viruses were found to be bat variants and clustered with *D. rotundus* variant sequences from South America. Phylogeographic analyses indicated three successive viral introductions from the mainland during the period 1972-2004, from which Trinidadian rabies virus lineages arose. Microsatellite analysis revealed the presence of two distinct population groups of bats with varying levels of admixture, which suggested gene flow between the island and mainland bat populations. Bat herpesviruses and coronaviruses were identified by both Sanger and NGS sequencing methods, with an additional 5 viral families identified by the NGS platform.

**CONCLUSIONS:** These results suggested that bats move freely between Trinidad and South America, endorsing the role of *D. rotundus* bats in rabies virus translocation between the South American mainland and Trinidad. This work also highlighted the potential for the similar introduction of other viral diseases of public health concern by bat dispersal.

## 2 OHS B07 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 2 - SALONS CD

## Nematode co-infections, environmental factors and weather impact infection with the zoonotic bacterium, *Bartonella tribocorum*, in urban Norway rats (*Rattus norvegicus*)

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**BACKGROUND:** Traditional zoonotic pathogen ecology studies in wildlife examine the interplay among hosts, their demographic characteristics and their pathogens. But pathogen ecology is also influenced by factors that traverse the hierarchical scale of biological organization, ranging from within host factors including co-infections at the molecular, cellular, tissue and organ levels, all the way to the host population within a larger environment. The influence of the environment and co-infections on zoonotic pathogen carriage in hosts may provide key information to create a holistic understanding of pathogen ecology in wildlife hosts, which are a major source of emerging infectious diseases in humans. Using wild, urban Norway rats (*Rattus norvegicus*) as a model species, the purpose of this study was to investigate associations among environmental factors, co-infections and *Bartonella tribocorum*.

**METHODS:** During a systematic trap and removal study of rats in Vancouver, Canada, between Sept. 2011 and Aug. 2012, city blocks were assessed for relative rat abundance and 48 microenvironmental characteristics. We also constructed 32 time-lagged temperature and precipitation variables. Rats were tested for the presence of *B. tribocorum* using culture and confirmatory PCR and the presence of invasive nematode infections using macroscopic assessment and/or histopathology. We then fitted multi-level multivariable logistic regression models with *B. tribocorum* status (positive/negative) as the outcome and city block as a random effect to account for clustering. For the environmental analysis, abundance, microenvironment and weather variables were potential independent variables, and for the co-infection analysis, nematode infections were independent variables.

**RESULTS:** Rats originated from 32 city blocks and the prevalence of *B. tribocorum* was 25.7% (101/393) and. The odds of a rat testing positive for *B. tribocorum* were significantly lower for rats in city blocks with one or more low-rise apartment buildings compared to blocks with none. Rats had significantly increased odds of being infected with *B. tribocorum* when there were high minimum temperatures for several time periods prior to rat capture and when rats had a nematode infection in one or more organ systems (*Eucoleus* sp. in the stomach, *Capillaria hepatica* in the liver, enteric nematodes, and/or *Trichosomoides crassicauda* in the urinary bladder or renal pelvis).

**CONCLUSIONS:** A baseline minimum temperature may be necessary for flea survival and *B. tribocorum* transmission among rats, which may lead to fluctuations in the number of infected rats and potentially, the risk to humans. Our results also suggest that nematode parasitism and the environment may have important roles in the ecology and epidemiology of *B. tribocorum*. Our approach may be applicable to future studies of zoonotic pathogens in rats and other wildlife hosts. A nuanced appreciation of how co-infections and specific environmental factors influence pathogen ecology in wildlife host systems may be particularly useful for surveillance and disease prevention activities.



## 3 OHS B07 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 2 - SALONS CD

## Environmental Change Increases Human-Macaque Interactions and the Risk of Zoonotic Disease Spillover

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**BACKGROUND:** Environmental change is not a new issue in the study of public health. Many public health studies have been conducted that link environmental changes to emerging and re-emerging viruses. However, these studies rarely examine human-animal interaction in relation to environmental change. Zoonotic diseases have been considered a major public health concern, and one pathway through which disease risk is heightened is from environmental changes that increase interaction between humans and rhesus macaques (*Macaca mulatta*).

**METHODS:** Three sites of increasing local land-use change in Bangladesh—old Dhaka, Madaripur, and Chandpur—were selected after preliminary key informant interviews and field observations. This qualitative study employed anthropological research methods including participant observation, ethnographic in-depth interviews (58) and focus group discussions (3) to understand local experiences of environmental change and patterns of human-macaque interactions. Interviews and focus group data were coded using computational data analysis software (MaxQDA), and emergent themes were identified using a modified grounded theory approach.

**RESULTS:** Environmental changes are clear in each of the study sites, visible in the significant anthropomorphic landscape transformations. This qualitative study found that all the three areas went through significant landscape transformation due to the construction of roads or apartment buildings on open or agricultural land, to be used for both business and human settlement purposes. Disappearance of forestland has increased macaques' dependence on fruit trees of household backyards. As a result, residents often cut down fruit trees as macaques eat fruits from their trees and instead started planting woody trees so that macaques cannot disturb them. Natural water resources such as rivers and ponds were filled to support the development of roads and homes. As natural water sources were depleted, macaques became more dependent on human water sources, allowing possible water source contamination. Macaques in all three regions have expanded their foraging areas and are now invading new areas where people are not culturally habituated to living with macaques. In response, many residents have reacted aggressively, leading to more frequent biting and scratching events. Many respondents accepted the presence of monkeys at their home, and few consider monkeys as a threat for disease transmission. As a result, they do not mind sharing food or water with macaques. Monkey bites/scratches are not always taken seriously, in some cases victims are not taken to the hospital.

**CONCLUSIONS:** Macaque-human interaction is on the rise in many areas of Bangladesh due to increased dependence on the same land, water, and food resources. This frequency of interaction increases the risk of zoonotic disease transmission. Human behavior is greatly responsible for human-macaque interaction and zoonotic disease transmission. Behavior change interventions should be developed to reduce zoonotic spillover by mitigating the risks associated with human-macaque interaction due to land use change.

## 4 OHS B07 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 2 - SALONS CD

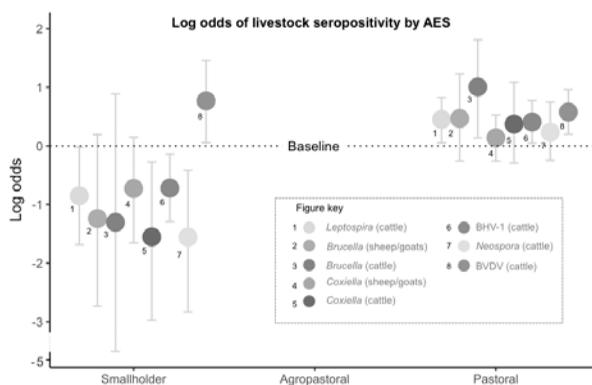
## Explaining variation in human and animal zoonotic infection risk in northern Tanzania: defining agro-ecological systems and their contribution to risk

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**BACKGROUND:** The risks of human infection with livestock-associated zoonoses depend on a complex interplay of factors, including local livestock infection prevalence, contact with animals and contaminated environments, and food preparation and consumption behaviours. Zoonotic disease risk is therefore highly context-dependent. Quantifying the degree to which social and environmental conditions shape variation in infection risk can help identify health inequalities, and provide targets for interventions to reduce them.

**METHODS:** We describe the outputs from a cross-sectional survey conducted in northern Tanzania in 2016. A mixed methods approach was employed, including household surveys (n=404) and serological testing of humans (n=351), cattle (n=3133), sheep (n=2178) and goats (n=2554) for a range of zoonotic pathogens. Prevalence of *Brucella* and *C. burnetii* exposure was generated for livestock and people, and *Leptospira borgpetersenii* serovar Hardjo for cattle. To explore variation in livestock infection risk more broadly, cattle sera were tested for exposure to several non-zoonotic pathogens, including bovine viral diarrhoea virus (BVDV), bovine herpes virus-1 (BHV-1) and *Neospora caninum*. A data-driven approach was used to classify livestock-keeping households into groups based on indicators considered to represent agro-ecological system (AES). These included livestock demographics, management, crop agriculture, and land use. Classification was performed using factor and hierarchical cluster analysis. Multi-level logistic regression models were built for each pathogen with a focus on examining relationships between individual seropositivity and AES.



**RESULTS:** The overall prevalence of cattle, small ruminant and human exposure to *Brucella* was 2.8%, 3.3%, and 5.1%, respectively. For *C. burnetii*, this was 4.1%, 24.4%, and 3.7%. Bovine *N. caninum*, *Leptospira*, BVDV, and BHV-1 seroprevalence was 12.6%, 23.6%, 36.1%, and 66.3%, respectively. Three household clusters were derived that corresponded with historical descriptions as smallholder (n=39 households), agro-pastoral (n=217), and pastoral (n=124) AES. Whilst relationships were not significant for all pathogens, a general trend for elevated livestock infection risk in pastoral systems and reduced risk in smallholder systems was apparent (Figure). There

was no evidence for differences in the risk of human exposure to *Brucella* or *C. burnetii* between AES.

**CONCLUSIONS:** We demonstrate the value of using data-driven approaches for household classification in a setting with a range of livestock-based livelihoods. Important variation in livestock pathogen exposure risk was observed between systems, with the highest overall infection pressure in pastoral households. Further work is underway to identify correlates of human *C. burnetii* and *Brucella* exposure that may better explain variation in zoonotic disease risk in northern Tanzania.

## 5 OHS B07 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 2 - SALONS CD

**Building collaborative capacity to evaluate zoonotic viral sharing among bats, primates, and people in Tanzania**

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**BACKGROUND:** As human populations expand, people are living in closer contact with wildlife, altering human-animal interactions and increasing the risk of disease transmission. Viruses traced to bats and primates have caused significant human epidemics and pandemics, but these animals also play critical ecological roles. In the biodiverse Udzungwa Mountains, one of Tanzania's last areas of undeveloped mountain forest, bats and primates live in close proximity to human communities, creating a high-risk interface for zoonotic disease transmission. Using a One Health approach to surveillance and capacity building, we investigated the presence of and risk factors for viral sharing among geographically overlapping bat, primate, and human populations.

**METHODS:** We built an interdisciplinary team to integrate human, animal, and environmental sampling in the Udzungwa Mountains of Tanzania. Partnering with four village-based human health clinics, we enrolled and collected samples from febrile patients (March 2016 – January 2018). Patients were screened for malaria using a rapid, field diagnostic test (mRDT), and a behavioral survey was conducted to assess contact with forest environments and wildlife. From neighboring town and forest habitats, we captured and sampled fruit bats and insectivorous bats and non-invasively collected feces and saliva from non-human primates (May 2016 – January 2018). Using data on bat movement and feeding patterns, we sampled fallen fruits discarded by foraging bats and used camera traps to assess connections to other species that contact these foods through scavenging or play. For biological samples (blood, oral swabs, feces or fecal swabs, and swabs or sections of fruit), we performed RNA extraction, cDNA synthesis, and viral family level consensus PCR screening (corona-, filo-, flavi-, influenza-, and paramyxoviruses) at laboratories in Tanzania. Confirmatory sequencing of suspect positive samples is currently being performed at University of California, Davis.

**RESULTS:** Our One Health team sampled 1,920 human patients, 1,037 bats, 339 primates, and 108 fruits discarded by foraging bats. Family-level PCR screening identified suspect positive samples from multiple viral families in human and wildlife samples. Confirmatory sequencing of these samples will be completed by May 2018 to allow for full analysis of viral sharing among people, bats, and primates in overlapping habitats. Following confirmatory testing, we will assess spatial, temporal, and behavioral risk factors for viral infection. During the project, our team trained 72 individuals, including veterinarians, human health professionals (clinicians and nurses), animal and human health students, and wildlife officers, building partnerships with diverse community, government, and university groups.

**CONCLUSIONS:** Preliminary evidence supports the potential for viral sharing among overlapping populations of bats, primates, and people in Udzungwa forest environments. Connections with communities, government, and interdisciplinary research partners allowed us to successfully integrate human, animal, and environmental sampling, enhancing capacity for future viral surveillance and One Health project implementation.

# AMR ANTIMICROBIAL AGENTS AND RESISTANCE

## AMR USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE LINK TO AMR AND ENVIRONMENTAL IMPACT

### 1 AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE LINK TO AMR AND ENVIRONMENTAL IMPACT - GALLERY CD

## Reduced and responsible use of antibiotics in food-producing animal in The Netherlands

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**BACKGROUND:** In the period 2008-2011 the outline of the Dutch policy for a substantial reduction and a more responsible use of antibiotics in the livestock industry was drafted as a reaction to the persistent high level of antibiotic use in the livestock sector and public concerns about any transfer of antimicrobial resistance from livestock to humans. Sales of veterinary antimicrobials dropped by more than 64% between 2009 and 2016, and antimicrobial resistance levels decreased substantially as a result of the reduced use. These results are achieved by intensive collaboration between government, the veterinary association and stakeholders within the major livestock sectors.

However the main reduction was achieved in the first years whereafter the reduction leveled off. The idea was that a more targeted and sector specific approach should be developed. For this reason research was performed on the critical success and fail factors of a low usage of antibiotics in the different sectors.

**METHODS:** First of all the changes in usage on farm level were analysed to see whether there are structural high and structural low users and to define the farms to be incorporated in the study. After that different characteristics of the farms in the low and high users groups were further analysed e.g. farm type, farm size, farm management, construction of farm, health of the animals, education and knowledge of farmer etc.. Statistical analyses were performed to show possible associations between certain factors and high/low usage of antibiotics.

**RESULTS:** For all sectors certain associations were found e.g. for the veal calf and pig sectors the small farms have a lower usage where the association is the other way around for poultry, large farms have a lower usage of antimicrobials. In all 3 sector clear leads were found to decrease the usage in the high user group.

In the poultry sector associations were found with the different market concepts, slower growing breeds use less antimicrobials. Management practices like thinning the flocks increase the usage.

In the veal sector management, ventilation and feeding but also nationality of the calves are points of attention. In the pig sector associations were found with management, vaccination and the number piglets. Not all results can be clarified and not all associations are causal relationships. Further in depth research will be needed on certain aspects of the current results, however these results can be a basis for more sector specific plans to further reduce the antimicrobial usage.

**CONCLUSIONS:** The reduction targets for antimicrobial usage in livestock production in the Netherlands was -70% in 2015 with reference to the amount of effective substance sold in 2009. The last few years it became clear that the general approach would not lead to this reduction. By making an analysis of the critical success and fail factors of the different sectors, a sector specific approach can be developed. The outcomes of these studies will be presented.

## 2 AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE LINK TO AMR AND ENVIRONMENTAL IMPACT - GALLERY CD

### Antimicrobial resistance in wildlife species: the potential for sentinel surveillance in a ONE HEALTH perspective

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**BACKGROUND:** Antimicrobial resistance (AMR) is an emerging problem worldwide, and is widely spread in many environments. The use of antibiotics and other drivers for AMR development in humans, livestock or agriculture may have a direct impact on wildlife, and wild animals may provide a biological mechanism for the spread of antibiotic resistance genes. The wild reservoirs of resistance remain poorly understood, even though its origins and mechanisms are of paramount relevance to human health. We have conducted several studies with different wildlife species in Norway to monitor AMR and understand the potential for these to both work as sentinels/bio indicators for AMR spread, and help explain the dynamics and driver for resistance in the environment.

**METHODS:** Between 2013-2017 faecal samples were collected from different wild species in continental Norway: wild birds (ducks and gulls) (n=357); red foxes (n=387); wild reindeer (n=265); roe deer (n=301). In addition faecal samples were collected from 27 wild reindeer from the arctic archipelago of Svalbard. Resistant bacteria were identified by culturing on selective media and/or by susceptibility testing of randomly chosen *E. coli* from the samples. Microbroth dilution were conducted to assess phenotypic resistance.

**RESULTS:** *Wild birds:* *E. coli* resistant to extended-spectrum cephalosporins (ESC) were detected in 31 samples (8.7%) and quinolone resistant *E. coli* in 74 samples (5.6%). Additional resistance to one or more agents was found in 45.9% of the isolates.

*Red foxes:* The occurrence of AMR was 9.2%, 6.3% and 14.7% in areas of low, medium and high human population density, respectively. A statistically significant difference in AMR occurrence was observed between medium and high population density areas. Resistance to fluoroquinolones occurred in 76 foxes (14.4%) with a statistical relevance between density areas.

*Roe deer and wild reindeer:* *E. coli* was isolated and susceptibility tested from 274 out of 301 (91%) roe deer, and from 230 out of 265 (86.8%) wild reindeer. Resistance to streptomycin was detected in 1.7% of wild reindeer and in 5.1% of roe deer. The overall occurrence of *E. coli* resistant to ESC was 0.3% in roe deer. This is the first finding of an ESBL from a wild cervid in Norway.

*Svalbard reindeer:* Fifteen isolates (55%) were resistant to more than one antimicrobial agent. Resistance regions with high homology to plasmid regions previously described in bacteria from swine in the Netherlands and poultry in China were identified.

**CONCLUSIONS:** Results from these studies demonstrate that AMR is present in the environment even in pristine ecosystems such as the Arctic. Longitudinal and spatial broad studies should be prioritized in order to better understand this problem and elucidate the role of wildlife species in the spread of AMR in a one-health perspective.

3 AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE LINK TO AMR AND ENVIRONMENTAL IMPACT - GALLERY CD

**Comparative human exposure to antimicrobial-resistant *Campylobacter* species, *Escherichia coli*, *Salmonella enterica* from food animals using integrated assessment modelling: A farm to fork approach.**

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3: Population Medicine, University of Guelph

**BACKGROUND:** Antimicrobial resistance (AMR) is an important public health concern and there is a large body of research on this topic. To further understand AMR, there is a need to synthesize existing information and our objective was to develop quantitative models to synthesize existing data and assess human exposure to extended-spectrum cephalosporin-resistant *E. coli* (ESC-*E. coli*) and *Salmonella enterica* (ESC-*Salmonella*), and fluoroquinolone-resistant *Campylobacter* (FQ-*Campylobacter*) from chicken, beef or pork consumption in Canada.

**METHODS:** Individual farm-to-fork quantitative models for ESC-*E. coli*, ESC-*Salmonella*, and FQ-*Campylobacter* from beef cattle, chickens and pigs were constructed using data from the Canadian Integrated Program for Antimicrobial Resistance Surveillance and a comprehensive literature search. Using a branching probability tree approach, the models propagated a baseline probability of AMR modified by 1) the odds ratio between factors and the occurrence of AMR, and 2) the frequency of occurrence of the factors (Figure 1) through the agri-food chain. Estimates of Canadians' exposures to resistant bacteria through beef, chicken and pork were obtained by adjusting the calculated probabilities by Canadian consumption patterns and population.

**RESULTS:** All models included management system (e.g., organic) and antimicrobial use. The chicken models also included other factors (e.g., type of litter, chilling at abattoir, type of retail packaging). A FQ-*Campylobacter* model for beef cattle could not be constructed as there were no data about factors linked with AMR reported in the reviewed literature relevant to Canadian beef production. There was higher exposure to AMR through chicken when compared to beef or pork. The highest exposure was to ESC-*E. coli*, then ESC-*Salmonella* and lowest exposure to FQ-*Campylobacter*. There was comparatively lower exposure to ESC-*E. coli* and ESC-*Salmonella* from beef or pork and lowest exposure to FQ-*Campylobacter* from pork.

**CONCLUSIONS:** The comparative human exposure to antimicrobial resistant bacteria was highest from chicken. This observation was attributable in part to higher baseline probabilities of AMR from chickens, higher bacterial recovery rates at retail, and higher consumption rates. However, there are substantial data gaps in the models including factors such as animal density, factors affecting pathogen load, and vaccination. Filling these data gaps will enable us to build models that more adequately represent the agri-food system in Canada and identify plausible interventions to reduce exposure to AMR. Further development of this integrated assessment model includes filling data gaps, addressing other pathways of AMR (e.g., environment, human pathways) and incorporating whole genome sequencing resistance data.

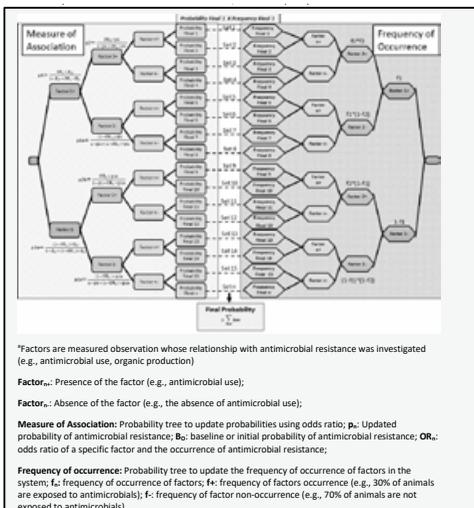


Figure 1. Branching probability tree of propagation of the probability of antimicrobial resistance (AMR) modified by the odds ratio between factors and AMR, and the frequency of occurrence of factors.

#### 4 AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE LINK TO AMR AND ENVIRONMENTAL IMPACT - GALLERY CD

### Assessing Impacts of Antibiotic Therapy in Neonatal Dairy Calves on Gut and Animal Health

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2: Field Disease Investigative Unit, Washington State University, United States of America

**BACKGROUND:** Diarrhea and pneumonia are commonly observed in pre-weaned calves on dairy farms and account for > 50% of all calf deaths. There is evidence that these diseases are over treated with antibiotics which may disrupt colonization of gastrointestinal tract (GIT) microbiota. The aim of this study is to better understand the impacts of intramuscular antibiotics on dairy calves' growth rate, health and microbiotic density of beneficial bacteria in the GIT. The study hypothesis was: antibiotics given to healthy calves created a GIT dysbiosis and subsequent negative health and productivity outcomes.

**METHODS:** The study was conducted on a commercial dairy farm in the Pacific Northwest USA. The farm milked 3000 Holstein and Holstein-Jersey mix cows and raised all their replacement stock. Study personnel worked with on-farm staff to conduct the study and identify animals to be included. The study was a clinical trial design with calves initially enrolled at the first sign of disease (usually diarrhea) and an age-matched calf with no clinical signs. This was determined by on-farm calf caretakers. Subsequently, calves in each group (healthy and unhealthy) were randomly assigned to be treated with a parenteral antibiotic or palliatives and oral electrolytes. Body weight at enrollment and weaning were recorded. Daily health scores (appetite, fecal consistency, fecal dry matter, pre-feeding attitude and body temperature) were recorded twice daily before, during and post treatment. Calves were regrouped for analysis to reflect disease status based on daily health scores collected by study personnel. *Bifidobacteria*, an anaerobic Gram- negative bacteria associated with decreased *E. Coli* and overall good health was quantified from fecal samples before, during and after treatment using pPCR.

**RESULTS:** A total of 121 pre-weaned dairy calves were enrolled into one of four groups. An important finding was a disconnect between the decision made by farm personnel to identify a calf as sick and criteria based on clinical signs observed and measured by the investigators. Across the four groups, 26 percent of calves enrolled into groups by farm personnel did not accurately correspond to disease groupings based on daily health scores. Average daily gain was not significantly impacted by the use of antibiotics or by disease groupings. Inappropriate use of antibiotics (treating healthy animals or not treating clinically sick animals) was associated with decreased *Bifidobacteria* quantities in the GIT.

**CONCLUSIONS:** Inappropriate antibiotic use had a negative impact on GIT *Bifidobacteria*. Also, these data illustrate the importance of effective communication between veterinarians and farm personnel to improve disease diagnosis and better promote understanding and definition of the on-farm treatment decision-making process and encourage appropriate antibiotic use protocols.

**5 AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE LINK TO AMR AND ENVIRONMENTAL IMPACT - GALLERY CD****Prevalence and Antimicrobial Resistance profile of *Salmonella* spp. in retail meats of Super Shop: a food safety risk**

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*Salmonella* spp has represented as the primary cause of foodborne diseases in human. Immunocompromised people and infants are mainly vulnerable to Salmonellosis. *Salmonella* spp can be found in many foods and food products including retail meat where multi-drug resistant *Salmonella* spp evolves a robust challenge to food safety. The aim of this study was to determine the prevalence and antimicrobial resistance profile of *Salmonella* spp in retail meat of super shop at Dhaka City, Bangladesh. During July 2015 and June 2016, a total of 476 samples were collected from 10 super shop of Dhaka city; categorized in chicken meat (n=170), beef (n=68), mutton (n=34) and environment (n=204). *Salmonella* spp. were isolated from the samples by using selective enriched media and confirmed by real-time PCR. Phenotypic resistance was determined by disk diffusion method. Extended-spectrum  $\beta$ -lactamases (ESBLs) and quinolone resistance genes were determined by PCR. The overall prevalence of *Salmonella* spp. was 18.5% (n=88; 95% C.I.15-22%) comprising in chicken meat 26% (n=44; 95% C.I.19.5-32.5%), beef 15% (n=10; 95% C.I.7-23%), mutton 18% (n=6; 95% C.I.6-30%) and environment 14% (n=28; 95% C.I.9.5-18.5%). In antimicrobial assay, 55% isolates were found multi-drug resistant (MDR). Among 22 tested antibiotics, extreme level of resistance was observed against Tetracycline and Erythromycin 99.1% (n=87, 95% CI: 94.5-99.9%), followed by Doxycycline 98%, Pefloxacin 93.9%, Azithromycin 92.2%, Enrofloxacin 91.2%, Moxifloxacin 89.7%, Nalidixic Acid 87.1%, Trimethoprim/Sulfamethoxazole 75%, Ciprofloxacin 53.4% and Streptomycin 49.6%. Nevertheless, only Ceftriaxone, Cefotaxime, Imipenem, Amoxicillin/Clavulanic acid showed good level of sensitivity as 82%, 73%, 73% and 68% respectively. In minimum inhibitory concentration (MIC) assay, high level of MIC<sub>50</sub>/MIC<sub>90</sub> were observed against Amoxicillin (512/>1024), Flucloxacillin (512/1024), Cephadrine (256/1024), Cefixime (2/512), Gentamycin (4/512), Chloramphenicol (32/512), Azithromycin (512/1024), Erythromycin (1024/>1024), and Sulfamethoxazole (512/ >1024). Among the phenotypically resistant isolates, ESBL encoding genes were observed as bla (TEM) 80% (n=40/50), bla (shv) 10% (n=5/50), bla (ctx) 34% (17/50), bla (cmv) 8% (4/50); and Quinolone resistance genes qnrA 10.63% (5/47) gyrA 57.45 % (27/47) and gyrB 23.40% (11/47). High level prevalence of MDR *Salmonella* spp in retail meat which could cause foodborne illness is a great alarming issue for public health.



# AMR GENOMIC EPIDEMIOLOGY / EVOLUTION OF AMR TRANSMISSION

## 1 AMR 02 - GENOMIC EPIDEMIOLOGY / EVOLUTION OF AMR TRANSMISSION - GALLERY CD

### The human resistome within the Dutch pork production chain, a metagenome-wide study among farmers and slaughterhouse workers.

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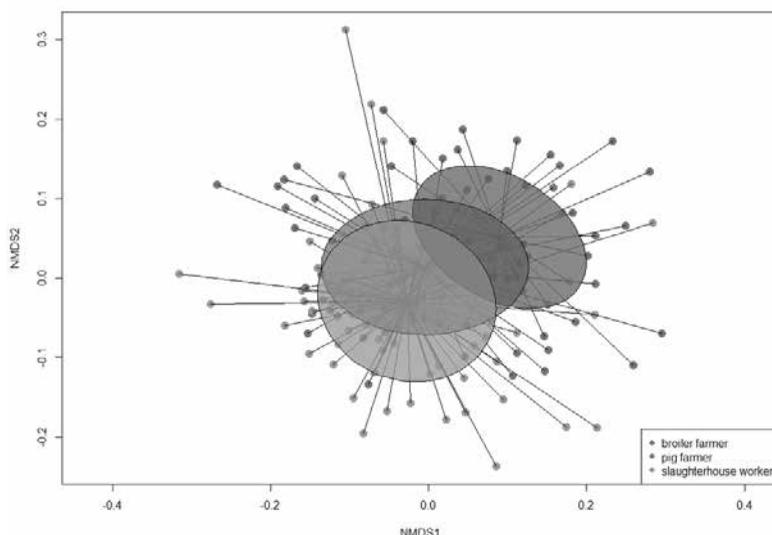
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This study is part of the European EFFORT project (<http://www.effort-against-amr.eu>).

**BACKGROUND:** Studies investigating antimicrobial resistance (AMR) in humans working in the meat production chain have primarily focused on specific bacterial species and types of AMR. However, larger scale resistome and microbiome studies, to our knowledge, have never been reported. This study analyzes (dis)similarities in faecal microbiome and resistome composition within and between farmer (pigs and poultry) and slaughterhouse populations (pig slaughterhouse employees, pig carcasses and faeces).

**METHODS:** Between October 2014 and December 2015, faecal samples were collected from 79 Dutch pig and poultry farmers, their families and co-workers (age: 18-65 years). Subsequently in two sampling rounds (June 2015 and July 2016) within one slaughterhouse, we collected faecal samples from in total 70 pig slaughterhouse workers (age: 21-59 years), 60 pigs (colon samples) and 480 pigs (carcass: cork borer). The latter two sample types were pooled by slaughter step and sampling round (carcass: 12 pools, pig faeces: 2 pools). All participants filled out a personal questionnaire regarding past antimicrobial use, animal contact, travelling, hospitalization, and meat consumption. DNA was extracted from all 163 samples and acquired resistomes and microbiomes were determined by metagenome (Illumina HiSeq4000) sequencing to 40M PE150 clusters. Bacterial genome and antimicrobial resistance genes (ARGs) were classified by mapping to NCBI bacterial reference genomes and the 90% identity/AMR-class clustered resfinder database. Fragments Per Kilobase ARG per Million bacterial fragments (FPKM) was used for relative abundance comparisons. Finally, necessary data transformations (incl. outlier removal) and descriptive and multivariate analyses were performed (NMDS, PERMANOVA, SIMPER analysis).

**RESULTS:** Significant differences in relative ARG load (total FPKM) were observed between the three human populations (Kruskal-Wallis:  $p < 0.005$ ), with pig farmers (median: 782) and slaughterhouse workers (median: 768) carrying the highest relative loads, and broiler farmers (median: 433) the lowest. Relative abundance of tetracycline resistance was highest among all samples, followed by  $\beta$ -lactam (humans) and macrolide resistance (humans, carcasses, pig faeces). Within the farmers' group, significant differences were observed between the farmers' partners and the other family members/farmers/employees (Kruskal-Wallis:  $p < 0.05$ ). Furthermore, we observed differences between relative ARG loads along the slaughter line (humans) with higher abundances in samples at the beginning (lairage-scalding) and at high-risk positions (evisceration, removal heart-lung-tongue) (Kruskal-Wallis:  $p < 0.01$ ). Multivariate results indicate resistome composition differences between the different human populations (PERMANOVA  $p < 0.001$ ; Figure 1).



**CONCLUSIONS:** Differences in ARG abundances were observed within and between farmers and slaughterhouse workers populations. Further work on the microbiome and the comparison of the microbiome and resistome is forthcoming.

Figure 1: NMS2 plot: Resistome clusters by human sample type. ARGs were used at the aggregated AMR class level (Bray-Curtis dissimilarity, data = square root transformed, stress=0.16). PERMANOVA on sample type:  $p < 0.001$ ,  $R^2 = 0.056$ , after removal of outliers, 'R' software v.3.4.2.

## 2 AMR 02 - GENOMIC EPIDEMIOLOGY / EVOLUTION OF AMR TRANSMISSION - GALLERY CD

### Genomic and evolutionary analysis of *Clostridium difficile* sequence type 11: a genetically diverse lineage of significant One Health importance

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**BACKGROUND:** In the last decade, *Clostridium difficile* infection (CDI) has reached an epidemic state in some parts of the world with sources outside the healthcare system, particularly livestock, identified as potential reservoirs. *C. difficile* sequence type (ST) 11 is a diverse evolutionary lineage comprising at least 5 PCR ribotypes (RTs) that contribute considerably to the global burden of CDI in humans and production animals. Increasing evidence of a shared ancestry and genetic overlap of RT078, the most common ST11 sublineage, between these populations suggests that CDI may have a zoonotic or foodborne aetiology.

**METHODS:** Whole-genome shotgun sequencing and core genome phylogenetics were performed on a diverse collection of 207 ST11 isolates of clinical (n=150) and veterinary/environmental (n=57) origin from Australia and 12 countries across Asia, Europe and North America (16 RTs including major ST11 sublineages 078, 126, 127, 033 and 288).

**RESULTS:** Phylogenies based on core orthologous genes (1276 loci) showed clustering of clinical and veterinary isolates indicative of very recent shared ancestry. Core genome single nucleotide variant (SNV) analysis provided

ultra-fine scale resolution of this lineage, identifying multiple intra- species and inter-species clonal groups (isolates separated by  $\leq 2$  SNVs in their core genome) in all the major RT sublineages. Many clonal groups comprised isolates spread over a vast geographic area (different states, countries, and continents), indicative of reciprocal long-range dissemination and possible zoonotic/foodborne transmission. Antimicrobial resistance genotypes and phenotypes varied across host species, geographic regions and RTs, and included macrolide/lincosamide resistance (Tn6194; *ermB*), tetracycline resistance (Tn6190; *tetM* and Tn6164; *tet44*), fluoroquinolone resistance (*gyrA/B* mutations) as well as several aminoglycoside resistance cassettes. *C. difficile* ST11 is defined by a large 'open' pan-genome (10378 genes) comprising a core genome of 2058 genes (remarkably, accounting for only 19.8% of the total gene repertoire) and an accessory genome of 8320 genes containing a large and diverse collection of clinically important prophages of the Siphoviridae and Myoviridae.

**CONCLUSIONS:** This study provides novel and critical insights on strain relatedness and genetic variability of *C. difficile* ST11, a lineage of significant One Health importance.

### 3 AMR 02 - GENOMIC EPIDEMIOLOGY / EVOLUTION OF AMR TRANSMISSION - GALLERY CD

## Whole genome sequencing reveals limited contribution of non-intensive chicken farming to extended-spectrum beta-lactamase producing *Escherichia coli* colonization in humans in southern Vietnam

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**BACKGROUND:** Overuse of antimicrobials in agriculture in Asia has been reported, but the risk of acquisition of extended-spectrum beta-lactamase (ESBLs) in humans through non-intensive chicken farming still remains unclear. We conducted this study to investigate the contribution of transmission of ESBL-producing *Escherichia coli* (ESBL-Ec) from poultry to ESBL-Ec colonization in humans.

**METHODS:** We collected faecal samples from 204 randomly selected farmers and their chickens, and from 306 community-based individuals who did not raise poultry in Vietnam. ESBL-Ec was isolated from MacConkey agar with and without antimicrobials supplemented. Logistic regression model was built to investigate risk factors associated with ESBL-Ec colonization in humans. A total of 486 ESBL-Ec isolates were sequenced to examine genomic relatedness of ESBL-Ec colonizing chickens and humans in Vietnam.

**RESULTS:** The prevalence of ESBL-Ec colonization was 20.0% in chicken farms, 31.1% in chicken farmers, 49.5% in rural individuals and 38.3% in urban individuals. Multivariable analysis showed that colonization with ESBL-Ec in humans was associated with human usage of antimicrobial drugs (OR=2.52, 95%CI=1.08–5.87) but not with involvement in chicken farming (OR= 0.71, 95%CI=0.43–1.19).

Whole-genome sequencing revealed that CTX-M genes were the most predominant ESBL genes, found in 468/486 (96.2%) of ESBL-Ec isolates. However, the distribution of CTX-M genes across chicken and human isolates was different (Figure 1). CTX-M-55 was identified as the most common ESBL-encoding gene in chicken isolates (72.1% versus 12.9% in human isolates,  $p < 0.001$ ), whilst CTX-M-27 was more prevalent in human isolates (44.2% versus 7.0% in chicken isolates;  $p < 0.001$ ).

On 16/204 farms (6.9%; 95%CI=3.4–10.3%) ESBL-Ec were detected phenotypically in both the farmers and their chickens. On 3/204 farms (1.5%; 95%CI=0–3.1%), ESBL genes of ESBL-Ec isolated from the farmers and their chickens were identical. However, we detected identical sequence types of ESBL-Ec between chicken and farmer isolates in only one farm. Isolates also revealed 0 pairwise SNP distance based on core genome alignment, indicating potential sharing of ESBL-Ec between the chickens and farmer on that farm.

**CONCLUSIONS:** The findings in this study suggest that non-intensive chicken farming is not a major source of ESBL-Ec colonization in humans and that human antimicrobial drug usage appears to be a more important driver of ESBL-Ec colonization in humans in Vietnam.

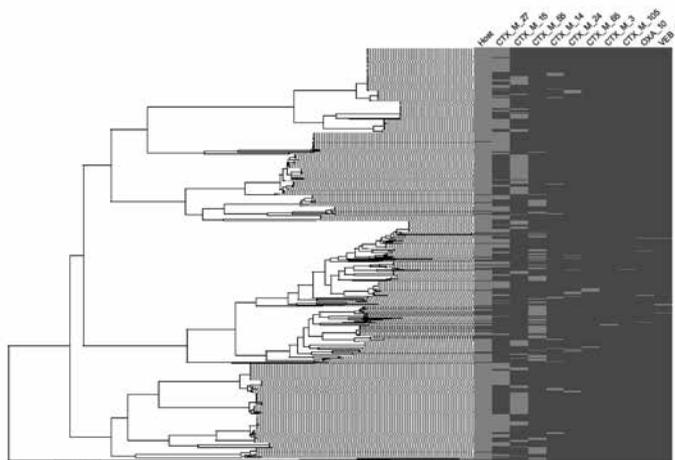


Figure 1 Distribution of ESBL genes across the phylogeny of ESBL-Ec isolated from chickens and humans in Vietnam. On the left is the maximum-likelihood phylogeny based on 230791 single nucleotide polymorphisms (SNPs) in the core genome of 486 ESBL-Ec isolates. The first column at the termini of the phylogeny represents the host of the isolates (red indicates human isolates, blue indicates chicken isolates). The presence (red) and absence (blue) of ESBL genes is shown in the next ten columns.

#### 4 AMR 02 - GENOMIC EPIDEMIOLOGY / EVOLUTION OF AMR TRANSMISSION - GALLERY CD

### Associations between antimicrobial use and the fecal resistome on broiler farms in nine European countries

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**BACKGROUND:** Several studies have suggested that antimicrobial use (AMU) selects for antimicrobial resistance (AMR). The association has never been determined specifically for the resistome of broiler fecal samples on farm level though. The aim of this study is to determine associations between farm and flock level AMU and the

abundance of antimicrobial resistance genes (ARGs) in broiler fecal samples from nine European countries. Also the association between farm biosecurity status and ARGs is explored.

**METHODS:** In the cross-sectional pan-European EFFORT-study, conventional broiler farms were visited to collect feces and to record biosecurity and AMU. The resistome (all known resistance genes included in the Resfinder database) of a pooled fecal sample was determined by metagenomic analysis for 176 farms. To take a potential country effect into account, meta-analysis was used to relate total and class-specific ARGs to AMU. ARGs, clustered at a 90% identity level, were quantified by metagenome short read mapping expressed as Fragments Per Kilobase ARG-reference per Million bacterial fragments (FPKM). AMU is measured by Treatment Incidence per Defined Daily Doses Animal (TI-DDDvet) for group treatments of the sampled flock, or products purchased by the farm in the year before sampling. In a similar way, the association between biosecurity status of a farm (defined with Biocheck.UGent) and the resistome was explored. All associations were adjusted for multiple testing by controlling the False Discovery Rate.

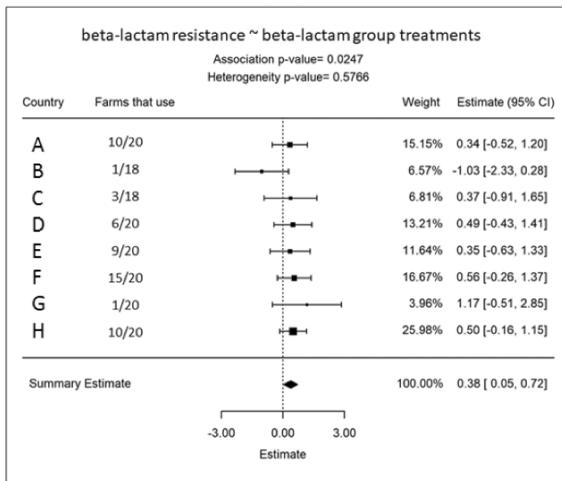


Fig. 1. Meta-analysis of associations between beta-lactam ARG presence and beta-lactam usage as group treatment in the sampled flocks, with number of farms that use AM, the weight of the individual association in the summary estimate and the 95% confidence intervals per country. At the bottom the summary estimate for the overall association. Country I reported no usage.

**RESULTS:** For 66 (38%) flocks there was no report of group treatments. These flocks show a similar resistome composition and roughly similar FPKM levels as AM-treated flocks. Nevertheless, we found significant positive associations between class-specific antimicrobial flock treatments and ARG clusters conferring resistance to the same class, for beta-lactams (fig.1), tetracyclines, macrolides, trimethoprim and aminoglycosides. Similar associations were found between ARG clusters and purchased products, which represent usage on farm level. In a gene level analysis for the class beta-lactam, a significant positive association was found for *bla<sub>TEM</sub>* and *bla<sub>ACT</sub>* gene clusters, which are in the top five most abundant gene clusters for this class. Little evidence was found for associations between resistance genes and biosecurity. No indications for confounding by age and biosecurity status were found.

**CONCLUSIONS:** The fecal microbiome in European broilers contains many resistance genes, even in the absence of current antimicrobial selection pressure. Despite this, the relative abundance of genes and composition of the resistome is positively related to the antimicrobial use in European broiler farms for several antimicrobial classes.

## Epidemic clones of community-acquired methicillin-resistant *Staphylococcus aureus* in slaughter pigs, Cuba

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The WHO, FAO and OIE, promote a global action plan under the One Health approach for a rapid containment antimicrobial resistance (AMR). In 2011 in Cuba, human infections caused by MRSA were predominantly associated with the USA300 clone, and the Latin American variant (USA300-LV) was not identified. Although these lineages are generally not associated with nasal carriage in pigs, which usually harbor the livestock-associated MRSA (LA-MRSA) lineage ST398, the presence of human epidemic clones in pigs cannot be excluded. Following the One Health recommendation, the epidemiological MRSA situation in slaughter pigs from three Cuban provinces was investigated. From May to July 2015, 22 of 285 nasal swabs taken at one central slaughterhouse from fattening pigs raised in the provinces of Mayabeque (n=67), Matanzas (n=90) and Cienfuegos (n=128) were found to carry MRSA (prevalence 7.7%). Isolates were obtained after two-step of enrichment and selective cultivation in Müller-Hinton (MH) broth. MRSA were identified by matrix-assisted laser desorption/ionisation time of-flight mass spectrometry (MALDI-TOF/MS) and by detection of the methicillin resistance gene *mecA* by PCR. The minimum inhibitory concentrations (MICs) were determined by microdilution in MH broth using the Sensititre susceptibility plate EUST. Antibiotic resistance and virulence genes were detected using microarrays (Alere). Isolates were characterized using pulsed field gel electrophoresis (PFGE), multilocus sequence typing (MLST), *Staphylococcus* protein A (*spa*) typing, *SCCmec* typing, ACME typing and *mec*-associated direct repeat unit (*dru*) typing. PFGE revealed three groups of MRSA. The MRSA isolates gathering into PFGE cluster I shared the same PFGE profile as the USA300 epidemic clone as well as the same genetic properties (ST8 except one ST173, *SCCmec* IVa, *dru* dt9g, PVL+, ACME I +). The isolates belonged to *spa* type t024 also contained the *sek* and *seq* enterotoxin genes. The strains were resistant to  $\beta$ -lactams (*mecA*, *blaZ*), macrolides [*msrA*, *mph(C)*], aminoglycosides [*aph(3')-III*] and fluoroquinolones [*GrlA(S80-Y)* and *GyrA(S84-L)*]. MRSA clones of PFGE cluster II were characteristic to USA300-LV (ST8, *spa* t008, *SCCmec* IVc, *dru* dt7j, PVL+ and ACME-). These clones were resistant only to  $\beta$ -lactam antibiotics (*mecA*, *blaZ*). The third PFGE cluster (cluster III) contained clones belonging to ST5, *spa* t010, *SCCmec* IVc, *dru* dt10a. They were all PVL- and ACME-, contained the enterotoxin genes *sea(N315)*, *seb*, *sel*, *selm*, *seln*, *selo*, *egc* and *selu*, and were resistant to  $\beta$ -lactams (*mecA*, *blaZ*) as well as to the aminoglycosides gentamicin and kanamycin [*aac(6')-Ie-aph(2'')-Ia*]. These findings demonstrate that pigs from Cuba carry MRSA belonging to the same clonal lineages than those found in humans causing infection in the community. It is therefore of major veterinary and public health importance to take specific preventive measures and antimicrobial stewardship in both human and animal settings to limit the spread of MRSA.

## AMR REAL LIFE APPLICATIONS OF WHOLE GENOME SEQUENCING

### 1 AMR 03 - REAL LIFE APPLICATIONS OF WHOLE GENOME SEQUENCING - GALLERY CD

#### Comparative Genomics of Vancomycin-Resistant *Enterococcus* spp. isolated from Wastewater Treatment Plants

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**BACKGROUND:** Wastewater treatment plants (WWTPs) are considered hotspots for the environmental dissemination of antimicrobial resistance (AMR) determinants and receive antimicrobial residues and resistant microorganisms from a variety of sources. Vancomycin-Resistant *Enterococcus* (VRE) is a candidate indicator organism for gauging the degree of AMR contamination in water environments. The multi-drug resistant nature of vancomycin-resistant *E. faecalis* and *E. faecium*, their ubiquity in wastewater and the gastrointestinal tracts of mammals, and the use of the genus as an indicator organism for fecal contamination make these species ideal candidates for this purpose.

**METHODS:** Three hundred and thirteen presumptive VRE isolates from two WWTPs from the same municipality were selected using selective broth containing vancomycin (4mg/L). In this study, a total of 39 isolates were selected for whole genome sequencing based on source, species (determined by groEL loci) and AMR phenotype (disc diffusion antimicrobial susceptibility). These genomes included *E. faecalis* (n=24), *E. faecium* (n=11), *E. casseliflavus* (n=2) and *E. gallinarum* (n=2). The presence of AMR genes, virulence genes, bacteriophage, and CRISPR/Cas arrays was determined using a variety of databases. Analysis of the phylogeny and the pangenome was also conducted with the inclusion of genomes of *E. faecium*, *E. faecalis* and *E. casseliflavus* from NCBI.

**RESULTS:** All but 3 isolates (2 *E. gallinarum* and 1 *E. faecalis*) exhibited resistance to three or more antimicrobials. The AMR phenotype generally aligned with genotype which confirmed the presence of multi-drug efflux proteins and specific resistance genes. Genes conferring vancomycin resistance were detected in 20 of the genomes. Vancomycin resistance was conferred by vanA (*E. faecium*), vanM (*E. faecium*), vanG (*E. faecalis*) and vanC (*E. casseliflavus* and *E. gallinarum*). A minimum of 18, 5, 6 and 3 virulence genes were detected in *E. faecium*, *E. faecalis*, *E. casseliflavus* and *E. gallinarum* genomes, respectively. Functional CRISPR/Cas arrays were detected in 10 *E. faecalis* genomes and 1 *E. gallinarum* genome. All of the *E. faecalis* genomes with CRISPR/Cas arrays also contained at least one prophage. The accessory genomes for each species show clear differentiation between isolates from wastewater, livestock, food products and clinical sources and could provide candidate biomarkers for microbial source tracking.

**CONCLUSIONS:** This study characterized the genomes of isolates from various species of VRE. It includes not only multi-drug resistant *E. faecium* and *E. faecalis*, commonly associated with humans, but also environment-associated *E. casseliflavus* and *E. gallinarum*. Analysis using additional genomes from the NCBI database demonstrated differential clustering of isolates from wastewater, clinical and other sources suggesting that these strains are specifically adapted to their environments.

2 AMR 03 - REAL LIFE APPLICATIONS OF WHOLE GENOME SEQUENCING - GALLERY CD

## Integrating whole genome sequencing data into quantitative microbial risk assessment modeling: a case study for *Salmonella* Heidelberg resistant to third-generation cephalosporins in Canadian broiler chicken production

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**BACKGROUND:** *Salmonella* Heidelberg resistant to third-generation cephalosporins (3GC) in chicken products has been identified as an important foodborne antimicrobial resistance concern by the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS). Primarily under the Genomics Research and Development Initiative on Antimicrobial Resistance (AMR) (GRDI-AMR), approximately 2,000 *S. Heidelberg* isolates collected in Canada were subjected to whole-genome sequencing (WGS). The objective of this study was to explore applications and added value of integrating WGS data into a farm- to-fork quantitative microbial risk assessment (QMRA) model for 3GC-resistant *S. Heidelberg* in broiler chicken.

**METHODS:** A QMRA framework was developed in accordance with the Codex Alimentarius guidelines for risk analysis of foodborne AMR (Figure 1). Using data from a literature review and consultation with WGS experts, we identified potential areas where WGS data could be integrated into the QMRA model through refinement of the hazard identification, exposure assessment and hazard characterization steps, in order to produce a more accurate estimate of the public health risk associated with the occurrence of 3GC-resistant *S. Heidelberg* in chicken in Canada.

**RESULTS:** Applications of WGS data were identified at each step of the QMRA model (Figure 1). For hazard identification, WGS data can refine the AMR profile of the hazard of interest by providing a comprehensive list of AMR genes present and describing their location on the chromosome or on mobile genetic elements. The latter is critical to determine whether horizontal gene transfer should be considered in the risk pathway and if so, at which steps along the farm-to-fork continuum. Additionally, WGS data can be used to determine the virulence profile of the hazard and any associations with AMR. By quantifying the relatedness of isolates collected along the agri-food chain using phylogenetic approaches, the proportion of hazards carried through each step (i.e., farm, abattoir, retail) can be integrated into the exposure assessment to better characterize how upstream events affect consumer exposure.

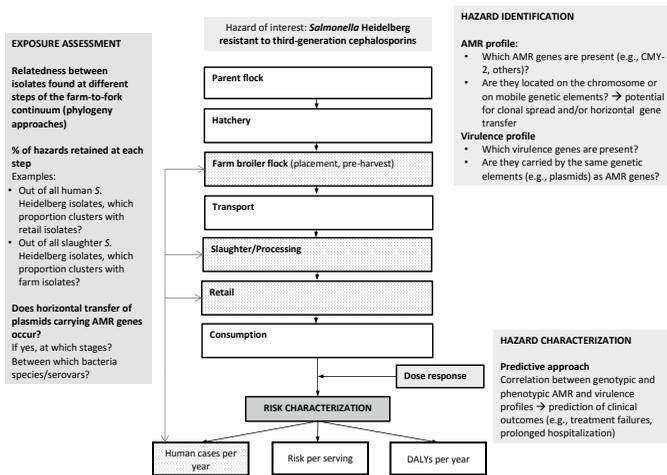


Figure 1. Potential added value of whole-genome-sequencing data to quantitative risk assessment of *S. Heidelberg* resistant to third-generation cephalosporins in broiler chicken

Colored boxes indicate key areas where whole-genome-sequencing data could inform quantitative risk assessment steps as defined by the Codex Alimentarius guidelines for risk analysis of foodborne antimicrobial resistance  
Dotted blue boxes: steps where *S. Heidelberg* isolates were sequenced via whole-genome sequencing primarily under the Canadian Genomics Research and Development Initiative on Antimicrobial Resistance

For the hazard characterization, virulence profiles can be integrated into novel dose-response models. As well, WGS data are expected to better predict clinical outcomes following exposure to the hazard, although correlations between genotypic and phenotypic profiles need to be validated first.

**CONCLUSIONS:** WGS data have the potential to make a huge improvement to QMRA modeling, which has been traditionally performed using phenotypic information. Some of the possible improvements described herein will be tested under the GRDI-AMR project using 3GC-resistant *S. Heidelberg* as a case study.



## 3 AMR 03 - REAL LIFE APPLICATIONS OF WHOLE GENOME SEQUENCING - GALLERY CD

**Whole Genome Sequence Profiling of Antibiotic Resistant *Staphylococcus aureus* isolates from Livestock and Farm Attendants in Ghana**

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3: Livestock and Poultry Research Centre Institute of Agricultural and Consumer Sciences, University of Ghana

**BACKGROUND:** Recent studies in Ghana have indicated the presence of epidemic methicillin resistant *S. aureus* clones among carriage and clinical *S. aureus* isolates. Information on the epidemiology of *S. aureus* among livestock in Ghana is, however, not available. Therefore, the objective of this study was to characterize *S. aureus* isolates from livestock and farm attendants to determine the differences, if any, with respect to antimicrobial resistance, genotypic diversity and virulence gene content.

**METHODS:** Swab samples were collected from the anterior nares of cattle, pigs, goats, sheep and farm workers from selected farms. Identification of *S. aureus* was done by MALDI-TOF MS. Antimicrobial susceptibility testing was performed by VITEK (Biomérieux) and interpreted according to EUCAST guidelines. Whole genome sequencing was done using the illumina Miseq Platform.

**RESULTS:** Twenty-six (26) *S. aureus* isolates were recovered from a total of 401 nasal swab samples collected. Isolates were frequently resistant to penicillin (65%), tetracycline (42%), ciprofloxacin (31%), clindamycin (9%) and ceftiofur (7%). Genome sequencing of 15 out of the 26 isolates revealed that the isolates belonged to ST8 (n=1), ST152 (n=4) (humans); ST9 (n=1), ST97 (n=4) (Pigs) and ST133 (n=5) (Goats). Almost half (46%) of the isolates were multi-drug resistant. The two MRSA isolates detected (belonged to ST8 and ST152) were from humans; none was found among livestock. Panton Valentine leucocidin toxin gene was detected among 27% of the isolates (mainly from humans).

**CONCLUSIONS:** The detection of ST152 as MRSA was particularly interesting; although this clone was dominant in a collection of carriage and clinical isolates in previous studies in this country, none was MRSA. ST152 MRSA has been reported in Central Europe, the Balkan, Switzerland and Denmark as a community acquired MRSA. All isolates detected in this study belonged to global lineages (ST133, ST9, ST97, ST8, ST152). The finding of 46% multidrug resistant isolates is worrying as routine detection of resistant bacteria species are not performed on these farms due to limited microbiological infrastructure in Ghana. This calls for capacity building to prevent the spread of these resistant bacteria species in the country.

## Phenotypic and genomic analysis of antimicrobial resistant *E. coli* isolated from ready-to-eat food in Singapore

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**BACKGROUND:** Antimicrobial resistance (AMR), especially multidrug-resistance, of bacteria is posing a great threat to public health. This study aimed to determine the phenotypic antimicrobial resistance (AMR) profiles of *Escherichia coli* isolated from ready-to-eat retail food in Singapore. *E. coli* is widely recognized as a food safety indicator and a high priority Gram negative bacterium for studying antimicrobial resistance. We then compared the phenotypic traits of these isolates with the antimicrobial resistant genes identified by next-generation sequencing (NGS) technique which can serve to support further work on elucidating the genetic mechanisms involved.

**METHODS:** A total of 99 *E. coli* isolates (77 were from poultry-related food, 22 were from fish-related food) from ready-to-eat retail food were included in this study. Disk diffusion was conducted to determine the phenotypic AMR profiles of isolates against 12 antimicrobials. Isolates resistant to ceftriaxone (30 µg) were subjected to double-disk synergy test using amoxicillin and clavulanate (20/10 µg), ceftazidime (30 µg), and cefotaxime (30 µg) for the phenotypic confirmation of Extended-Spectrum β-lactem (ESBL)- production. Isolates resistant to at least one antimicrobial were subjected to micro-dilution against 33 antimicrobials (including classes of β-lactem, aminoglycosides, tetracycline, fluoroquinolones, polymyxin et. al.). These isolates were also subjected to whole genome sequencing (WGS) using Illumina HiSeq2500 sequencer. Short reads were assembled by Velvet. Resfinder, an online tool, was used to analyze WGS data for the detection of AMR genes.

**RESULTS:** Based on disk diffusion results, 24.2% (24/99) of the *E. coli* isolates from ready-to-eat retail food were resistant to at least 1 antimicrobial agent, and 68.7% (68/99) isolates were sensitive to all 12 antimicrobials tested. Poultry-related *E. coli* isolates showed a higher resistance rate (29.9%, 23/77) to at least 1 antimicrobial agent than fish-related isolates (4.5%, 1/22). No resistance to amikacin, amoxicillin/ clavulanic acid and meropenem was observed. The most common resistance pattern observed was tetracycline resistance (17.2%), followed by ampicillin resistance (15.2%). Two ceftriaxone-resistant isolates were confirmed as ESBL-producing *E. coli*. Of 24 isolates subjected to micro-dilution, 70.8% (17/24) were resistant to tetracycline, followed by chloramphenicol (50%, 12/24), ampicillin and trimethoprim (41.7%, 10/24). Genomic analysis of 24 *E. coli* isolates revealed the presence of 9 classes of AMR genes; 20 isolates carried at least one AMR gene. High agreement (79.2% to 95.8%) between AMR phenotypes and genotypes across all antimicrobials was observed, with exceptions for aminoglycosides (79.2%) and colistin (79.2%). Differences observed between phenotypic and genomic findings of isolates could be due to unknown or noble resistance mechanisms of the bacteria or it could be due to the limited range of antimicrobials used in phenotypic tests.

**CONCLUSIONS:** The detection of *E. coli* harboring antimicrobial resistance traits in ready-to-eat food can be of potential public health concern. Although these are non-pathogenic *E. coli* strains and are unlikely to cause foodborne disease, they can still be good reservoirs for the acquisition and transmission of AMR genes in bacteria in retail food and the environment. This study illustrates the usefulness of WGS in supporting work for understanding the genetic mechanisms of antimicrobial resistance traits in bacteria. With the advancement in technology and the general declining cost in sequencing, WGS is a promising tool that can be applied even for routine surveillance for the monitoring of AMR trends in human pathogens and environmental bacteria.

## 5 AMR 03 - REAL LIFE APPLICATIONS OF WHOLE GENOME SEQUENCING - GALLERY CD

## Antibiotic use and biosecurity in pig farming are determinants for antimicrobial resistance, a metagenome-wide association study in nine European countries.

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**EFFORT GROUP:** Haitske Graveland (UJVM), Alieda van Essen (WBVR), Bruno Gonzalez-Zorn (UCM), Gabriel Moyano (UCM), Pascal Sanders (ANSES), Claire Chauvin (ANSES), Julie David (ANSES), Antonio Battisti (IZSLT), Andrea Caprioli (IZSLT), Thomas Blaha (TIHO), Katharina Wadepohl (TIHO), Maximiliane Brandt (TIHO), Tine Hald (DTU), Ana Sofia Ribeiro Duarte (DTU), Dariusz Wasyl (NVRI), Magdalena Skarzyńska (NVRI), Magdalena Zajac (NVRI), Hristo Daskalov (NDRVI), Helmut W. Saatkamp (BEC), Katharina D.C. Stärk (SAFOSO). This study is part of the EFFORT project (<http://www.effort-against-amr.eu>).

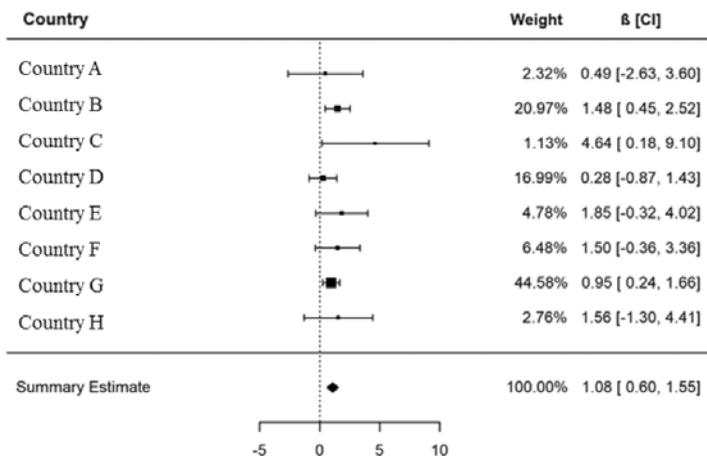
**OBJECTIVES:** Previous studies in food-producing animals have shown relationships between antimicrobial use (AMU) and resistance (AMR) in specifically isolated bacterial species. Multi-country data is scarce and only describes between-country differences. Here we investigate associations between the pig faecal mobile resistome (based on Resfinder, i.e. full collection of horizontally acquired antimicrobial resistance genes (ARGs)) and characteristics at farm-level across Europe.

**METHODS:** A cross-sectional study was conducted among 176 conventional pig farms from nine European countries. Twenty-five pig faecal samples were pooled per farm and acquired resistomes were determined by shotgun metagenomics and clustered. Normalized Fragments resistance genes Per Kilobase reference per Million bacterial fragments (FPKM) were calculated. Specific farm-level data (AMU, biosecurity) was collected. Random-effects meta-analyses were performed by country, relating farm-level data to ARG abundances (FPKM).

**RESULTS:** Total AMU during fattening was positively associated with total ARG (total FPKM). Positive associations were especially observed between widely used macrolides (e.g. Figure 1) and tetracyclines, and ARGs corresponding to the respective antibiotic classes. Significant AMU/ARG associations were not found for  $\beta$ -lactams and no colistin-encoding ARGs were found, despite being the antimicrobial classes used highest in younger pigs. An increased internal biosecurity was directly related to higher abundances of ARG mainly encoding macrolide resistance. These effects of biosecurity were independent of AMU in mutually adjusted models.

**CONCLUSIONS:** Using resistome data in associations studies is unprecedented and adds accuracy and new insights to previously observed AMU-AMR associations. The major components of the pig resistome are positively and independently determined by on-farm AMU and biosecurity conditions.

Figure 1: Meta-analysis: A positive association was observed between macrolide and lincosamide use and macrolide resistance (FPKM) (forest plot)



Macrolide resistance =  $f(\text{Macrolide and lincosamide use during the fattening phase}^*)$

Legend:  $q$ -value summary estimate < 0.01,  $p$ -value heterogeneity test > 0.5. Weight for country 'i' is dependent on the inverse of the sum of the within-country variance for country 'i', plus the between-country variance tau-squared. CI = confidence interval. \*Includes lincomycin-spectinomycin antimicrobial use. One country couldn't be included in the above association as a consequence of no macrolide/lincosamide use during the fattening phase in the respective farms of this country.

## AMR PREVALENCE AND SURVEILLANCE OF RESISTANCE

### 1 AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE - GALLERY CD

#### Temporal Changes in Antibiotic Resistance in Common Bottlenose Dolphins (*Tursiops truncatus*), a Sentinel Species

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An increase in resistance to antibiotics among common bacterial pathogens is one of the most significant threats to public health. Increases in antibiotic resistance (AR) have been documented globally in isolates from humans, wildlife and the environment. To date, few studies have examined long-term trends in AR in organisms isolated from marine mammal populations despite the potential role of aquatic environments in the proliferation of resistance genes. The objective of this study was to examine temporal trends in resistance to antibiotics among pathogens isolated from common bottlenose dolphins (*Tursiops truncatus*) between 2003 and 2015. Individual dolphins, resident to the Indian River Lagoon, FL, an ecosystem with significant human impacts and a large coastal population, were sampled as a part of the Bottlenose Dolphin Health and Environmental Risk Assessment Project. Swab samples for microbiological analyses were taken from the blowhole, stomach and anus as a part of a comprehensive health examination. Isolates were identified using gram stain morphology and growth on selective media. Antibiotic resistance was measured using disc diffusion on Mueller Hinton agar. The multiple antibiotic resistance index (MAR) was calculated for each isolate. A total of 733 isolates were obtained from 171 individual dolphins. The most commonly cultured pathogens included *Aeromonas hydrophila*, *Escherichia coli*, *Edwardsiella tarda* and *Vibrio alginolyticus*. The MAR was compared between 2003-2007 and 2010-2015 for each organism and was significantly higher for *Pseudomonas aeruginosa* and *Vibrio alginolyticus* during the later period. For all bacterial isolates, resistance to cefotaxime, ceftazidime and gentamicin increased significantly between sampling periods. This represents the first study to use multiple antibiotic resistance indexing for bacterial isolates from a marine mammal. The significant increases in resistance for some bacterial species likely reflect shared environmental exposures to antibiotics and transfer of resistance from terrestrial sources, and animal or human populations to dolphins.

## Antimicrobial Resistance in *Salmonella enterica* Isolates from Wildlife in Virginia

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2: Ohio State University, United States of America;

3: Virginia State University, United States of America;

4: Division of Consolidated Laboratory Services, Virginia Department of General Services, United States of America

**BACKGROUND:** A large majority of national surveillance efforts for enteric bacteria in the United States currently come from clinical isolates from humans or samples from the agriculture and livestock domain. However, there has recently been a drive to implement surveillance efforts with a more One Health approach and focus. Wildlife has the potential to serve a critical role in the dispersal and dissemination of antimicrobial resistance (AMR) genes. Wildlife may carry a wide array of AMR genes and can potentially introduce these genes into the soil and water through excrements. These genes may then proliferate in the environment and be transmitted to humans and domestic animals through indirect or direct exposures.

**METHODS:** A total of 65 *Salmonella enterica* isolates from two studies between 2010-2012 involving birds, reptiles, and mammals sampled in the Eastern region of Virginia were tested for AMR by two different methods. The first method performed antimicrobial susceptibility testing by the traditional Kirby-Bauer disk diffusion method (phenotypic resistance) following Clinical and Laboratory Standards Institute concentrations and guidelines against a panel of 12 antibiotics representing nine antimicrobial categories. Whole genomic sequencing (WGS; genotypic resistance) was also performed on the isolates. The CARD database in conjunction with the ARIBA platform tool was used to identify genes associated with the different antimicrobial categories.

**RESULTS:** The prevalence of AMR in the samples by Kirby-Bauer disk diffusion was 61/65 (94%) with most samples demonstrating at least intermediate resistance to streptomycin. Over 10% (7/65) of the isolates showed resistance to three or more antimicrobial categories; therefore, classifying them as multidrug resistant. An isolate of *Salmonella* Senftenberg from a bird was resistant to eight drugs. Overall, phenotypic resistance showed a high correlation with genotypic resistance for the 65 *Salmonella enterica* isolates. From an epidemiological perspective, an overall sensitivity of 86.8% and specificity of 87.0% were observed. The concordance between tests was categorized as 'good' as shown by the kappa value of 0.59. The overall agreement between all of the calls (9 antimicrobial categories\* 65 isolates=585 total calls) was 87% (509/585).

**CONCLUSIONS:** Antimicrobial resistance was present in many of the wildlife samples likely indicating that AMR is present in their environment. Different measures for test performance demonstrate that WGS can be used to predict AMR phenotypic resistance for *Salmonella* in wildlife. It is highly recommended to pursue more research in this area as the numbers are small for any analysis performed by species or antimicrobial class and that a standard for be developed to compare WGS technology to current gold standards.

## 3 AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE - GALLERY CD

## Antibiotic resistance and epidemiology of *Campylobacter* recovered from humans, animals and environmental sources in Ghana

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2: Kwame Nkrumah University of Science and Technology, Ghana;

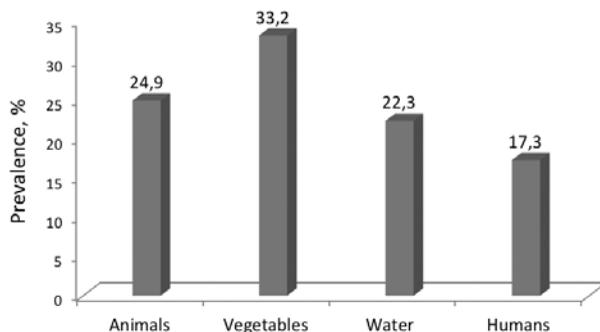
3: Kwame Nkrumah University of Science and Technology, Ghana;

4: Department of Microbiology & Infection Control, Statens Serum Institute, Copenhagen, Denmark

**BACKGROUND:** Antibiotic resistance is a major challenge in public health especially in developing countries where antibiotic use is widespread and poorly moderated. This study highlights the resistance trends in environmental water sources, human and veterinary public health.

**METHODS:** The research was carried out in the Kumasi Metropolis in Ghana from March 2013 to May 2016. *Campylobacter* were isolated using standard bacteriological methods and speciated on API CAMPY kit. Isolates were confirmed using multiplex PCR targeting the *lpxA* gene of *Campylobacter*. The antibiogram profile of species were determined by the CLSI's Kirby-Bauer disk diffusion method against 13 relevant antibiotics.

**RESULTS:** A total of 635 faecal and 595 carcasses of livestock and poultry, 241 farm and market vegetables, 188 water samples from different sources and 202 human samples were analysed. Prevalence of *Campylobacter* in the animals were 23.4%, 27.2%, 21.2%, 32.5% and 22.3% respectively in cattle, sheep, goat, pigs and poultry. In farm and market vegetables, prevalence was 23.9% and 41.9% respectively, as 17.3% and 22.3% were recovered from humans and water sources respectively. Species identified were *C. Campylobacter*, *C. Campylobacter sub sp. doylei*, *C. coli*, *C. lari* and *C. hyointestinalis* with *C. Campylobacter* and *C. coli* being the dominant specie (>80%). Resistance of the species from humans, animals, vegetables and water sources respectively were 34-46%, 17-74%, 33-49% and 48-69% to the quinolones, 9-43%, 4-29%, 20-31% and 45-55% to aminoglycosides, 97-100%, 80-100%, 95-100% and 100% to  $\beta$ -lactams, 96-100%, 98-100%, 96-100% and 88-100% to erythromycin, 54-56%, 68-87%, 90-96% and 75-93% to chloramphenicol, 92-100%, 62-98%, 64-75% and 50-100% to tetracycline and 67-81%, 46-92%, 57-67% and 25-100% to trimethoprim sulphonamides.



Resistance to imipenem was 0%, but a proportion of the *Campylobacter* strains exhibited intermediate susceptibility from all sources.

Fig. 1: Prevalence of *Campylobacter* isolated from animals, vegetables, water and humans.

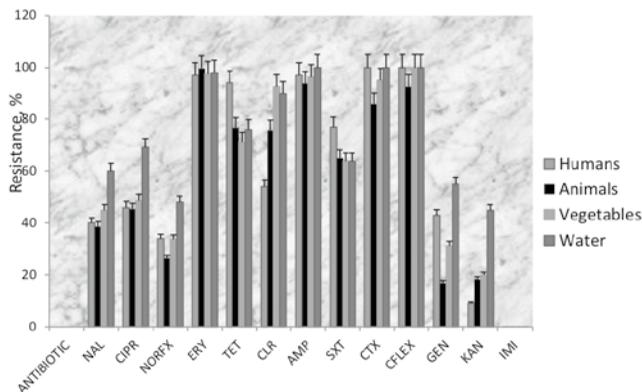


Fig. 2: Antibiotic resistance profile of *Campylobacter* species recovered from various sources

**CONCLUSIONS:** The study established multidrug resistant *Campylobacter* as widespread in the environment, present in the food chain and among patients presenting with gastroenteritis in Ghana. The high resistance rates observed against erythromycin and other commonly prescribed antibiotics is worrying, which necessitates the establishment of a national antibiotic resistance management team to monitor and control antibiotic use in agriculture, veterinary and human medicine.

#### 4 AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE - GALLERY CD

### A longitudinal evaluation of *Salmonella* Typhimurium AMR prevalence and transmission using whole genome sequencing and phenotyping in a poultry population with no antimicrobial selection pressure.

**Crabb, Helen Kathleen**

The University of Melbourne, Australia

**BACKGROUND:** Australia released its first National Antimicrobial Resistance Strategy in 2015 and the implementation plan for this strategy in 2016 (Commonwealth of Australia, 2016). The use of antimicrobials in food producing animals in Australia is strictly regulated and few antimicrobial classes are available for use in poultry. It is currently unknown what the long term impact of the reduction in use of antimicrobials will have on antimicrobial resistance in specific pathogens. An ongoing longitudinal study investigating the transmission of *Salmonella* Typhimurium within an “antibiotic free” vertically integrated chicken meat enterprise has been conducted. This study evaluated the impact of antimicrobial prescribing on the prevalence of antimicrobial resistance in *Salmonella* Typhimurium isolates in this poultry population.

**METHODS:** No antimicrobials have been used in the studied population for a period of 5 years. Three hundred and twenty-seven *S. Typhimurium* isolates were screened for antimicrobial susceptibility using the calibrated dichotomous sensitivity test (CDS) method. Four hundred and eleven isolates were whole genome sequenced using Illumina HiSeq and sequence reads were screened for the carriage of known antibiotic resistance genes using SRST2.

**RESULTS:** Two clonal lineages of *S. Typhimurium* were identified in this population. The phenotypic test identified 16.5% of isolates susceptible to all antimicrobials tested and three resistant phenotypes; sulphafurazole (68.5%), streptomycin (56.5%), and ampicillin (10.1%). No fluoroquinolone, cephalosporin or ESBL producing phenotypes were identified. Genotyping identified four TEM  $\beta$ -lactamase resistance genes in 11 isolates (3.4%). Nine of the 11 isolates were resistant to ampicillin (MIC  $\geq$  8mg/L). These genes were identified on two occasions only. No transmissible genes conferring resistance to sulphonamides or streptomycin were identified in this population.



**CONCLUSIONS:** Two *S. Typhimurium* lineages were clonally disseminated through a vertically integrated poultry operation with their origin at the parent sites. Whole genome sequencing failed to identify the similar dissemination of antimicrobial resistance genes within this *Salmonella* population. The presence of phenotypic resistance (streptomycin MIC  $\geq$  16mg/L), in the absence of known resistance genes, at minimum inhibitory concentrations for antimicrobials not permitted nor available for use in poultry for nearly 20 years suggests factors other than direct antimicrobial use maintain phenotype presence in this *S. Typhimurium* population. These findings have important ramifications with regards to the current drive for the reduction in the use of antimicrobials in food producing animals and its' impact on the prevalence of antimicrobial resistance and subsequent transmission via the food chain.

## 5 AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE - GALLERY CD

### Antimicrobial resistance in *Escherichia coli* from dairy farms of Quebec, Canada, and identification of Extended-Spectrum- $\beta$ -lactamase/AmpC resistance

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Faculty of Veterinary Medicine, University of Montreal, Canada

Passive surveillance of antimicrobial resistance (AMR) in dairy pathogens in Québec, Canada, has revealed resistance to various antimicrobials including third generation cephalosporins. Some studies have also suggested that calves may be a greater source of antimicrobial resistant bacteria than mature cows. Third generation cephalosporins are of very high importance in human health medicine in Canada and one of these, ceftiofur, is used in the dairy industry. This usage could contribute to the emergence of resistance due to bacterial production of AmpC beta-lactamases and extended-spectrum beta-lactamases (ESBL). In addition, the prevalence of AMR, other than to ceftiofur, at the dairy farm, which includes bacterial isolates from healthy and sick animals, is unknown in Québec because passive surveillance programs focus on pathogenic bacteria. The hypothesis of the present study is that the prevalence of AMR in enteric bacteria is higher in calves than in cows for Québec dairy farms. Thus, an objective of this study was to determine the prevalence of AMR in the enteric indicator bacterium *Escherichia coli* in adult cows and calves on farms in Quebec using faecal and manure pit samples. Dairy farms ( $n=102$ ) were recruited randomly on a voluntary basis for the one-year study period between March 2017 and April 2018. For each farm, composite manure samples were collected from three different sources: up to five randomly chosen preweaning calves, five random lactating cows and two locations of the manure pit. Farms were visited twice at an interval of 6 months. Faecal samples ( $n=602$ ) were stored at  $-80^{\circ}\text{C}$  with a preservative medium for 2 – 6 months before processing. Each sample was streaked on MacConkey agar for isolation of up to 5 lactose positive colonies. Also, fecal samples from the first visit ( $n=302$ ) were pre-enriched with buffered peptone water then streaked on MacConkey agar supplemented with  $1\mu\text{g/ml}$  of cefotaxim for recovery of presumptive ESBL/AmpC colonies. *Escherichia coli* were identified by Matrix-assisted laser desorption ionization time of flight mass spectrometry (MALDI-ToF MS). Minimum inhibitory concentration (MIC) was performed by the broth microdilution technique for one *E. coli* isolate per fecal sample ( $n=602$ ). MIC results are presently being analysed. Following selective enrichment of samples, presumptive ESBL/AmpC *E. coli* were found in lactating cows (11/102; 0.11 [IC 95% : 0.06 - 0.18]), manure pit (24/102; 0.24 [IC 95% : 0.16 - 0.33]) as well as calves (53/98; 0.54 [IC 95% : 0.44 - 0.64]). Hence, our preliminary data indicate that calves may represent a greater risk for carrying ESBL/AmpC *E. coli* than lactating cows in dairy farms in Québec. Production of ESBL/AmpC by dairy commensal bacteria could contribute to the dissemination of this resistance and this warrants further investigation.

## AMR NOVEL STRATEGIES FOR AMR INTERVENTIONS / PREPAREDNESS

### 1 AMR 05 - NOVEL STRATEGIES FOR AMR INTERVENTIONS / PREPAREDNESS - GALLERY CD

## Operationalising One Health Approaches to Surveillance for Antimicrobial Resistance

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2: Mott MacDonald Ltd, London, United Kingdom;

3: Morvet Ltd, Masterton, New Zealand

**BACKGROUND:** Antimicrobial resistance (AMR) is a truly ‘wicked’ global health issue that requires a One Health approach to understand the complex range of interacting factors involving humans, animals and the environment that may be associated with its emergence. One Health is a fundamental principle of the WHO-FAO-OIE Global Action Plan for AMR and the UK Department of Health and Social Care’s Fleming Fund Programme. The Fleming Fund Country Grant and Fellowship programmes are designed to strengthen collaborative and integrated surveillance in South and Southeast Asian and sub-Saharan African countries to produce data on AMR and AMU in humans, animals, farmed aquatic species, the environment and agriculture that over time will support development of evidence-based policies and programmes to mitigate AMR risks.

**METHODS:** The Fleming Fund Management Agent, Mott MacDonald, and technical partner, Massey University, are working with the Ministries of Health, Agriculture/Livestock and other related Ministries in multiple countries to design and implement integrated One Health AMR/AMU surveillance systems. Key design aspects that support integrated surveillance are:

- a common set of zoonotic bacteria/ antibiotic combinations
- standardised diagnostic approaches to antibiotic sensitivity testing
- equivalent laboratory quality assurance systems
- comparable recording of diagnostic results
- sampling strategies that facilitate comparison of AMR/AMU patterns in related human and animal populations

In addition to supporting implementation of the surveillance programmes through Country Grants, supporting the establishment of multi-sectoral technical and policy-making bodies, and facilitating collaboration within these, is critical to operationalisation of One Health. The Fleming Fellowship Scheme supports technical leaders share and interpret their surveillance results, identify epidemiological links and design future surveillance to strengthen the relatedness of the AMR/AMU information generated by each sector. Collaboration amongst members of policy-making bodies is supported through critical decision-making meetings throughout the Fleming Fund programme.

**RESULTS:** The extent to which a One Health approach to AMR/AMU surveillance is operationalised varies considerably amongst countries which have different cultural and political environments. A key influencing factor is the extent to which the national AMR committee leadership facilitates engagement and collaboration amongst the sectors within the committee, which guides implementation of the country’s national action plan for AMR. Other factors reflect the extent to which professionals from different sectors know each other and have worked together in the past. Collaboration is most effective amongst people who respect each other and enjoy working together.

**CONCLUSIONS:** Moving from words to action in operationalising One Health is challenging as it involves engaging with increased complexity and requires building relationships, respect and trust amongst people from different sectors to work effectively together to address a common health issue. On-going facilitation is necessary to strengthen collaboration towards a transdisciplinary approach through building a shared vision and understanding of AMR, building relationships, understanding, respect and trust amongst the multidisciplinary teams.

## #AMR: Exploring the role of social media in addressing antimicrobial resistance

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1: University of Saskatchewan, Canada;

2: University of Frederickton

**BACKGROUND:** Despite the pervasiveness of social media (SM) today there is limited discussion about the value of these platforms in addressing issues of antimicrobial resistance (AMR). The Pew Research Center indicated the increasing use of SM in 2018, including significant advances in the 30-49 and 50-64 age groups. This trend aligns with producer demographics and animal agriculture organizations are increasingly promoting SM use to their members. However, there is little exploration of use of these media as a means for knowledge dissemination, community building, and/or intervention in the AMR literature. The aim of this research was to determine the volume, reach, and engagement of AMR discourse on SM in the four months immediately preceding the conference to deliver near real-time data on the potential role of these media as a mass scale AMR health information sharing platform.

**METHODS:** This study began with a comprehensive review of the existing literature on SM and AMR using a combination of related terms in the CABI, Medline, and AGRICOLA databases. This search resulted in limited relevant literature (N=10) and demonstrated a lack of SM AMR content analysis and analytics. To address this gap, a fit-for-purpose Twitter-stream monitoring application was created using Python and the tweepy library to collect AMR posts using predetermined SM hashtags. In the four months immediately preceding the conference the Python scraper will continue to retrieve AMR related tweets to populate a SQL database. Using Python and the natural language toolkit, the raw Tweets will be analyzed for trends and common themes, including separating original Tweets from re-Tweets, assessment of tone using sentiment scores, and the identification of the most impactful Tweets in terms of volume and reach.

**RESULTS:** The relative frequencies of the retrieved hashtags were evaluated over an initial two-week period allowing for refinement of the Python code to establish a robust tracking system. Within the first 24 hours 1625 posts were captured, with more than 15 000 at the conclusion of the two-week test period. There was a significant change in the hashtag capture during the test period, and the researchers will continue to refine the code as needed to elicit the most comprehensive dataset. In the week immediately preceding the conference a full suite of analytics, as previously detailed, will be completed.

**CONCLUSIONS:** This research will deliver a near-real time characterization of the current SM AMR discourse to attendees of the 5th International One Health Congress, a critical first step in determining the efficacy of SM in reaching knowledge users. There is an increasing volume of AMR data being exchanged through SM platforms and yet the role of these media in monitoring trends, influencing dialogue and producer practice, and for knowledge translation is largely uninvestigated.

3 AMR 05 - NOVEL STRATEGIES FOR AMR INTERVENTIONS / PREPAREDNESS - GALLERY CD

## Development of 2-Aminoimidazole Compounds that Enhance Antibiotic Activities to Reduce Antibiotic Usage

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- 1: Agile Sciences, Inc, United States of America;
- 2: University of North Carolina - Chapel Hill;
- 3: Geffen School of Medicine at UCLA LABioMed at Harbor-UCLA Medical Center

**BACKGROUND:** A novel strategy to reduce antibiotic usage is to develop 2-aminoimidazole (2-AI) compounds that enhance the activity of antibiotics. These compounds inhibit the response regulator of bacterial two component systems, so bacteria cannot sense and respond to their environment and are unable to turn on defense mechanisms (i.e. biofilm formation, efflux pump upregulation, and membrane modification). Here we present the efficacy of two compounds in increasing antibiotic sensitivity in vitro and in two rodent models in vivo.

**METHODS:** Minimum inhibitory concentration (MIC) were determined following the CLSI microdilution method. CD-1 mice were infected with 10<sup>6</sup> CFU of *Pseudomonas aeruginosa* PAK, and administered the treatments (Figure 1). Sprague-Dawley female rats were infected with 10<sup>5</sup> CFU of MRSA Xen30, and administered the treatments (Figure 2).

**RESULTS:** MIC assays show 2-AI compounds lower the MICs of antibiotics (Table 1). The mouse lung infection model shows combination treatment with AGL-503 + colistin reduced bacterial counts versus colistin alone (Figure 1).

Pathogen	Antibiotic	Antibiotic MIC value (µg/mL)	
		w/o <i>cmpd</i>	with <i>cmpd</i>
<i>Pseudomonas aeruginosa</i> (cystic fibrosis isolate)	Imipenem	16	4
	Meropenem	8	1
	Ceftazidime	32	8
<i>Acinetobacter baumannii</i> (clinical isolate)	Imipenem	16	4
	Meropenem	64	4
<i>Klebsiella pneumoniae</i> NDM-1 ATCC BAA-2146	Imipenem	256	4
	Meropenem	128	16
<i>Acinetobacter baumannii</i> ATCC 4106	Colistin	>128	2
MRSA (10 isolates)	Oxacillin	32	0.5

Table 1: Antibiotic MIC with/without 2-AI compound.

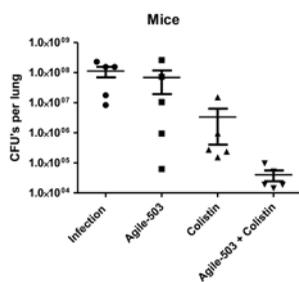


Figure 1. Bacterial burden after colistin, AGL-503, and combination treatments in a mouse lung infection model. Treatments started 2 hours after infection q12h for 36 hours.

The rat infection model show combination treatments with AGL-324 + antibiotic had statistically significant lower MRSA densities versus antibiotic alone (Figure 2).

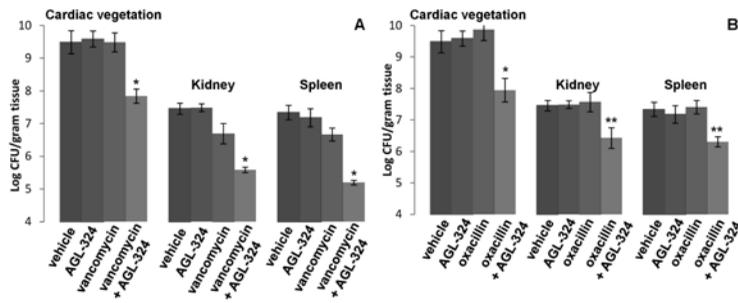


Figure 2. Bacterial burden in target tissues after antibiotic (vancomycin panel A; oxacillin panel B), AGL-324, and combination treatments. Treatments started 24 hours after infection, twice a day for three days. \*  $P < 0.05$ ; \*\*  $P < 0.05$  versus all other tissues

**CONCLUSIONS:** These experiments display the activities of these novel 2-AI compounds in enhancing antibiotic activity and supports the development of these compounds to reduce antibiotic usage.

#### 4 AMR 05 - NOVEL STRATEGIES FOR AMR INTERVENTIONS / PREPAREDNESS - GALLERY CD

### A novel participatory strategy to reduce antimicrobial use in agricultural systems

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**BACKGROUND:** Agricultural antimicrobial use (AMU) is recognized as being closely linked to the development of antimicrobial resistance (AMR) (Chantziaras et al. 2014). AMR is recognized as one of the greatest risks to human health globally (O'Neill, 2015), and agriculture uses the majority of antimicrobials globally.

The New Zealand Veterinary Association (Anon, 2015) has set an aspirational goal of reducing AMU to zero by 2030, and has embarked on a number of projects in an attempt to achieve this.

Participatory development (PD) has been used to help facilitate farmer projects previously (Reyher, 2016). This paper reports on the interim results of a three-year project using PD in farmer-led groups to help formulate AMU reduction strategies in New Zealand.

**MATERIALS AND METHODS:** This project is currently active in the lower region of New Zealand. Farmers and veterinarians across the lower South Island have been invited to participate in 4 strategic farmer groups comprising up to 12 farmers per group, from sheep, beef, deer (red meat) sectors, and from the dairy sector.

Each group has a facilitator, who is a trained agricultural consultant with a background in group facilitation. The groups are initially given a comprehensive AMR workshop, where they are introduced to the concept, to the risks and history, data around AMU and other background. This material is subsequently made available to them during the project in a variety of formats; and they are also given regular technical briefings.

**RESULTS:** The goal is for each group to develop separate novel AMU reduction strategies. The 4 groups to date have developed 10 quite distinct and quite varied strategies. These have been crystallised into a format for communicating to other farmers via presentations, social media and other vehicles. The strategies will then be implemented across a number of farms to effect change.

**CONCLUSIONS:** This study intends to facilitate farmers to create a range of strategies for reducing AMU which they will feel ownership of, and then to test these strategies in the field, with regard to ease of implementation, level of effect, consequences and other impact. From this, effective, simple strategies are hoped to be identified by farmer leaders and adopted by the farming community, because farmers will feel the ownership of these strategies themselves. The goal is to facilitate farmer uptake and effect reduction in AMU by farmer-led initiatives. Monitoring of AMU as part of this project will help determine the quantitative effect of the various strategies. The ultimate goal is to reduce AMU on farm by 20% by 2020.

## Can inhibition of transmission of KPC and CTX-M producing plasmids reduce the spread of AMR?

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2: School of Pharmacy, University College London, United Kingdom

**BACKGROUND:** Antimicrobial resistance (AMR), including resistance to carbapenem and extended spectrum beta-lactam antibiotics, poses a serious threat to modern medicine. Genes encoding resistance to these and other antimicrobials are frequently located on plasmids, which can be transmitted between distantly related bacteria. AMR plasmids and bacterial hosts can co-evolve, resulting in plasmids being maintained over long periods of time. Plasmid transmission occurs on a global scale. AMR plasmids can move between humans, domestic, livestock and wild animals, agricultural soil, and the wider environment. Furthermore, the global movement of people, animals and products such as food, provides a direct mechanism for AMR plasmids to traverse the globe. Some compounds have been identified which reduce plasmid carriage, however most are highly toxic. Therefore, alternative approaches to identify compounds that prevent transmission of large, complex, and clinically important plasmids could help reduce the global burden of AMR.

**MATERIALS/METHODS:** Using cloning techniques developed for this purpose, we have engineered two clinically successful plasmids pCT<sub>CTX-M-14</sub> and pKpQIL<sub>KPC</sub> to encode fluorescent protein genes. The modified plasmids were inserted into *E. coli* and *K. pneumoniae*, respectively. Plasmid transmission within a population was monitored using flow cytometry and confocal microscopy. To validate this assay, we have previously shown it was able to identify characterized plasmid-inhibiting compounds, including chlorpromazine, ascorbic acid, and linoleic acid. Using this system, we have now screened one drug library plus natural products to identify novel and non-toxic compounds which inhibit AMR plasmid transmission and/or persistence. Identified compounds were tested for impact upon bacterial growth, and the optimal concentration using dose-response assays for anti-plasmid activity was determined.

**RESULTS:** Our screen of over 2,000 compounds has identified Compound E, which has novel and strong potential as an anti-AMR plasmid compound. Compound E is neither an antibiotic nor a biocide. Compound E inhibited transmission at concentrations which did not significantly impact upon bacterial growth. The dose-response experiments revealed the optimal concentrations for anti-plasmid activity.

**CONCLUSIONS:** Using our fluorescent transmission assay, we have identified a compound which prevents the spread of "real-world" AMR plasmids amongst clinically relevant Gram-negative bacteria. Compound E has the potential to be used to reduce the prevalence of AMR plasmids found in critical priority antibiotic-resistant pathogens. This compound could be used in a variety of settings, including in humans, animals, and/or the environment. The use of non-toxic, transmission inhibiting compounds, such as compound E, could be a viable strategy to reduce the global spread and prevalence of AMR.

# AMR ALTERNATIVE APPROACHES TO TACKLING RESISTANT INFECTIONS

## 1 AMR 06 - ALTERNATIVE APPROACHES TO TACKLING RESISTANT INFECTIONS - GALLERY CD

### Antibiotics usage by pastoralists in livestock in North-central Nigeria: The socio-cultural drivers for antibiotic resistance emergence and public health implications

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**BACKGROUND:** Improper use of antibiotics in food animals contributes to the development of antibiotic resistance, a global health threat. Exploration of pastoralists' local knowledge and practices towards antibiotics usage is crucial for development of antibiotics surveillance in extensive husbandry system and control of antibiotic resistance in food animals. Study objectives were: to assess pastoralists' local knowledge and practices regarding antibiotics usage and pathways for resistant pathogens transmission from animals to humans. Our Null hypothesis was that pastoralists' socio-cultural activities cannot influence antibiotic resistance emergence and spread through food chain.

**METHODS:** Interview structured questionnaire-based cross-sectional study was conducted in systematic randomly selected household heads in pastoral settlements of North-central Nigeria in 2015. Pastoralists' communities in Nigeria herd about 90% of ruminants and practice year-round nomadism in rural areas. Descriptive and multivariable logistic regressions analyses were performed at 95% confidence level.

**RESULTS:** All 384 recruited pastoralists participated in the study. Majority (58.0%) of them had no formal education. Only 8.1% of the respondents knew antibiotics misuse to be when given under-dose, 7.3% indicated when given over-dose and 70.1% had no idea of what misuse entails. Nearly two-thirds (64.8%) of respondents did not know consequences of improper antibiotics uses in animals. More than half (58.3%) reported self prescription of antibiotics used in animals. Regarding antibiotics dosage determination before use, two-thirds (67%) of pastoralists reported arbitrary applications. More than half (54.4%) of participants used antibiotics mainly for therapeutic purposes, less than half (40.6%) of them for preventive purposes, and 4.9% of them as growth promoters (Table 1). Frequently used antibiotics by pastoralists were penicillin (94.0%), gentamicin (75.5%), streptomycin (93.0%), tetracycline (96.6%), tylosin (95.6%), neomycin (67.2%) and sulfonamides (92.4%).

Table 1. Practices of antibiotics usage in food animals by pastoralist in North-central Nigeria

Practice	Frequency (n)	Proportion (%)	95% CI
<b>Antibiotics used in animals were prescribed by</b>			
Animal health officials	117	30.5	26.0, 35.2
Self prescription	224	58.3	53.4, 63.2
Friends and relations	43	11.2	8.3, 14.7
<b>Purchased antibiotics from</b>			
Veterinary drug shops	229	59.6	54.7, 64.5
Human drug shops	21	5.5	3.5, 8.1
Animal drug hawkers	134	34.9	30.3, 39.8
<b>Antibiotics were administered on animals by</b>			
Self administer	251	65.4	60.5, 70.0
By animal health officials	133	34.6	30.0, 39.5
<b>Frequency of antibiotic usage on sick animals</b>			
As prescribed	103	26.8	22.6, 31.4
Once	109	28.4	24.0, 33.1
Once daily until recovered	172	45.6	40.6, 50.6
<b>Dosage determined before use</b>			
From instructions on the label	125	32.6	28.0, 37.4
Arbitrary	259	67.4	62.4, 72.0
<b>Frequently used route of administration</b>			
Injection	215	56.0	51.0, 60.9
Mouth (POS)	96	25.0	20.9, 29.5
On the skin (topical)	42	10.9	8.1, 14.4
In feed	31		
<b>Observed antibiotics withdrawal periods</b>			
Yes	61	15.9	12.5, 19.8
No	323	84.1	80.2, 87.5
<b>Purpose for antibiotics usage</b>			
Treatment of infections	209	54.4	49.4, 59.4
Prevention of infections	156	40.6	35.8, 45.6
Growth promotion	19	4.9	3.1, 7.5

CI - Confidence interval

**Table 2.** Identification of pathways for transmission and spread of antibiotic resistant pathogens to humans through food animals in North-central Nigeria

Pathway	Frequency (n)	Proportion (%)	95% CI
<b>Contaminated food animal products</b>			
Raw milk	96	25.0	20.9, 29.5
Raw cheese	101	26.3	22.1, 30.9
Under cooked meat	142	37.0	32.3, 41.9
I don't know	45	11.7	8.8, 15.2
<b>Contacts: direct or indirect</b>			
Humans with contaminated animals	294	76.6	72.1, 80.6
Humans with contaminated fomites	32	8.3	5.9, 11.4
I don't know	58	15.1	11.8, 18.9
<b>Environmental releases and wastes</b>			
Discharged contaminated faeces (manure)	214	55.7	50.7, 60.7
Aerosols from herd facilities	56	14.6	11.3, 18.4
Flies attracted to the contaminated faeces	93	24.2	20.1, 28.7
I don't know	21	5.5	3.5, 8.1

CI - Confidence interval

**Table 3.** Factors that influence emergence and spread of antibiotic resistance through food animals to humans in pastoral settlements of North-central Nigeria

Factors	Poor influence (%)	Satisfactory influence (%)	Odds ratio (OR)	95% CI	P-value
<b>Improper use of antibiotics</b>					
No	28 (63.6)	16 (36.4)	1.00		
Yes	20 (5.9)	320 (94.1)	28.00	13.06, 60.02	<0.001
<b>Non enforcement of laws regulating antibiotics usage</b>					
No	37 (52.1)	34 (47.9)	1.00		
Yes	60 (19.2)	253 (80.8)	4.59	2.67, 7.91	<0.001
<b>Weak financial status of pastoralists</b>					
No	37 (56.1)	29 (43.9)	1.00		
Yes	68 (21.4)	250(78.6)	4.69	2.69, 8.17	<0.001
<b>Low education and expertise of pastoralists</b>					
No	46 (73.0)	17 (27.0)	1.00		
Yes	74 (23.1)	247 (76.9)	9.03	4.89, 16.69	<0.001
<b>Mobile culture of pastoralists</b>					
No	55 (73.3)	20 (26.7)	1.00		
Yes	68 (22.0)	241 (78.0)	9.75	5.47, 17.38	<0.001
<b>Husbandry system: extensive system</b>					
No	32 (54.2)	27 (45.8)	1.00		
Yes	91 (28.0)	234 (72.0)	3.05	1.73, 3.57	0.001

Statistically significant at p<0.05

Pathways for transmission of antibiotic resistant pathogens through food animals were identified as: consumption of contaminated animal products (raw milk); direct and indirect contacts with contaminated animals and fomites; and environmental wastes (faeces) (Table 2). Factors that significantly influenced antibiotic resistance emergence and spread were: improper use of antibiotics (P<0.001), non enforcement of laws regulating antibiotics usage (P<0.001), weak pastoralists' financial status (P<0.001), pastoralists' low education and expertise (P<0.001), pastoralists' mobile culture (P<0.001), and extensive husbandry system (P=0.001) (Table 3).

**CONCLUSIONS:** The study revealed that the majority of pastoralists had low levels of knowledge and practices regarding antibiotics use in livestock. Antibiotic emergence and spread through livestock may not be unconnected with pastoralists' socio-cultural activities. To combat antibiotic resistance menace effectively, it is imperative to raise pastoralists' knowledge/awareness on effects of antibiotics misuse and promotion of prudent use in livestock through only registered veterinary services. Gradual reform of these socio-cultural activities through multifaceted strategies, in line with the 'One Health' approach, is recommended so as to assured food safety, food security, public and environmental health.



## 2 AMR 06 - ALTERNATIVE APPROACHES TO TACKLING RESISTANT INFECTIONS - GALLERY CD

## Extent of dispensing prescription-only medications without a prescription in community drug retail outlets in Addis Ababa, Ethiopia: a simulated-patient study

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**PURPOSE:** This study was aimed at assessing the extent of dispensing prescription-only medications without a prescription in community drug retail outlets (CDROs) of Addis Ababa, Ethiopia.

**METHODS:** A descriptive cross-sectional observational study design was used to sample 31 pharmacies, 25 drug stores, and two rural drug vendors from August 11, 2015, to October 21, 2015, through a simple random sampling method. A simulated-patient method of visit was implemented to collect data. Requests of six tracer prescription-only medicines (amoxicillin + clavulanic acid capsule, amitriptyline, captopril, glibenclamide [also known as glyburide], omeprazole capsule, and sildenafil citrate) and upper respiratory tract infection were selected as the simulated clinical scenario.

**RESULTS:** Amoxicillin–clavulanic acid capsule was dispensed when requested in 87.93% of the dispensaries. All of the CDROs dispensed omeprazole upon request. Sildenafil citrate (Viagra) was in stock in 96.55% of the CDROs, all of which issued the requested number of tablets without asking why or for whom the drug was needed. Amitriptyline, captopril, and glibenclamide (glyburide) were dispensed in 84.48%, 89.65%, and 87.93% of CDROs upon the provision of an empty container. Antibiotics were obtained from 75.86% of CDROs for presentation of upper respiratory tract infection symptoms. Among the dispensed antibiotics, the most common was amoxicillin (93.18%), followed by amoxicillin–clavulanic acid capsule (72.72%), and azithromycin (50%). Only 4.5% of the dispensaries asked about drug allergies, and 15.9% of the CDROs informed the simulated patient about the possible side effects of the drugs.

**CONCLUSIONS:** This study revealed a very high rate of dispensing of prescription-only medicines without a prescription. Antimicrobials and drugs for chronic diseases were obtained with ease from almost all of the randomly sampled CDROs. Putting good dispensing practice into effect and adhering to the existing national laws and regulations regarding the same are necessary. It is also necessary to adopt a strong and explicit line of action, especially toward the irrational use of antibiotics.

## Towards a Global Database of Emerging Antibiotic Resistance

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**BACKGROUND:** Antimicrobial resistant (AMR) pathogens are on the rise globally, making infections harder to treat and cure. However, the underlying patterns and mechanisms in where and when AMR is emerging are not clearly understood, making control and prevention difficult. There is a need to better catalog the emergence of AMR to allow for targeted research into the drivers of emergence and assist in the development of a rigorous One Health approach to prevent future resistance. We have built a surveillance database of the first reported emergence in humans of a specific of an antibiotic-resistant bacterium and characterized these events by extracting information on the geographic, demographic, and temporal scale associated with their emergence.

**METHODS:** We conducted an extensive systematic literature review of all the publications contained in PubMed, Embase, and ProMed Mail databases ranging from 2006 to 2017. We then used this dataset to identify the first temporal emergence of an AMR in a human population. We used PRISMA guidelines to structure the review, with each abstract screened twice, and final inclusion as a “new emergence event” determined after full-text review and background corroboration that the event was the first recorded instance of a specific resistance type. Articles selected for inclusion were summarized in a database of emerging antibiotic resistance with available information on pathogen, drug or drug combination resistance, location, and event date.

**RESULTS:** Our initial search identified 22,770 publications to be reviewed for inclusion in our database. The majority of publications were from 2015, with an overall increase in publications from 2006 onward. To this date we have identified 882 publications that will be reviewed in detail. This database includes information on the location, bacterial pathogen, clinical disease, and drug resistance, which can be used to analyze trends in global emergence. The dynamic structure of the AMR database easily allows the systematic and continuously updated of new AMR disease events as they may arise.

**CONCLUSIONS:** To our knowledge, this is the first comprehensive review of the *first emergence* of antibiotic resistance and first database of this kind. Treating AMR as an emerging threat allows for targeted measures to *prevent* new resistance combinations from emerging. Coupled with existing measures to reduce current AMR, more targeted surveillance and prevention could be a key measure in reducing the burden of AMR on human health and increasing the longevity of current antimicrobial treatments. Our comprehensive database will act as a critical resource for evaluating the current state of emerging AMR bacteria and creating strategies to mitigate the impact of novel AMR, as well as support further research into the origins of resistance in people. Developing this database is an important first step in understanding the drivers of new resistance globally.

## 4 AMR 06 - ALTERNATIVE APPROACHES TO TACKLING RESISTANT INFECTIONS - GALLERY CD

**Current Patterns of Antibiotic Resistance in High Density Livestock-Human Populations in Western Kenya****Kemp, Steven Alan**

University of Liverpool, United Kingdom

Over the last 80 years, correlation between antimicrobial use and resistance has been observed, and extensive use of antimicrobials in human and veterinary medicine has resulted in the widespread emergence of multi-drug resistant bacterial infections. Kenya has a rapidly growing livestock industry; thus, various antimicrobials are used to maintain livestock health. The purpose of this work was to determine if there were similarities in the patterns of antimicrobial-resistant bacteria (AMR) in farmers, their animals and their immediate environment. This was undertaken in Western Kenya, representing an area with a high density of livestock and using *E. coli* as our sentinel organism.

Water, environmental swabs and human and animal faeces were collected from 70 mixed crop-livestock smallholder farms across Busia county, Western Kenya. A questionnaire regarding access to and understanding of antimicrobials was given to each farmer; up to 3 fresh faecal samples were collected from each species of animal and human volunteers. Water samples were collected from wells, boreholes or stored rainwater. Living areas were sampled using bootsocks to determine contamination with representative bacteria and their AMR patterns. Faecal samples were cultured on eosin-methylene blue (EMBA) agar, 5 colonies representative of *E. coli* were selected and susceptibility determined via antibiotic disc diffusion and using human EUCAST breakpoints; extended-spectrum  $\beta$ -lactamase-producing *E. coli* were selected on EMBA containing 1mg/l cefpodoxime, and then confirmed by double-disc test (cephalosporin with, and without clavulanic acid). Water samples and environmental swabs were pre-enriched in tryptone-soya broth for 24 hours and then processed as per faecal samples.

261 samples were processed and AMR *E. coli* was detected in 96.0% of samples with the following breakdown for other resistance outcomes: tetracycline (91.2%, n=238), ampicillin (83.1%, n=217), sulfathiazole (79.7%, n=208) trimethoprim (62.1%, n=162), chloramphenicol (9.6%, n=25), ciprofloxacin (3.4%, n=9) and gentamicin (2.3%, n=6). Multi-drug resistant *E. coli* (to 3 or more drug classes) was found in 77.4% samples. ESBL-producing *E. coli* was detected in 24 (9.3%) of all samples, and the majority of isolates were MDR. The most common resistance pattern (tetracycline, trimethoprim, and sulfathiazole) was observed in all three groups, indicating potential sharing of AMR-bacteria.

This study demonstrated a high prevalence of AMR and MDR *E. coli*. The high prevalence of tetracycline and sulfa-drug resistance is reflective of the antimicrobials which are commonly cited as being used in Kenyan livestock. Further investigation of isolates will include full genotyping by whole genome sequencing and the phylogenetic background of strains and resistance determinants and their genetic context determined. This further work should elucidate sharing of MDR bacteria and/or resistance elements between animals, people and their shared environment. Such data is important for informing veterinary public health and our methodology has already been shared with key Kenyan stakeholders for this purpose.

## 5 MR 06 - ALTERNATIVE APPROACHES TO TACKLING RESISTANT INFECTIONS - GALLERY CD

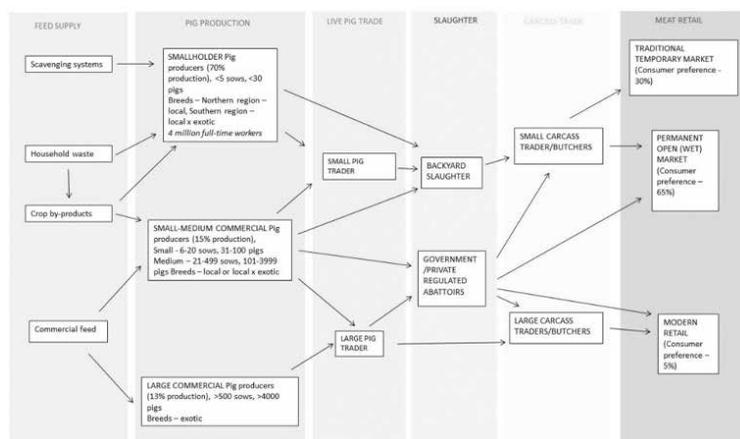
## Antimicrobial use behaviours, the economics of animal disease and perceptions of antimicrobial policy in pig production in Vietnam

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**BACKGROUND:** Antimicrobial resistance is influenced by antimicrobial use in the human and animal health sectors, exerting selection pressure on pathogen populations that encourage the development of resistance and exchange of resistance genes. The scale of antimicrobial resistance in Vietnam remains unknown, however, studies suggest that it is a major issue in both human and animal health.



Around three quarters of all meat consumed in Vietnam is pork identifying pigs as a priority species for further research. The limited data on antimicrobial use in pigs highlight high risk behaviours such as high overall antimicrobial use, large proportions of commercial feed containing antimicrobials and poor adherence of farmers to meat withdrawal periods.

*Pork Supply Chain – movement of feed, pigs and pork*

**METHODS:** The study explored antimicrobial use in 20 farms in the Nam Dinh Province (North) and 20 farms in the Dong Nai Province (South) of Vietnam. Data were collected through a structured interview and the collection of discarded antimicrobial packaging over a 6 week period. The study sought to explore how and why antimicrobials were used in pig production; including a focus on the economic costs and benefits of use for the producer.

**RESULTS:** Overall antimicrobial use was found to be high with frequent reported use of the World Health Organisation highest priority critically important antimicrobial classes and antimicrobials routinely used in combinations of two or more active ingredients. Farmer awareness of what constituted an antimicrobial was poor and there was little knowledge or understanding of policy to prohibit the use of antimicrobials as growth promoters (introduced on 31 December 2017). Overall, farmers perceived a low risk to human health from antimicrobial use in pigs. Economic assessment of the benefits of antimicrobial use was challenging as record keeping on productivity, health and veterinary costs was poor.

**CONCLUSIONS:** The study results provide insight into antimicrobial use behaviours by Vietnamese pig farmers and highlight areas such as poor farmer awareness of antimicrobial use and resistance, limited knowledge of antimicrobial use regulation and poor record keeping as areas of priority for future interventions to reduce antimicrobial use and promote responsible behaviours. These data may form the basis of further research to inform policy makers in supporting economically sustainable production systems, with minimum risk from antimicrobial use and which focus on food safety. The data collection framework will be made available for use in other countries to address similar antimicrobial use knowledge gaps.

## AMR RAPID DIAGNOSTICS

### 1 AMR 07 - RAPID DIAGNOSTICS - GALLERY CD

## Analysis of single nucleotide polymorphism in katg gene in isoniazid resistant *Mycobacterium tuberculosis*

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*Mycobacterium tuberculosis* (MTB) is one of the most wide spread bacterial pathogens. The emergence of drug-resistant tuberculosis is a significant problem worldwide. Multiple drug-resistant tuberculosis (MDR-TB) results when *Mycobacterium tuberculosis* becomes resistant to most of the baseline anti-TB drugs such as isoniazid (INH) and rifampicin (RIF). Genetic alterations in the genome of MTB such as mutation in katG gene are involved in the development of resistance to INH. The present study aimed to explore mutations in KatG gene in *Mycobacterium tuberculosis* isolates resistant to isoniazid by sequencing.

The sputum samples (n=390) were collected from suspected patient for tuberculosis during the year 2015-2016. Collected samples were decontaminated using N-Acetyl-L-Cysteine-Sodium Hydroxide (NALC-NaOH) solution. All the samples were screened for *Mycobacterium tuberculosis* through GeneXpert MTB/RIF analysis, Fluorescent Microscopy and MGIT Culturing. The culture positive samples were then checked for antibiotics resistance using drug susceptibility test (DST).

Genomic DNA was extracted from *Mycobacterium tuberculosis* isolates resistant to isoniazid using QIAamp DNA Mini Kit(Qiagen Germany). The extracted DNA was amplified in Thermal cycler (Kyratec, Australia). The PCR products were run on 2% agarose gel (Thermo Scientific). The PCR products were then cleaned-up and sequencing was performed. Each sample was sequenced in both directions. Contig sequences were generated using Sequencher 5.3. KatG gene sequence of *M. tuberculosis* H37Rv (Accession No. NC000962.3) was used as a reference. Multiple alignment of the sequences was performed using BioEdit. Deduced amino acid sequences were generated from the nucleotide sequences using MEGA 6 software.

Of the 390 sputum samples from TB suspected patients 145, 110 and 119 samples tested positive in GeneXpert MTB/RIF, FM and MGIT Culturing, respectively. The relative sensitivity of GeneXpert on samples which were positive both in FM and MGIT culture was found to be 98.8% (80/81).

The culture positive samples (n=119) were checked for drug susceptibility test (DST) using first line antibiotics such as Streptomycin, Isoniazid, Rifampicin, Ethambutal and Pyrazinamide and second line antibiotics i.e. Amikacin, Capriomycin and Ofloxacin. It was found that 29% (n=35), 53% (n=64), 38% (n=45), 19% (n=23), 11% (n=13) 6.7% (n=8), 8.4% (n=10), 37.8% (n=45) were resistant to the first and second line drugs, respectively. In DST 44 samples were also confirmed to be MDR-TB samples. Out of 64 Isoniazid, 20 selected samples were further preceded for direct DNA sequencing of KatG gene of which 10 isolates had substitution mutation at codon 315 (AGC=ACC) that resulted in change in amino acid from Serine=Threonine while mutation at codon 463 (CGG=CTG,) was detected in all the INH resistant *Mycobacterium tuberculosis* sequenced. This mutation resulted in change in amino acid from Arginine to Valine.

High resistance rates were found in MDR-TB against first-line and second-line anti-tuberculosis drugs. This study also shows high frequency of mutation in KatG gene in isoniazid resistant *Mycobacterium tuberculosis*.

## 2 AMR 07 - RAPID DIAGNOSTICS - GALLERY CD

**Exploiting the potential of flow cytometry in rapid antimicrobial susceptibility testing**

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**INTRODUCTION:** Conventional culture-based antimicrobial susceptibility tests (AST) are slow to deliver definitive results, forcing prescribers to counter the risk of antimicrobial resistance (AMR) with an excessive quantity and spectrum of antibiotics. Improved diagnostic methods have thus been identified as decisive AMR countermeasures, and rapid AMR detection has become a high priority.

**METHODS:** Recent attempts to solve this problem range from detection of specific AMR markers to broad-based genotypic and phenotypic characterisation of bacteria. We developed a flow cytometry-assisted susceptibility test (FAST) that combines reference method accuracy with unprecedented speed. FAST methods exploit reproducible changes in bacterial physiology during the early stages of antimicrobial exposure that predict the Minimum Inhibitory Concentration.

**RESULTS:** We have expanded our repertoire to a range of antimicrobial agent families and to additional multidrug resistant bacteria. The FAST method reduced the time to an accurate, objective AST result by one to three days and remained accurate across the wider range of antimicrobial agents and bacterial species we tested. These included ceftriaxone and gentamicin with multidrug resistant *Enterobacteriaceae*, and isoxazolyl penicillins and ceftazidime with *Staphylococcus aureus*. Accurate FAST results were completed for Gram negative bacteria without identification beyond Gram stain.

**CONCLUSION:** The FAST method addresses the trade-off between accuracy and time to result by using a rapid AST measurement technique. Alternative rapid AMR detection methods do not predict true susceptibility, and rely on prior identification of bacteria from pure culture. There are a few technical obstacles to translation of these FAST methods into standard laboratory procedures. The principal challenges are regulatory compliance, integration with existing clinical laboratory systems and upscaling for high laboratory throughput.

## 3 AMR 07 - RAPID DIAGNOSTICS - GALLERY CD

## Novel and Rapid Multiplex Allele-Specific PCR (MAS-PCR) Test for Rapid Detection of MDR and XDR-TB from the Sputum of Lung TB Patients in Makassar, Indonesia

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- 5: Hasanuddin University Medical Research Center, Medical Faculty, Hasanuddin University, Indonesia.

**BACKGROUND:** Until now, Multi-Drug Resistant TB (MDR-TB) and Extended Drug Resistant TB (XDR-TB) are still difficult to rapidly detect, due to the length of time it takes (eight weeks) for the gold standard culture method to arrive at a diagnosis. In this research, we designed a rapid and accurate detection method applicable in developing countries such as Indonesia.

**METHODS:** The study was done in Makassar, Indonesia and sputum samples were taken from TB suspect patients and Mycobacterium tuberculosis (MTB) sample collection from the HUMRC-TB Laboratory, Makassar. The rapid and accurate detection method to detect MDR and XDR-TB pathogen types was designed using a PCR technique called Multi-Allele Specific Polymerase Chain Reaction (MAS-PCR) to detect a combination of specific genes encoding susceptibility to first and second line anti-TB drugs. The sequence of amplified PCR products was analysed with BLAST.

**RESULTS:** From 89 sputum samples tested with MGIT 960 culture method for first-line drugs, 43 samples (48.3%) were susceptible, 5 samples (5.6%) were mono-resistant R and 41 samples (46.1%) were MDR. Based on SLD-DST, amongst 46 samples resistant to FLD, 36 samples (78.3%) were susceptible to SLD, 5 samples (10.8%) were resistant to OFX, 4 samples (8.7%) resistant to KAN, and 1 sample (2.2%) were resistant to both OFX and KAN. The MASPCR test demonstrated 97.7% and 95.5% specificity in MDR-TB and XDR-TB detection, respectively.

**CONCLUSIONS:** The MAS-PCR technique allows rapid detection of TB pathogens that are resistant to INH, RIF, FQ, and KAN in a simple and cost-effective manner to enable early diagnosis and treatment of MDR and XDR-TB patients, and in turn may prevent further spread to their surrounding contacts.

## 4 AMR 07 - RAPID DIAGNOSTICS - GALLERY CD

**Presence of *oqxA* and *oqxB* genes in a multidrug resistant *Salmonella* Typhimurium isolate recovered from swine in Brazil**

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- 5: Food Research Center, University of São Paulo, Brazil

**BACKGROUND:** Fluoroquinolones (FQs) are often first-choice antimicrobial agents used to treat adult salmonellosis. However, a global rise in the number of *Salmonella* with reduced susceptibility to the FQs has been observed in isolates recovered from food, animals, the environment and humans, thus confounding treatment options. Therefore, we designed this study to determine the molecular characteristics of *oqxA* and *oqxB* genes in *Salmonella enterica* isolated from swine in Brazil.

**METHODS:** In this study, 14 *Salmonella enterica* isolates (Typhimurium, n=8; Infantis, n=3; 4[5],12:i:-, n=2; and Panama, n=1) with known resistance profiles were analysed for the presence of plasmid-mediated quinolone resistance (PMQR) determinants and mutations in the quinolone resistance-determining region using PCR and sequencing techniques.

**RESULTS:** Only one *S. Typhimurium* isolate recovered from the stomach of one pig was positive for a plasmid carrying *oqxA* and *oqxB* genes (Table 1). A mutation in the *gyrA* gene (Asp87Asn) was observed in codon 87 with replacement of the amino acids asparagine (Asn) by aspartate (Asp). In addition to the PMQR genes, WGS analysis revealed the presence of resistance genes for aminoglycoside (*strA*, *aph(6)*-I<sub>d</sub>), β-lactam (*bla*<sub>TEM-1A'</sub>), phenicol (*floR*), sulphonamide (*sul2*) and tetracycline (*tetB*). Five of these genes (*strA*, *aph(6)*-I<sub>d</sub>, *bla*<sub>TEM-1A'</sub>, *floR* and *sul2*) were located in the same plasmid identified as IncR. The sequence type (ST) was determined to be ST19. There was 99% concordance between *oqxB*, *oqxA*, *floR*, *sul2* and the backbone molecular structure of *S. Typhimurium* strains isolated from human and poultry samples reported worldwide.

**CONCLUSIONS:** Although other plasmid-types are most often harbored by *S. Typhimurium*, our results demonstrate multi-drug resistance associated with the IncR replicon type. Additionally, ST19 is a particularly virulent sequence type of *Salmonella*. The global spread of this plasmid-encoded multidrug efflux pump *oqxA*, *oqxB* and other resistance determinants represents an emerging resistance problem of great concern.



## 5 AMR 07 - RAPID DIAGNOSTICS - GALLERY CD

## Inter-laboratory validation for antimicrobial susceptibility testing of highly pathogenic bacteria performed by an European laboratory network

### Wahab, Tara

Public health agency of Sweden, Sweden

**OBJECTIVES:** The antimicrobial susceptibility testing (AST) of highly pathogenic bacteria is difficult due to incomplete breakpoint definitions and the lack of standardized regulations. Up to now, guidelines are only available from the Clinical and Laboratory Standards Institute (CLSI) and from WHO manuals for *Bacillus anthracis* and *Francisella tularensis*. The CLSI M45 3rd ed. document gives recommendations for testing conditions (microdilution), but breakpoints are lacking for several relevant antibiotics. Furthermore, the breakpoints are only available for the category susceptible. The AST working group from the European network EMERGE (Efficient response to highly dangerous and emerging pathogens at EU level) consists of 14 laboratories specialized in highly pathogenic bacteria in their countries and is working on a suitable standard operation procedure (SOP) for AST of highly pathogenic bacteria.

**METHODS:** The broth microdilution method with user-defined commercial microdilution plates was chosen and the tests were performed according to CLSI recommendations. The reproducibility was investigated in a multicenter study involving six European institutes, specialized in highly pathogenic bacteria. 35 bacterial isolates of *Bacillus anthracis*, *Brucella spp.*, *Burkholderia pseudomallei*, *Burkholderia mallei*, *Francisella tularensis* and *Yersinia pestis* from the EMERGE repository were tested via intra- and inter-laboratory-validation towards antimicrobial substances typically used for therapy of these agents.

**RESULTS:** Overall the broth microdilution method showed good practicability and concordance for all highly pathogenic bacteria. In the intralaboratory validation between 97,8% and 86,5% of the MIC results were within one log<sub>2</sub> dilution step from mode. The lowest conformity was observed for slow growing bacteria *Francisella tularensis* and *Brucella spp.* For *Bacillus anthracis* and for *Brucella spp.* the method showed need for improvement due to differences between two categories.

**CONCLUSION AND PERSPECTIVES:** The microdilution method is applicable for AST of all highly pathogenic bacteria, but needs optimization for *Brucella spp.* Further interpretation of the variances observed during this inter-laboratory validation is difficult due to the small set of data for each stain/substance combination. Therefore, after adaptation of the SOP a follow-up inter-laboratory-validation using a set of clinical strains including only one strain per species and 10 replicates per site was conducted and the results are still pending. After validation, the SOP is planned to be used to get MIC distribution of wild type strains and to produce epidemiological cutoff values by testing the strain collections from all partners. These data can be used to complete the clinical breakpoints for all agent-relevant substances and to implement the method to the European Committee on Antimicrobial Susceptibility Testing (EUCAST) guidelines.

Additionally to the presenting author listed above, the EMERGE AST working group consists of the following persons and institutions: Tscherne A, Zöller L, Georgi E, Hinz C, Vollmar P and Zange S (Bundeswehr Institute of Microbiology, Germany), Jacob D and Grunow R (RKI, Germany), Henczko J (National Public Health Institute, Budapest), Manzulli V, Fasanella A (IZSPB, Italy); Papaparaskevas J (NKUA, Greece); Pelerito A, Nuncio S ( INSA, Portugal); Thomann S, Schürch N (SPIEZ, Switzerland); Nenova R (NCIPD, Bulgaria); Elschner M, Tomaso H (FLI, Germany); Jureen P, Boskani T (FoHM, Sweden); Feruglio SL, Johansen T, Jensen V (NIPH, Norway); Wojciech I, Kedrak-Jablonska A (NVRI, Poland); Bertolini B, Di Caro A (INMI, Italy); de Vries MC (RIVM, The Netherlands); Machoaizpurua M (BIOEF, Spain); Bolton PF (PHE, United Kingdom).

# LATE BREAKERS

## 1 LB1 - LATE BREAKERS 1 - SALON AB

### Coronavirus bio-surveillance of the insectivorous bats at the Matlapitsi cave in the Limpopo province, South Africa

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Bats host a large diversity of coronaviruses, many of which have been associated with a history of cross-species transmission and co-evolution. Several examples of coronavirus cross-species transmissions and adaptations to new hosts have been documented in the past 16 years. These include human coronaviruses such as severe acute respiratory syndrome coronavirus and Middle East respiratory syndrome coronavirus. Recently in Asia, a fatal enteric disease (porcine enteric alphacoronavirus) emerged in porcine populations from a novel bat-borne alphacoronavirus previously identified within the *Rhinolophus* bat genus. Continued coronavirus surveillance is thus essential to build on the known diversity of bat-associated coronaviruses and enable investigation into the emergence of viral species of public health and veterinary importance. We therefore aimed to expand on the known diversity of bat-associated coronaviruses from South African bat species. We focused on the species present at a specific cave-system (Matlapitsi) in the Limpopo province in South Africa, which is rich in species diversity, with high abundance of certain hosts. We analyzed samples collected from insectivorous bats from 2013 to 2017, such as fecal material (n=58) from caught-and-released bats as well as the rectal/intestinal samples (n=59) of bats collected as vouchers. The samples were investigated for coronavirus RNA with a hemi-nested RT-PCR assay targeting a conserved region of the RdRp gene. This region was extended with an assay from the literature for better phylogenetic resolution. Of the 117 samples tested thus far, 44 were found to harbor coronavirus RNA. The high positivity rate (37.6%) identified from the bats at this site was mainly attributed to the high positivity encountered from the large number of sampled *Miniopterus natalensis* species that roost in the cave. Overall, nearly half of all sampled material from the species collected over five years were found positive for coronaviruses. The *Rhinolophus* spp., *Myotis* sp. and *Pipistrellus* sp. were shown to harbor coronavirus RNA with low levels of positivity. Preliminary analysis of the sequenced regions show three lineages of novel *Miniopterus* alphacoronaviruses as well as a novel lineage of a *Rhinolophus* alphacoronavirus. There is a significant lack of comparable sequence data for some of these lineages, and this study also constitutes the first reports of coronavirus sequences from South African *Rhinolophus* species. These preliminary findings show the presence of a large coronavirus diversity within just one site. These bats were sampled over five years, also showing persistence within these hosts. The *M. natalensis* species can be highlighted as a model to study the factors involved in the persistence, maintenance and shedding of coronaviruses that may be applied to investigating emerging coronaviruses among human and livestock populations.

## 2 LB1 - LATE BREAKERS 1 - SALON AB

## Zika Virus Surveillance at the Animal-Human Interface in Brazil, Colombia, and Peru, 2017-2018

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- 9: Centro de Reabilitação de Animais Silvestres (CRAS), Campo Grande, Brazil

**BACKGROUND:** Zika virus (ZIKV) was first discovered in 1947 in Uganda, but was not considered a public health threat until 2007 when found to be the source of epidemic activity in Asia. Epidemic activity spread to Brazil in 2014 and continues to spread throughout the tropical and subtropical regions of the Americas, where *Aedes aegypti* mosquitoes are abundant. Despite ZIKV being zoonotic in origin, information about potential vertebrate hosts and invertebrate vectors for ZIKV in the Americas and the role they play in virus maintenance and transmission is lacking.

**METHODS:** We conducted active surveillance of native primates, as well as other non-human vertebrates and mosquitoes to ZIKV virus in Brazil, Colombia, and Peru at established field sites up to 5 times per year, where there was evidence of recent or active ZIKV transmission in humans. Trapping efforts focused on abundant wildlife and domestic animals, as these would be candidate reservoirs or amplifiers if they are hosts. We screened whole blood and mosquito samples for ZIKV nucleic acid by a pan flavivirus real time RT-PCR and confirmed by ZIKV specific real time RT-PCR. We tested plasma samples for presence of anti-ZIKV antibodies by plaque reduction neutralization testing (PRNT).

**RESULTS:** From February 2017 to March 2018, we collected 4,727 animal and roughly 27,000 mosquito samples. Preliminary test results, for the subset of the samples from Brazil and Colombia with test results to date, reveal that 7.7% (144/1,863) of animal and 26.4% (146/554 mosquito pools; 1,115 total pools collected) of pooled mosquito samples are positive for flavivirus by RT-PCR and 8.9% (68/761) of animal plasma samples show evidence of anti-ZIKV antibodies by PRNT. Laboratory analysis for the remaining 70% (7,391/10,569) of individual and pooled samples is underway.

**CONCLUSIONS:** Results of this study will facilitate a better understanding of ZIKV's ability to establish a sylvatic cycle outside of human transmission, shape future surveillance strategies for ZIKV in tropical ecosystems, and inform the need for public health intervention efforts like vaccine development.

## 3 LB1 - LATE BREAKERS 1 - SALON AB

**Avian-origin PB1 gene confers selective advantages to 2009 pandemic H1N1 virus RNA transcription and replication**

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**BACKGROUND:** Polymerase functions of avian influenza viruses were restricted in mammals due to host restrictions. To overcome restrictions on heterotrimeric polymerase complex, diverse adaptive strategies has been deployed by viruses. PB1 gene originated from avian strains has been frequently observed in seasonal and pandemic strains. Nevertheless, the biological significance and corresponding molecular mechanism by which avian-origin PB1 emerged in these strains have long been elusive.

**METHODS:** To elucidate the effects of avian-origin PB1 on the functions of viral polymerase complex and pandemic formation, we introduced avian-origin PB1 into the background of 2009 pH1N1 virus, which naturally lacks avian-origin PB1 segment and the well characterized PB2 E627K mutation. Viral polymerase activities were measured using mini-replicon assay or primer extension assay. cRNA stabilization assay was used to dissect the influence of avian-origin PB1 on different step of viral RNA synthesis.

**RESULTS:** We showed that avian-origin PB1 can markedly elevate polymerase activity of pH1N1 in human cells. Notably, acquisition of avian-origin PB1 can assist pH1N1 polymerase to compensate the lack of PB2-associated adaptive mutations in a similar manner as overexpression of chANP32A, the recently identified major host factor underlying host restrictions on viral polymerase complex. Analysis of viral RNAs synthesis indicated avian-origin PB1 enhanced both replication and transcription of pH1N1 polymerase. Further cRNA stabilization assay results suggested that avian-origin PB1 facilitated the vRNA synthesis from cRNA template in a *trans*-activating manner.

**CONCLUSIONS:** Our results demonstrated that avian-origin PB1 can boost the viral polymerase activity, or even compensate the function of the canonical adaptive mutation in 2009 pH1N1 polymerase. These data implicated that avian-origin PB1 should be regarded as one of the adaptation markers in the surveillance for pandemic strains, especially in the frequent reassortment events occurred between avian and human strains. Moreover, the proposed mechanism used by avian-origin PB1 to facilitate vRNA synthesis might be applicable to other adaptive mutations such as PB2 E627K. Both of these findings will promote studies on host adaptation of influenza polymerase complex.

## 4 LB1 - LATE BREAKERS 1 - SALON AB

**Learning form an evolutionary host: IRF3 signaling is critical to prevent Middle East respiratory syndrome (MERS) coronavirus propagation in big brown bat cells**

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**Rationale:** Insectivorous bats are speculated to be evolutionary hosts of Middle-East respiratory syndrome (MERS) coronavirus (CoV) and Jamaican fruit bats experimentally infected with MERS-CoV do not exhibit symptoms of disease. MERS-CoV causes disease in humans with a thirty-five percent mortality. MERS-CoV has evolved proteins that can counteract human antiviral responses that are mediated via interferon regulatory factor 3 (IRF3). Since bats experimentally infected with MERS-CoV do not develop classical signs of disease, we tested the hypothesis

that MERS-CoV cannot subvert antiviral interferon responses in bat cells. Methodology and results: We infected human and big brown bat cells with MERS-CoV and observed that the virus propagated significantly more in human cells. MERS-CoV effectively suppressed antiviral interferon beta (IFN $\beta$ ) response in human cells, unlike in bat cells. By studying the response of IRF3 to poly(I:C), a synthetic analogue of viral double-stranded RNA, we observed that bat IRF3 responded to poly(I:C) by phosphorylation and nuclear translocation; hallmarks of IRF3 activation. The role of IRF3 in antiviral signaling is not known in bat cells. By knocking down IRF3 in bat cells by small interfering RNA (siRNA), we demonstrated that IRF3 is critical in poly(I:C) and MERS-CoV mediated IFN $\beta$  gene expression. We performed a kinome analysis on poly(I:C) treated bat and human cells and observed that similar pathways were up-regulated. We also infected IRF3 knocked-down bat and human cells with MERS-CoV and observed that MERS-CoV propagated to significantly higher levels in IRF3 knocked-down bat cells.

**CONCLUSION:** Our study was able to identify a unique IRF3 mediated antiviral signaling process in bat cells that is resistant to subversion by MERS-CoV. Future studies will enable us to adapt these strategies to restore antiviral signaling in coronavirus infected human cells.

**FUNDING:** NSERC Discovery, Saskatchewan Innovation and Opportunity and Dept. of Vet. Micro.

## 5 LB1 - LATE BREAKERS 1 - SALON AB

### Anti-viral activity of HDAC6 against influenza A virus mediated via suppression of viral RNA polymerase subunit PA

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**BACKGROUND:** Influenza A virus can cause lethal disease in humans and animals. The virus can trigger severe pneumonia and lead to acute respiratory distress syndrome. The life cycle of influenza A virus (IAV) is modulated by various cellular host factors, which either promote or dampens virus infection at different stages. However, the precise mechanism of IAV infection eliciting the unique host response is still not well understood. Thus, it is critical to find new strategies to control IAV infection

**METHODS:** To obtain a better understanding of the molecular events of IAV replication, we used the IAV mini-genome construct to quantify the IAV RNA polymerase activity in 293T and MDCK cells. Results: Our data revealed that HDAC6 plays an important role in fine-tuning IAV RNA replication and transcription. Specifically, we found that HDAC6 physically interacts with three subunits of the IAV RNA polymerase, PA, PB1 and PB2, as well as nucleoprotein NP. Interestingly, the protein stability of PA is preferentially decreased via HDAC6-mediated deacetylation. We also found that overexpression of HDAC6 attenuates the expression of PA protein during IAV infection, concomitantly with a decrease in synthesis of both viral genomic RNA (replication) and viral mRNA (transcription). In contrast, upon treatment with Tubacin, an HDAC6 specific inhibitor, IAV RNA replication and transcription are enhanced potentially due to elevated viral RNA polymerase activity. Consistent with this, we showed that depletion of HDAC6 increases the level of PA protein as well as IAV RNA replication and transcription.

**CONCLUSIONS:** Our study provides important mechanistic insight into the understanding of IAV replication via suppression of viral RNA polymerase. Taken together, our findings indicate that HDAC6 plays a negative role on IAV RNA polymerase activity via deacetylating PA protein and thus restricts IAV RNA transcription and replication. Thus, HDAC6 could be a potential candidate as the therapeutic target for treating IAV infection.

**FUNDING:** This work was supported by the Fundamental Research Funds for the Central Universities (KYHW201702), the National Natural Science Foundation of China (Grant No. 31472218), and the Priority Academic Program Development of Jiangsu Higher Education Institutions (PAPD).

## 6 LB1 - LATE BREAKERS 1 - SALON AB

### Rapid and sensitive molecular detection of viruses, bacteria, and parasites without sophisticated laboratory equipment

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**BACKGROUND:** On-site rapid-diagnostic tests (RDTs) can have limited accuracy, whereas molecular genetics-based diagnostics such as real-time PCR can overcome accuracy limitations by offering high sensitivity, but require significant infrastructure with constant power requirements. We have developed a new low-resource molecular genetics workflow that enables accurate disease identification without any sophisticated equipment (not even a centrifuge). Only a battery-operated heating block is required for incubation at 39 °C. We demonstrated this workflow can be applied widely for detection of parasites, bacteria, and viruses in crushed tissue and whole blood.

**METHOD:** Malaria parasites were detected from cultured *Anopheles* mosquitoes (n=116) or red blood cells infected with *Plasmodium falciparum*. *Wolbachia* bacteria was detected from infected *Aedes* mosquitoes (n=79). Prawn hepatopancreatic parvovirus detection was demonstrated using fresh and wild-caught *Fenneropanaeus merguensis* prawns (n=30). Analytical sensitivity was determined using dilutions of synthetic plasmid material. Our rapid detection workflow consisted of a simple three-step detection process (see Figure): (1) Mosquitoes, tissue, or blood were homogenized in a novel single-solution extraction buffer for 5 minutes, before (2) specific disease identification using recombinase polymerase amplification (RPA) and incubation at 39 °C for 10-30 minutes, followed by (3) a 5 minute lateral flow strip detection.

**RESULTS:** Analytical sensitivity of *Plasmodium falciparum* detection was 30 gene copies/μL, which was sufficient to detect a single oocyst within a single infected *Anopheles* mosquito, even when pooled with 19 uninfected mosquitoes, and when mosquitoes were left in traps for up to 8 days; diagnostic sensitivity and specificity for detection in *Anopheles* mosquitoes was 100% and 94% respectively. Pilot studies indicated detection of *Plasmodium falciparum* in cultured red blood cells could also be achieved, with a sensitivity down to 50 parasites/μL. Analytical sensitivity of *Wolbachia* detection was 200 gene copies/μL, which enabled detection of a single infected *Aedes* mosquito, even when pooled with 4 uninfected mosquito, and even when mosquitoes were left in traps for up to 7 days; diagnostic sensitivity and specificity for detection in *Aedes* mosquitoes was 96% and 97% respectively. Analytical sensitivity for detection of prawn hepatopancreatic parvovirus was 200 copies/reaction which enabled detection of homogenized *Fenneropanaeus merguensis* tissue with PCR-determined viral loads of 34.8 copies/μg; diagnostic sensitivity and specificity for detection in *Fenneropanaeus merguensis* were both 100%.

**CONCLUSION:** We demonstrated a rapid three-step detection workflow for sensitive and accurate pathogen detection with broad applicability for the detection of parasites, bacteria and viruses in a variety of different sample types. Our workflow could enable accurate on-site detection of pathogens for rapid and decentralised monitoring of diseases during elimination programs and outbreak management.

## 1 LB2 - LATE BREAKERS 2 - SALON CD

## One Health in History: Bison, Parks Canada and the Emergence of Tuberculosis in the Canadian Arctic

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**BACKGROUND:** Tuberculosis has been described as the defining disease of the Canadian Inuit. By the mid 1940s, the Canada operated a mass evacuation program Inuit sick with TB to the south. While researchers have focussed on the experiences of TB patients and the operation of the evacuation program, this research focuses on the initial reports of tuberculosis in the eastern Arctic in the 1920s. Prior to the 1920s, tuberculosis was extremely rare in the region but by the mid 1930s, a TB ward was opened on Baffin Island, a sign of the growing threat of the disease. The emergence of TB in the region, marked by signs of extra-pulmonary infection, occurred as the Canadian government operated an emergency food ration program to alleviate periodic hunger among the Inuit. Dehydrated meat was provided from bison located at Wainwright, Alberta. Testing at the time of slaughter showed that the herd was seriously infected with disease. Infection from the Wainwright herd to other animal populations is well documented. This study is the first to link infection in the Wainwright herd with the outbreak of disease in a human population.

**METHODS:** This paper considers the relationship between TB among bison on the northern Great Plains and the emergence of the disease among the Inuit in the eastern Arctic. Data on the health of the bison herd was collected from veterinary records of Parks Canada, the organization that brought the species back from the brink of extinction. Canadian government correspondence was used to uncover the logistics of the food program including the distribution of the meat in the north and the debate over the use of the meat as food. Medical records and correspondence of officials in the north were used to illustrate the growing recognition of TB as a threat to human health in the Arctic.

**RESULTS:** This examines zoonotic disease transmission in the past. It establishes the presence of disease in herd of bison managed by the government of Canada. It considers the debate over the health of the animals and their fate along with their use in a program that provided meat to the Inuit at the same time that TB was first observed as a growing threat to human health in the region. It follows the chain of infection from an animal population to a new and susceptible human population a considerable distance away.

**CONCLUSION:** In detailing the relationship between infection in disparate populations of humans and animals in the past, this paper illustrates the value of applying principles of One Health to historical research.

## 2 LB2 - LATE BREAKERS 2 - SALON CD

## Alveolar echinococcosis – An emerging zoonosis in North America?

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Alveolar echinococcosis (AE) is a life-threatening medical condition that occurs when people are infected by the zoonotic cestode *Echinococcus multilocularis*. In the northern hemisphere, this parasite cycles between wild canid definitive hosts and rodent intermediate hosts, and people are accidentally infected by ingesting eggs shed in the fecal matter of infected foxes, coyotes, wolves, or dogs. Until recently, the distribution of *E. multilocularis* was thought to be limited to two geographic foci in North America- the Northern Tundra Zone and the North Central Region; however, reports in dogs and wild canids from outside these regions suggests that the distribution is expanding. Cases of domestic dogs infected with the larval stage of *E. multilocularis* (rather than adult cestodes)

have increasingly been reported since the index case was detected in 2009. Since then, AE cyst material from dogs across all 4 western Canadian provinces, and one human from Saskatchewan, have been genetically characterized. First, to confirm identity, parasite DNA was extracted from cysts, cyst fluid or free abdominal fluid, and amplified by a multiplex PCR designed to differentiate *E. multilocularis* from *E. granulosus* and *Taenia species*. Second, to identify haplotypes and analyze biogeographical origin, PCR was conducted at three additional loci - NADH dehydrogenase subunit 2 (nd2), cytochrome b (cob), and cytochrome c oxidase subunit 1 (co1). PCR products were purified, sequenced and aligned, and then compared to other *E. multilocularis* sequences by haplotype network analysis. Our analysis demonstrates that the genetic sequences of *E. multilocularis* causing AE in dogs and a person in Western Canada were more similar to European strains than North American strains. European strains appear to have greater zoonotic potential than endemic strains long established in the central region of North America. This work emphasizes the need to enhance North American capacity to detect and differentiate *Echinococcus* species in animals and people, and to develop enhanced AE surveillance and reporting in North America as the risk profile of AE might be changing. Finally, a One Health approach to risk mitigation and communication regarding AE is needed, involving (and not limited to) wildlife managers, urban planners, veterinarians, and medical professionals.

### 3 LB2 - LATE BREAKERS 2 - SALON CD

## Students' experiences during One Health field attachment: A case study of One Health Institute in Makerere University, Uganda

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**BACKGROUND:** Increasingly, it is getting clearer that solving complex global health problems requires interdisciplinary, intersectoral expertise and cooperation i.e. One Health (OH). Recent global movements and supporting evidence, including the report of the commission on the education of health professionals for the twenty-first century, have argued for a redesign of health professional education systems to better match the population needs and to produce a workforce that can meet complex health challenges. Universities are testing sites for education where innovative transdisciplinary approaches to training professionals are constantly introduced and refined, including One Health approaches. Makerere University implemented an innovative One Health Institute (OHI) in 2016 where undergraduate students were selected from different disciplines. The students were first taken through theoretical principles in OH followed by a field attachment in the communities. The field attachment exposed students to experiential educational opportunities. In this paper, we present students experience and their contributions in solving communities' health challenges.

**METHODS:** This was a cross-sectional study, utilizing qualitative data collection methods, involving students who participated in the OHI-field attachment and community members in Eastern Uganda. Six focus group discussions (FGDs) and four key informant interviews (KIs) were conducted among the students, while four FGDs and 14 KIs were conducted among community members. All interviews were audio-recorded, transcribed and analysed manually.

**RESULTS:** Two themes were identified: Students' gains and students' contribution to communities. Regarding students' gains; they appreciated the training sighting gaining skills in communication, team work and collaboration. Through the multi-disciplinary teams, the students appreciated that each discipline had something to contribute towards achieving health in the community. Students also reported a feeling of gratitude and accomplishment. They felt that they made a positive impact to the community by coming up with interventions to some of the challenges that the communities were facing. The students reported participating in creating awareness on water, sanitation and hygiene, prevention of zoonotic diseases like bovine TB and rabies. They also helped in



designing interventions such as briquette making by recycling waste and maintenance of safe water sources. The communities learnt and appreciated the concept of OH. The communities appreciated the students' contribution such as improving sanitation and hygiene in schools, abattoirs and markets. In addition, students were reported to raise awareness about general disease prevention and health promotion. Students were reported to exhibit a spirit of team work and collaboration in addition to showing love and care to the communities.

**CONCLUSIONS:** This exposure helped students experience working in interdisciplinary teams that value inputs from other disciplines and gained OH competencies like communication and collaboration. Adopting this model in university teaching system, is urgently needed as this kind of training imparts skills in disease detection, prevention and response including influenza.

#### 4 LB2 - LATE BREAKERS 2 - SALON CD

### A novel vaccine candidate for *Salmonella* gastroenteritis

**Sokaribo, Akosiererem Senibo:** Perera, Sumudu; Lam, Shirley; Deck, Will; Attah-Poku, Sam; White, Aaron P.

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Gastroenteritis (enterocolitis) caused by non-typhoidal *Salmonellae* (NTS) is one of the most common food borne diseases worldwide. Current global estimates are 94 million cases of gastroenteritis with 150,000 deaths annually. We have characterized a surface-associated polysaccharide capsule that is conserved in pathogenic *Salmonella* strains, and cross-reactive between the three most common North American groups of NTS: *Salmonella* serovars Typhimurium, Enteritidis and Heidelberg. We used a combination of random and targeted mutagenesis to generate a *Salmonella* strain that produces high levels of the capsule antigen, and have established optimal purification conditions. We performed an immunization trial in mice showing that the antigen can induce an immune response when delivered alone, and that conjugating the capsule to an immune stimulatory carrier protein can boost the response. Future challenge experiments with *Salmonella* will allow us to assess the level of protection achieved.

#### 5 LB2 - LATE BREAKERS 2 - SALON CD

### Core Competencies in One Health Education: What Are We Missing?

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**BACKGROUND:** Today's public health challenges are complex and crosscutting, such as antimicrobial resistance, food insecurity, and outbreaks of emerging infectious diseases. An important step toward synergistically addressing these issues would be to apply consistent One Health core competencies in education, in order to optimally prepare future One Health leaders. It is unclear if and how core competencies are currently being employed in One Health education. We assessed the evolution of existing One Health core competencies, how they are being applied in academic programs, and identified gaps that could be filled through our recommendations.

**METHODS:** We conducted a literature search for core competencies in One Health education, as well as searches for One Health academic degree programs in the United States. Post- secondary degree programs were included if they were taught with an interdisciplinary approach linking human, animal, and environmental health disciplines. We reviewed all available information online and contacted administrators by e-mail for each program.

**RESULTS:** Three separate groups developed One Health core competencies between 2008 and 2011, which were later synthesized in 2012. Since then, core competency recommendations have not been updated and provided as a public resource. A competency domain related to health sciences was missing from previously recommended competencies.

We identified at least 45 One Health degree programs in the US, of which 27 (60%) were master's level, 10 (22%) were bachelor's level, and 8 (18%) were doctoral programs. The majority (83%) of academic programs were established after 2001. Only 14 (31%) had core competencies publicly available. Among key areas that were evaluated, plant biology, antimicrobial resistance, and law were underrepresented in the programs, whereas epidemiology and environmental health/ecology were well represented.

**CONCLUSIONS:** The One Health approach has been embraced by a diverse and growing number of educational programs, but the product of such an education cannot be reasonably anticipated by prospective employers without consistency in One Health training objectives. We recommend One Health core competencies in (i) health knowledge, (ii) global and local issues in humans, animals, plants, and the environment, and (iii) professional characteristics, highlighting the importance of proficiency in health sciences, understanding complexities of real-life health challenges, as well as skills to apply scientific principles to solve them. One Health degree programs could be improved by voluntary commitments to core competencies, including proficiency in at least one health science, and to educating future professionals in disciplines that are both currently well represented as well as disciplines that are underrepresented. Furthermore, program administrators should continue to focus on practical training and communication. It is important to define, develop, evaluate, improve, and continue to refine One Health education, not only in One Health degree programs but also in existing public health, environmental, veterinary, and medical curricula.

## 6 LB2 - LATE BREAKERS 2 - SALON CD

### West Nile disease: possible epizootic transmission cycle in Southern Pakistan

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**BACKGROUND:** West Nile Virus (WNV) genus *Falavivirus*; is a cause of seasonal fever with neurotropic findings in countries that share borders with Pakistan; however data from Pakistan is very limited. The magnitude and distribution of WNV disease is poorly understood as Pakistan. The human and vector related part of this study was published in *Frontiers in Public Health*, 2018. In this abstract we have additional findings of WNV seropositivity from Equine animals suggesting maintenance of epizootic transmission of virus in southern region of Pakistan.

**METHODS:** A cross-sectional study was conducted to determine which flaviviruses were agents of seasonal febrile and related neurological disease in southern region of Pakistan 2015-2017. Patient with acute febrile illness with or without neurological complications were recruited from six different field sites. In addition mosquitoes and equine blood samples were collected (over limited geographical distribution) to see evidence for animal / vector positivity, confirming the epizootic cycle of WNV in Pakistan. For animal samples multispecies competitive ELISA to detect antibodies against WN pr-E envelope protein (cELISA; ID Screen®, West Nile Competition, ID Vet, Montpellier, France) were used. Statistical analyses were performed on clinical data using MedCalc version 17.9.7—64-bit, Logistic regression for dichotomous independent variables was performed. Odds ratios were calculated with 95% confidence intervals.

**RESULT:** This is the first report of WNV causing neurological disease in human patients in Pakistan. Of 997 enrolled patients presenting with clinical features suggestive of arboviral disease, 105 were positive for WNV IgM antibodies, and 71 of these patients possessed WNV-specific neutralizing antibodies. Cross-reactivity of WNV IgM antibodies with Japanese encephalitis virus (JEV) occurred in 75 of these 105 patients. Patients with WNV infections were more likely to present with altered mental status, seizures, and reduced Glasgow Coma scores when compared

with JEV-infected patients. Human WNV cases and vector numbers exhibited a temporal correlation with climate. Additionally we tested 39 equine sera (34 horse and 5 donkey) for West Nile seropositivity, using multispecies competitive ELISA to detect antibodies against WN pr-E envelope protein. The seropositivity in animal samples was 89.5% (34/39) from southern Pakistan.

**CONCLUSION:** The findings of WNV seropositivity from equine animals and temporal correlation of human WNV and vector numbers suggests maintenance of epizootic transmission cycle of virus in southern region of Pakistan, with horses/donkeys and humans infected in a spillover transmission as “dead-end” hosts. These findings are of great public health (both human and veterinarian) concern and alerts authorities for urgent initiation of one-health based control strategies to prevent epidemic outbreak in the country.

## 1 LB3 - LATE BREAKERS 3 - GALLERY AB

### Genetic diversity of VCC-1 carbapenemase-producing *Vibrio cholerae* in coastal waters of Germany

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**BACKGROUND:** Recently, we reported on seven VCC-1 producing *Vibrio cholerae* isolates that were recovered from coastal waters of the North and Baltic Sea in Germany. As *V. cholerae* non-O1/-O139 isolates are widely distributed in coastal waters with low salinity and sometimes are associated with wound infections and diarrheal diseases in humans, detailed information on the genetic background of these isolates is necessary to assess the risk for the distribution of this carbapenem resistance.

**METHODS:** In order to characterize the genetic diversity of the isolates, the genome of the reference strain VN-2997 was determined by PacBioRSII and MiSeq sequencing. PacBio reads were assembled using HGAP followed by mapping of the MiSeq raw reads against the PacBio genome. Bioinformatics, PFGE profiling, and DNA-DNA hybridization as well as conventional PCR were used to reveal the organization of the  $bla_{VCC-1}$  gene locus on other *V. cholerae* genomes. Furthermore, resistance testing of the isolates was performed by broth microdilution methods according to CLSI guidelines.

**RESULTS:** As initial MiSeq sequencing of all prevailing isolates did not reveal the genetic localisation of  $bla_{VCC-1}$  within the genomes, further dissection analyses were performed. PFGE profiling revealed that the isolates exhibit two distinct XhoI PFGE-patterns, which is in good agreement with the observed MLST-types of the isolates. DNA-DNA hybridization indicates that one or two copies of  $bla_{VCC-1}$  gene are present in different parts of the *V. cholerae* genomes. The presence of one or two  $bla_{VCC-1}$  genes did not correlate with the differences observed in the MLST-type or the observed MIC level. The organization of the  $bla_{VCC-1}$  harbouring genome region of the individual isolates will be presented in detail.

**CONCLUSION:** Our study indicates that VCC-1 carbapenemase-producing *V. cholerae* are frequently present in different regions of the German coastline. Despite of the close phylogenetic relationship of the two observed MLST-lineages the  $bla_{VCC-1}$  genetic context diverges from isolate to isolate.

## 2 LB3 - LATE BREAKERS 3 - GALLERY AB

## 6 years (2010-2016) lag phage of ESBL<sub>A</sub> - to ESBL<sub>Carba</sub> in Enterobacteriaceae isolated from wild birds: Towards the start of the environmental spread of Carbapenamse producers in Bangladesh?

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**BACKGROUND:** The dissemination of extended spectrum beta-lactamases (ESBL<sub>A</sub> and ESBL<sub>Carba</sub>) producing *S.* in clinical and environmental settings has become a global concern. ESBL<sub>A</sub> (CTX-M-15) has been reported in humans, livestock and the environment, and their isolation frequencies are increasing rapidly worldwide, however, ESBL<sub>Carba</sub> (NDM, KPC, OXA-48) has not been reported as frequently yet, but hospital wastes are believed to be the source in Bangladesh. To explore the molecular epidemiology of ESBLs (A and Carba) in the environment, birds foraging on hospital wastes in Bangladesh were examined for a period of 6 years (2010-2016) as wild birds are considered as bio-indicator.

**METHODS & MATERIALS:** During 2010 to 2016, once in every year 110 fecal samples were collected from the crows foraging on hospital wastes in the Rajshahi medical college and hospitals area. Fecal samples were enriched and cultured for ESBL-producers (A and Carba) during 2010 only, but later we screened for only ESBL<sub>Carba</sub> as it was a serious concern globally during 2011. Isolates were tested for susceptibility to 13 antibiotics including carbapenems according to EUCAST. ESBL producing Isolates were identified and characterized by PCR, rep-PCR, sequencing and MLST.

**RESULTS:** During 2010, 55% of the crows were positive for ESBL<sub>A</sub>, however no ESBL<sub>Carba</sub> was noticed. ESBL producers were belonging to several species of the Enterobacteriaceae family, for example, *E. coli*, *K. pneumoniae*, *R. terrigena* and *E. cloacae*. No ESBL<sub>Carba</sub> was found during the following years (2011-2015). The most common ESBL<sub>A</sub>-type was CTX-M-15, followed by CTX-M-55, CTX-M-1 and CTX-M-14. During 2016, ESBL<sub>Carba</sub> was found in 6% of the birds and *E. coli*, *K. pneumoniae* was the bacterial species so far recorded. NDM-1, NDM-5 and NDM-7 were found in *E. coli* and *K. pneumoniae*. Other than carbapenems and cephalosporins, *E. coli* and *K. pneumoniae* were resistant to broad spectrum antibiotics like ciprofloxacin, gentamycin, mecillinam, trimethoprim-sulfamethoxazole and chloramphenicols. Birds were sharing common clones closely related to clinical clones. Birds also shared clinically important sequence types with humans, including *E. coli* clone O25b-ST131.

**CONCLUSION:** In conclusion, ESBL<sub>Carba</sub>-producing bacteria with multi-resistance have started to spread from 2016 into the environment of Bangladesh and hospital wastes are attributing to the spread. High level of carbapenem resistant bacteria in the bird population of Bangladesh is worrying, and there is no easy solution in sight.

## 3 LB3 - LATE BREAKERS 3 - GALLERY AB

## Alternative Approaches to Managing Demand for Antibiotic Treatment in Dairying

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**BACKGROUND:** Regulations on antibiotics in animal agriculture have expanded over the past decade. Antibiotics have been administered to food production animals in feed to either prevent disease or improve feed efficiency, and also therapeutically. Our interest is in dairy farm use where purposes are therapeutic. Our focus is the managerial economics of farm-level antibiotics choices. Research in human medical practice reveals strong patient pressure on doctors to over-prescribe antibiotics (e.g., Linder et al. 2017). Evidence is also accumulating that agricultural decision-makers may, through rational inattention or irrationality, systematically mismanage their inputs (e.g., Perry et al. 2017). We seek to understand whether opportunities exist for behavioral economics approaches to reduce antibiotics demand on dairy farms.

**METHODS:** During mid-2017, paper and web surveys were sent to dairy farmers in Wisconsin, Minnesota and Michigan, requesting information about, among other matters, antibiotics input choices on the farm. One question presented a stylized decision environment. Four contexts were provided where in each two parameters were given: probability a single cow can be cured with antibiotics, and loss reduction if cured. Subjects were asked to provide willingness to pay (WTP) to treat the animal. Four versions were sent out. We received 648 responses of which about 480 completed the WTP queries.

**RESULTS:** Letting  $p$  = cure probability and  $L$  = reduction in loss then  $pL$  = expected reduction in loss. Analysis reveals that mean WTP exceeds expected loss at low losses and approximately equals expected loss at higher losses while strong sensitivity to probability is expressed. Least squares regression estimates confirm that WTP is more probability sensitive than loss sensitive. Sensitivity of WTP to expected loss is about 50%. A separate question for factors importance in management corroborates the finding that probability is the variable that managers focus on managing.

**CONCLUSIONS:** Our findings should alleviate concerns that growers far over-apply antibiotics from the private optimization viewpoint. What is best for society is a different matter. Our results also suggest that research and outreach efforts and practical tools which seek to better inform growers on probability of infection will be more effective than those addressing loss (e.g., more stringent rules about milk withdrawal from market after treatment) or emphasizing cost, perhaps through user fees as currently implemented in several European countries. Social Media: In managing antibiotics use, research and outreach efforts and practical tools that seek to better inform milk producers on probability of mastitis infection will be more effective than those addressing loss.

**REFERENCES:** Linder JA et al. 2017. J. Am. Med. Assoc. 318(14), 1391.  
Perry E et al. 2017. Selected paper, AAEA Annual Meetings, Chicago, IL.

#### 4 LB3 - LATE BREAKERS 3 - GALLERY AB

### Longitudinal field study in evaluating the ecological spillover of antibiotic-resistant *Escherichia coli* from poultry to humans in rural Ecuador

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Small-scale farming operations in rural communities often prescribe high amounts of antibiotics for industrial meat production breeds of chickens (e.g. broilers, Fig. 1A). In contrast, free-ranging local varieties of backyard chickens (Fig. 1B) receive almost no antibiotics. Recent evidence suggests that backyard chickens in proximity to broiler chickens have increased levels of phenotype and genotype antibiotic resistance. We conducted a seven-month longitudinal study aimed to examine whether backyard chickens and children serve as sentinels for detecting antibiotic resistance spread into the environment from broiler chickens in northwestern Ecuador. *Escherichia coli* isolates were identified from children ( $n = 1144$ ), backyard chickens ( $n = 1323$ ), and 1-day-old broiler chickens purchased from vendor sources ( $n = 253$ ). Isolates were examined for their resistance phenotypes to 12 antibiotics and selected resistance genes. Phenotype resistance profiles fluctuated over time for human and backyard chicken samples. In contrast, broiler chicken resistance profiles remained high for all antibiotics tested. We also detected that households closest to households raising broiler chickens yielded significantly greater phenotype resistance levels among avian and human samples (general additive model;  $p < 0.005$ ). The same *bla*CTX-M gene was detected in both human and chickens. These results likely suggest that small-scale broiler farming operations may function as sources of environmental antimicrobial exposure for the surrounding human and animal populations. Our results indicate that industrial meat-producing animals may introduce antibiotic resistance into other animal breeds, likely through horizontal gene transfer spillover events into backyard breeds and humans.

## 5 LB3 - LATE BREAKERS 3 - GALLERY AB

**Non-prescribed use of antibiotics in peri-urban small-holder dairy farms: A cross-sectional study of 510 farms across 5 cities in India**

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**BACKGROUND:** Non-prescribed use of antibiotics (NPAb) in dairy farms is long reported as a prevalent practice. It is perceived as a serious threat to antibiotic effectiveness in animals and humans and an inevitable challenge to the agroecology and sustainable production of 'healthy' dairy produce. However, the practices have not been adequately investigated. India is the largest milk producer in the world. Small holder dairy farms in peri-urban areas are a significant contributor to this production. This study investigated non-prescribed use of antibiotics by these farmers in India and determinants thereof.

**METHODS:** Using a multi-stage random cluster sampling, we selected small holder dairy farms ( $\leq 10$  cows) in peri-urban ecosystems of five cities of India. For quantitative surveys, we used a 'dairy farmer questionnaire' capturing antibiotic usage, farm and farmer characteristics, farming practices and farm environment. For direct observation, we used a 47-item 'observation checklist' assessing dairy and milking area, milk storage area, and hygiene. Milk samples were collected randomly from selected 'wet' cows from each farm and investigated for antibiotic residues. NPU was defined as self-reported use of allopathic medicine within the past 1 year for any of pre-specified 10 animal conditions without advice from a qualified veterinarian and/or detection of antibiotic residues from any of the milk samples.

**RESULTS:** Total 510 farms were included in the study. The rates of NPU in the study cities were as follows: Bengaluru, 40.2% (30.5-49.9); Bhubaneswar, 35.3% (25.9-44.7); Guwahati, 43.1% (33.4-52.9); Ludhiana, 53.9% (44.1-63.8); Udaipur, 76.5% (68.1-84.8). Antibiotic residues were detected in 14.3% (11.3-17.4) of the total farm. The most commonly used antibiotics in these farms were tetracyclines [10.0% (7.6-13.0)] followed by fluoroquinolones [2.8% (1.5-4.6)] and sulphonamides [1.8% (0.8-3.3%)]. Overall, about 26.2% (22.0-30.8) of the farms reported using medicines (antibiotics/ non-antibiotics) for purposes other than treating disease. The proportion of self-administration was significantly different ( $p=0.002$ ) between NPU farms (40.6%) and non-NPU farms (27.7%). Half of the NPU farm respondents said that they got advice from others on how to use these medicines as compared to 39.8% among non-NPU respondents ( $p=0.021$ ). In multivariate analysis, NPU was significantly associated with age of the farm beyond 5 years, self-administration of the veterinary antibiotics by the farmer, ease of administration, popularity of the drug, if the farmer had not visited the government veterinary hospital, and use of the drugs for diarrhea among specific conditions in the animal.

**CONCLUSION:** NPU was widespread across all the cities but rates varied from city-to-city. Antibiotic residues indicated that about 1 in every 7 farms were currently using antibiotics and for common conditions. Rates were likely to be higher in cities that were more likely to use intensified dairy farming. Such widespread use is likely to fuel AMR and reflects unsustainable farming practices.

## 6 LB3 - LATE BREAKERS 3 - GALLERY AB

**Population wide assessment of antimicrobial use in companion animals using a novel data source – a cohort study using pet insurance data**

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2: National Centre for Antimicrobial Stewardship, Peter Doherty Institute, Australia;

3: PetSure (Australia), Australia

**BACKGROUND:** Antimicrobial use in veterinary practice is under increasing scrutiny as a contributor to the rising risk of multidrug resistant bacterial pathogens. Surveillance of antimicrobial use in food animals is extensive, but population level data is lacking for companion animals. Lack of census data means cohorts are usually restricted to those attending veterinary practices, which precludes aggregating data from large cohorts of animals, independent of their need for veterinary intervention. The objective of this study was to investigate the exposure of companion animals to antimicrobials at a population level.

**METHODS:** A retrospective cohort study was performed using a novel data source; a pet insurance database. The rate of antimicrobial prescribing, and the rate of prescribing of critically important antimicrobials, was measured in a large population of dogs (813,172 dog-years) and cats (129,232 cat-years) from 2013 - 2017. Factors affecting the rate of prescription were explored using Poisson regression.

**RESULTS:** There were 222,069 dogs and 37,732 cats registered in the database in 2013. This increased to 385,915 dogs and 60,807 cats over the study period to the end of 2016. A total of 611,788 courses of antimicrobial treatment were prescribed. The incidence rate of antimicrobial prescribing was 5.8 prescriptions per 10 dog years (95% CI 5.8-5.9 per 10 dog years) and 3.1 prescriptions per 10 cat years (95% CI 3.1-3.2 per 10 cat years). Claims were submitted on average for 35% of insured dogs and 21% of insured cats each year. Among animals that had an insurance claim submitted, other than for routine preventative health measures (vaccination, parasite control, desexing), 53% received systemic antimicrobials (48% of cats and 54% of dogs). Critically important antimicrobials accounted for 8% of all the antimicrobials prescribed over the 4-year study. With the exception of 3rd-generation cephalosporins in cats, no other CIA represented more than 5% of the antimicrobial use in a species. Cats were 4.8-fold more likely than dogs to be prescribed 3rd-generation cephalosporins. A seasonal influence on prescribing was seen for dogs and cats. There was a small, but significant, reduction in the year-on-year rate of exposure to antimicrobials, after adjusting for species (RR 0.99, 95% CI 0.986-0.997, P=0.002).

**CONCLUSIONS:** The level of antimicrobial exposure in dogs and cats was less than half that for the coincident human community. Data such as this provides a unique opportunity to monitor antimicrobial prescribing in veterinary medicine, which is a critical component of optimal antimicrobial stewardship. While restricting all off-label use of antimicrobials in animals in Australia is likely to be detrimental to antimicrobial stewardship measures, and animal welfare in general, it may be necessary to restrict the use of 3rd-generation cephalosporins in this manner to reduce the inappropriate use of this antimicrobial.

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## PATHOGEN DISCOVERY

P001 - OHS A01 - PATHOGEN DISCOVERY

### Characterisation of Viruses in Australian Wild Birds using Metagenomics

**Vibin, Jessy** (1,2); Chamings, Anthony (1,2); Klaassen, Marcel (2); Nelson, Tiffanie (1,2); Alexandersen, Soren (1,2,3)

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P002 - OHS A01 - PATHOGEN DISCOVERY

### From SADS to STING: a story on bats

**Zhou, Peng** (1); Shi, Zheng-Li (1); Wang, Lin-Fa (2); Daszak, Peter (3); Tong, Yi-Gang (4); Ma, Jing-Yun (5)

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P003 - OHS A01 - PATHOGEN DISCOVERY

### Detection of MERS-related Coronavirus in Wrinkle-lipped free-tailed bats

Wacharapluesadee, Supaporn (1); Duengkae, Prateep (2); Kaewket, Chumphon (3); Yinsakmongkon, Sangchai (4); Kaewpom, Thongchai (1); Rodpan, Apaporn (1); Stokes, Martha M (5); Hemachudha, Thiravat (1); **Sininart, Petcharat** (6)

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P004 - OHS A01 - PATHOGEN DISCOVERY

### Discovery of Ecologically Distinct Clades within Pathogenic and Non-pathogenic Bacterial Taxa

Wood, Jason (1); Krizanc, Danny (2); Ward, David (3); **Cohan, Frederick** (2)

1: Jet Propulsion Laboratories, USA - 2: Wesleyan University, USA - 3: Montana State University, USA -

P005 - OHS A01 - PATHOGEN DISCOVERY

### Geostatistical analysis of the density of primary reservoir of plague in Armenia

**Danielyan, Ruben**; Sahakyan, Levon  
National Center for Disease Control and Prevention, Ministry of Health, Yerevan, Armenia -

P006 - OHS A01 - PATHOGEN DISCOVERY

### Towards bat coronavirus isolation – one cell culture at a time.

**Suliman, Tasnim** (1); Eckerle, Isabella (3); Cronjé, Nadine (1); Kotzé, Andrea (1); Mueller, Marcel (2); Drost, Christian (2); Preiser, Wolfgang (1)

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P007 - OHS A01 - PATHOGEN DISCOVERY

### DNA of human bocavirus origin detected in non-human primates in the Democratic Republic of the Congo

**Kumakamba, Charles** (1); Ngay Lukusa, Ipos (1); Mbala Kingebezi, Placide (1); N'Kawa, Frida (1); Atibu Losoma, Joseph (2); Mulembakani, Prime (1); Makuwa, Maria (1); Muyembe Tamfum, Jean-Jacques (3); Belais, Raphael (4); Gillis, Amethyst (1); Harris, Stephen (1); Rimoin, Anne (5); Hoff, Nicole (5); Fair, Joseph (6); Monagin, Corina (7); Ayuukebong, James (1); Saylor, Karen (1); Rubin, Edward (1); Wolfe, Nathan (1); Lange, Christian (1); Mazet, Jonna (7)

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P008 - OHS A01 - PATHOGEN DISCOVERY

### Ten year experience developing one health capacity in Africa

**Rweyemamu, Mark Marini**

Sokoine University of Agriculture, Tanzania, United Kingdom -

## SOCIAL SCIENCE AND POLITICS

P009 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### Environmental protection as an ethical requirement for community health

**Saleh, Gamil A.Rahim**

University of Aden, Yemen. Faculty of Medicine, Yemen -

P010 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### Culling as a Public Health Measure

**Lederman, Zohar**

National University of Singapore, Singapore -

P011 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### Differential impact of inequity on elimination of HIV in Nigeria: the intersection of policy, programme design and social norm

**Adeyinka, Daniel Adedayo** (1,2); Morka, Mercy (1); Ozigbo, Chamberline (1,3); Agogo, Emmanuel (4,5); Odoh, Deborah (1); Olakunde, Babayemi (4); Sambo-Donga, Finti (1); Onifade, Olufunke (1); Davies, Abiola (6); Amamilo, Ikechukwu (7); Mbori-Ngacha, Dorothy (6)

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P012 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### Expanding the umbrella of One Health – are there any outer boundaries or internal conflicts?

**Lerner, Henrik** (1); Berg, Charlotte (2)

1: Ersta Sköndal Bräcke University College, Sweden - 2: SLU Swedish University of Agricultural Sciences -

P013 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### Implications for the United States drawn from European Union experiences with antimicrobial use, policy, and resistance

**Vezeau, Neil Patrick**

Iowa State University College of Veterinary Medicine, Ames, IA, United States of America -

P014 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### International Circumpolar Partnerships in One Health; Role of the Arctic Council

**Corriveau, André Emile** (1,6); Hennessy, Thomas W. (2,6); Cox, Sarah (3,5); Oksanen, Antti (4,6)

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P015 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### Ensuring the viability and sustainability of One Health Platforms: Is Tackling Anti-Microbial Resistance the Answer?

**Martin, Jerry**

DAI Global Health, United States of America -

P016 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### The Health Belief Model and water testing behaviour: A qualitative study of rural well owners

**Munene, Abraham**; Lockyer, Jocelyn; Checkley, Sylvia; Hall, David  
University of Calgary, Canada -

P017 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### Politics before the First Cooperative Clinical Cancer Trial in Canada and Policies Thereafter

**Razumenko, Fedir**

University of Saskatchewan, Canada -

P018 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### High level of Pesticide Biomarkers among Bangladeshi villagers

**Das, Pritimoy** (1); Hossain, M S Sazzad (1); Mohammad, Abdullah Heel Kaf (1); Rahman, Mahmudur (2); Luby, Steve P (3); Gurley, Emily S (4)

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P019 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### One Health surveillance for brucellosis in Armenia: Approaches and a path forward for veterinary services

**Mkrtychyan, Hovhannes** (1); Markosyan, Tigran (2); Tumanyan, Pertch (3); Niazyan, Lyudmila (4); Ragan, Valerie (5); De Nardi, Marco (6)

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P020 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### Compassion Fatigue and One Health: supporting our relationship with the animals we care for thru an integrated One Health approach

**Pettan-Brewer, Christina** (1); Van Hooser, J.Preston (2); Rabinowitz, Peter (3); Thompson-Iritani, Sally (2)

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P021 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### Understanding the social lives of antibiotics and their policies in the UK dairy industry

**Begemann, Stephanie**; Christley, Robert; Perkins, Elizabeth; Vivancos, Roberto; Watkins, Francine

University of Liverpool, United Kingdom -

P022 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### Mentored research experiences in One Health: Increasing science identity and self-efficacy among undergraduate students from rural backgrounds

**Hueffer, Karsten** (1); Reynolds, Arkeigh (1); Cotter, Paul (2)

1: University of Alaska Fairbanks, United States of America - 2: Evalogic -

P023 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### The formulation of One Health policies: lessons from Burkina Faso

**Siri, Drissa** (1); Mele, Antonio (2); Youma, Joseph (3); Sawadogo, Issa (4); Landry Hien, Hugues (5); Yamèogo, Issiaka (5); Pissang-Tchangai, Dademanao (1); Pica Ciamarra, Ugo (2)

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P024 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### One Model for Generating Early Career Problem Solvers and Multi-Disciplinary Networks who place Global Issues in a One Health Framework

**Schneider, AnnMarie** (1); Wu, Huiyun (1); Weiskerger, Chelsea (1); Misra, Vikram (2)

1: Michigan State University, United States of America - 2: University of Saskatchewan, Canada -

P025 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### Operationalizing One Health: Strengthening Interagency Coordination through Systems Mapping and Analysis

**Pelican, Katey** (1); Myhre Errecaborde, Kaylee (1); **Vesterinen, Heidi** (1); Mahero, Michael (1); Macy, Katelyn (1); Tracey, Dutcher (1,2)

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P026 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### Power struggles, lack of leadership, and weak evidence on effective approaches are hindering collaboration between human, animal, and environmental health sectors

**S. Khan, Mishal** (1); McRobie, Ellen (2); Spencer, Julia (2); Dar, Osman (2)

1: London School of Hygiene & Tropical Medicine, United Kingdom - 2: Chatham House (the Royal Institute of International Affairs), United Kingdom -

P027 - OHS A03 - SOCIAL SCIENCE AND POLITICS

### Themes from One Health Zoonotic Disease Prioritization Workshops in 18 Countries, 2014-2017

**Barton Behravesh, Casey**; Ghai, Ria; Vikram, Krishnasamy; Goryoka, Grace; Varela, Kate; Oussayef, Nadia; Salyer, Stephanie

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## DRIVERS FOR EMERGING DISEASES

P028 - OHS A04 - DRIVERS FOR EMERGING DISEASES

### Reservoirs of Spillover Pathogens Exhibit Fast Life History Traits

**Plourde, Benjamin Thomas**

University of California, Davis, United States of America -

P029 - OHS A04 - DRIVERS FOR EMERGING DISEASES

### A quantitative exploration of Rift Valley Fever knowledge and associated social drivers in Fulani nomadic pastoral communities of North-central Nigeria

**Alhaji, Nma Bida** (001); Babalobi, Olutayo Olajide (002); Isola, Tajudeen Opayemi (003)

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P030 - OHS A04 - DRIVERS FOR EMERGING DISEASES

### Climate Change and Emerging Viral Threats in Canada: Modeling the Transmission Dynamics of Chikungunya Virus

**Khan, Salah Uddin** (1); Ng, Victoria (2); Fazil, Aamir (2); Greer, Amy L. (1); Ogden, Nicholas H. (2)

1: Department of Population Medicine, University of Guelph, Canada - 2: National Microbiology Laboratory, Public Health Agency of Canada -

P031 - OHS A04 - DRIVERS FOR EMERGING DISEASES

### Drivers for Emerging Zoonoses in Pastoralist Communities in Northern Tanzania: Using a mixed methods approach to determine animal-human interaction and rural health-seeking behaviours of livestock-keepers.

**Barasa, Violet Nasimiyu**

University of Sussex, United Kingdom -

P032 - OHS A04 - DRIVERS FOR EMERGING DISEASES

### Pregnancy and Other Drivers of Viral Detection in Bat Hosts

**Eskew, Evan A.** (1); Montecino-Latorre, Diego (2); Randhawa, Nistara (2); Olival, Kevin J. (1); Daszak, Peter (1); Mazet, Jonna A. K. (3); Consortium, PREDICT (2)

1: EcoHealth Alliance, USA - 2: One Health Institute, School of Veterinary Medicine, University of California - Davis, USA - 3: One Health Institute & Karen C. Drayer Wildlife Health Center, School of Veterinary Medicine, University of California - Davis, USA -

P033 - OHS A04 - DRIVERS FOR EMERGING DISEASES

### One Health in Thailand: Multisectoral contributing towards success addressing zoonotic EIDs

**Luangon, Woraya**

Bureau of Emerging Infectious Disease, Thailand -

P034 - OHS A04 - DRIVERS FOR EMERGING DISEASES

### Prevalence of vector-borne diseases in the Republic of Armenia

**Paronyan, Lusine**; Babayan, Lilit; Torosyan, Liana; Avetisyan, Lilit; Vanyan, Artavazd  
National Center for Disease Control and Prevention, Ministry of Health, Yerevan, Armenia -

P035 - OHS A04 - DRIVERS FOR EMERGING DISEASES

### Biological and anthropogenic drivers for emerging zoonoses from an interdisciplinary perspective

Swanenbug, Manon (1); de Lauwere, Carolien (2); Roest, Hendrik-Jan (1); **van der Poel, Wim H.M.** (1); de Boer, Fred (3); Vaandrager, Lenneke (4); Bergevoet, Ron (2); Hogeveen, Henk (5); Petie, Ronald (1); de Vos, Clazien J. (1)

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2: Wageningen University & Research, Wageningen Economic Research, The Netherlands -  
3: Wageningen University & Research, Resource Ecology, The Netherlands -  
4: Wageningen University & Research, Health & Society, The Netherlands -  
5: Wageningen University & Research, Business Economics, The Netherlands -

P036 - OHS A04 - DRIVERS FOR EMERGING DISEASES

### Understanding emerging infectious disease at the human-wildlife-environmental interface in Africa

**Alexander, Kathleen A.**

Virginia Tech, United States of America -

P037 - OHS A04 - DRIVERS FOR EMERGING DISEASES

### Seasonal reproduction of the Egyptian fruit bat drives viral infection dynamics

**Markotter, Wanda** (1); Dietrich, Muriel (1,2); Jansen van Vuren, Petrus (1,3); Mortock, Marinda (1); Storm, Nadia (3); Weyer, Jacqueline (1,3); Paweska, Janusz (1,3)

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2: UMR PIMIT (Processus Infectieux en Milieu Insulaire Tropical), Université de la Réunion, INSERM U1187, CNRS UMR 9192, IRD UMR 249, Sainte-Clotilde, Reunion Island -  
3: Centre for Emerging, Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases, National Health Laboratory Services, Sandringham, South Africa -

P038 - OHS A04 - DRIVERS FOR EMERGING DISEASES

### Identifying Avian Flu (H5N1 & H1N1) as an emerging disease to threaten both human and animal health especially to immunologically naïve communities.

**Sishuba Zulu**, Masibulele; Berani, Fjolla; Pokharel, Nikita; Mpofo, Bekithemba Brandon

Thammasat University, South Africa -

P039 - OHS A04 - DRIVERS FOR EMERGING DISEASES

### Recurrent crow (corvus spendens) mortality events linked to H5N1 influenza virus circulation in live bird markets, Bangladesh

**Islam, Ariful** (1); Islam, Shariful (1,2); Samad, Mohammad A (3); Rostal, Melinda K (1); Rahman, Md Kaisar (1,2); Karim, Md. Rezaul (3); Hossain, Mohammed Enayet (4); Rahman, Md Ziaur (4); Chawdhury, Md Golam Azam (5); Ferdous, Jinnat (1,2); Hagan, Emily (1); Giasuddin, Md. (3); Flora, Meerjady Sabrina (2); Epstein, Jonathan H (1)

1: EcoHealth Alliance, United States of America -  
2: Institute of Epidemiology, Disease Control and Research (IEDCR), Mohakhali, Dhaka-1212, Bangladesh -  
3: National Reference Laboratory for Avian Influenza (NRL-AI), Bangladesh Livestock Research Institute (BLRI), Savar, Dhaka-1341 -  
4: International Centre for Diarrheal Disease Research, Bangladesh (icddr), Dhaka, Bangladesh -  
5: Central Disease Investigation laboratory, Department of Livestock Services (DLS) -

P040 - OHS A04 - DRIVERS FOR EMERGING DISEASES

### Epidemiology of Brucella sp. antibody in cows of Chittagong Metropolitan Area, Bangladesh: A Prioritized Zoonotic Disease

**Islam, Shariful** (1,2,3); Barua, Shama Ranjan (3,4); Moni, Shahnaj Parvin (3); Rostrat, Melinda K. (1); Islam, Ariful (1,2); Rahman, A. K. M. Anisur (5); Chawdhury, Sharmin (3)

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2: Institute of Epidemiology, Disease Control and Research (IEDCR), Mohakhali, Dhaka-1212 -  
3: Chittagong Veterinary and Animal Sciences University (CVASU), Khulshi, Chittagong-4225 -  
4: Department of Livestock Services, Farmgate, Dhaka, Bangladesh -  
5: Bangladesh Agricultural University, Mymensingh-2202, Bangladesh -

P041 - OHS A04 - DRIVERS FOR EMERGING DISEASES

### Earth observation for environmental surveillance of pathogens

**Jutla, Antar** (1); Colwell, Rita (2)

1: West Virginia University, United States of America -  
2: University of Maryland, College Park -

P042 - OHS A04 - DRIVERS FOR EMERGING DISEASES

### Emergence of Extended Spectrum of $\beta$ -lactamase (ESBL) producing Enterobacteriaceae in migratory birds

**Samad, Mohammed A.** (1); Sagor, Md Shahjalal (1); Hossain, Muhammad Sazzad (1); Karim, Md Rezaul (1); Allied, Md Anamul Hassan (1); Khan, Fahria A (1); Mahmud, Mohammad Asheak (1,2); Miah, Md Sujan (1,2); Ali, Md Zulfekar (1); Giasuddin, Md (1)

1: Zoonoses and EID Laboratory, Animal Health Research Division, Bangladesh Livestock Research Institute, Savar, Dhaka-1341, Bangladesh. -  
2: Department of Microbiology, Jahangirnagar university, Dhaka, Bangladesh -

## VACCINES

P043 - OHS A06 A07- VACCINES

### Development of a mouse model for highly pathogenic avian H5N1 influenza virus

**Gaba, Amit** (1); Lu, Yao (1,3); Landreth, Shelby (1,2); Zhou, Yan (1,2,3)

1: Vaccine and Infectious Disease Organization-International Vaccine center, Canada -  
2: Vaccinology & Immunotherapeutics program, School of Public Health; University of Saskatchewan, Canada -  
3: Department of Veterinary Microbiology, Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, Saskatchewan, Canada -

## SURVEILLANCE AND EARLY DETECTION

P044 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Investigation and monitoring of Brucellosis associated abortion in a dairy cattle farm in Bhutan

**Gurung, Ratna B**; Dukpa, Kinzang

National Centre for Animal Health, Bhutan -

P045 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Contact tracing of dog-bites, disability-adjusted life year score and associated risk of rabies in four Government hospitals of Pakistan.

**Ahmad, Waqas** (1,3); Khan, Iahisham (1); Awais, Muhammad (1); Ali, Muhammad Amjad (2); Maolin, Zhang (3); Liu, Zengshan (3)

1: Section of Epidemiology and Public Health, College of Veterinary and Animal Sciences, Jhang, Pakistan -  
2: Department of Clinical Sciences, Faculty of Veterinary Sciences, Bahauddinzakriya University, Multan, Pakistan -  
3: Key Laboratory of Zoonosis, Ministry of Education, College of Veterinary Medicine, Jilin University, China -

P046 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Flaviviruses detected in wildlife and livestock in South African

**Steyn, Jumari** (1); Botha, Elizabeth (1); Steyl, Johan (2); Williams, June (2); Pretorius, Marthi (1); Stivaktas, Voula (1); Rakgotho, Mpho (1); Venter, Marietjie (1)

1: Department Medical Virology, University of Pretoria, Pretoria, South Africa - 2: University of Pretoria, Paraclinical Sciences, Pretoria, South Africa -

P047 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### **OHPIK (One Health Photography In Kinshasa)**

**Levy, Etienne**, Antoine-Moussiaux, Nicolas; Desmecht, Daniel  
Uliege, Belgium -

P048 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### **Environmental Sampling for the Surveillance of Swine Influenza Virus.**

**Prost, Karren** (1); Kloeze, Harold (2); Mukhi, Shamir (3); Bozek, Katie (1); Mubareka, Samira (1,4)

1: Sunnybrook Research Institute, Canada - 2: Canadian Food Inspection Agency - 3: Public Health Agency of Canada - 4: University of Toronto -

P049 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### **Identification of cereulide producing strains of Bacillus cereus group by MALDI-TOF MS**

**Ulrich, Sebastian** (1); Gottschalk, Christoph (1); Dietrich, Richard (2); Märtlbauer, Erwin (2); Gareis, Manfred (1)

1: Chair of Food Safety, Veterinary Faculty, Ludwig-Maximilians University, Germany - 2: Chair for Hygiene and Technology of Milk, Veterinary Faculty, Ludwig-Maximilians University, Germany -

P050 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### **A scoping review of Middle East respiratory syndrome coronavirus in natural animal hosts**

**Gardner, Emma** G (1,2); Kelton, David (1); Poljak, Zvonimir (1); von Dobschuetz, Sophie (2); Greer, Amy (1)

1: University of Guelph, Canada - 2: Food and Agriculture Organization of the United Nations -

P051 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### **Synchronized surveillance at the wildlife-livestock-human interface in Thailand: a novel approach to early detection of viral transmission across species interfaces**

**Thanapongtharm, Weerapong** (1); Wacharapluesadee, Supaporn (2); Nuansrichay, Bandit (1); Hoonsuwan, Wirongrong (1); Wongsathapornchai, Kachen (3); Claes, Filip (3); Black, Peter (3); Kalpravidh, Wantanee (3); Pornpattananikom, Sonjai (4); Duengkae, Prateep (5); Kaewchot, Supakarn (6); Hemachudha, Thiravat (2); Olival, Kevin J (7); Stokes, Martha (8); Damrongwatanapokin, Sudarat (9); Schar, Daniel L (9)

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P052 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### **Collaborative multiagency approach to melioidosis biopreparedness in Western Australia**

**Inglis, Timothy John Jay** (1,2); Merritt, Adam J (1,2); Buller, Nicky (3)

1: University of Western Australia, Australia - 2: PathWest Laboratory Medicine WA, Australia - 3: Department of Primary Industries and Regional Development, WA, Australia -

P053 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### **Recurrent Anthrax Outbreaks in Human, Livestock and Wildlife in the same Locality, Kenya, 2014-2017**

**Kung'u, Mathew Muturi** (1); Mwatondo, Athman Juma (1); Gachohi, John (2); Njagi, Obadiah (3); Oyas, Harry (3); Njenga, Kariuki (2)

1: Zoonotic Disease Unit, Kenya - 2: Washington State University Global Health Program, Washington State University, Pullman, Washington, USA. - 3: Directorate of Veterinary Services -

P054 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### **Zoonotic and vector borne agents causing disease in adult patients hospitalized due to fever of unknown origin in Thailand**

**Hinjoy, Soawapak** (1); Wacharapluesadee, Supaporn (2); Iamsirithaworn, Sopon (3); Smithsuwan, Punnarai (1); Padungtod, Pawin (4)

1: Bureau of Epidemiology Department of Disease Control, Thailand - 2: WHO Collaborating Center for Research and Training on viral zoonoses, Chulalongkorn University, Thailand - 3: Bureau of General Communicable Diseases, Department of Disease Control, Thailand - 4: Thailand Ministry of Public Health-US CDC Collaboration, Department of Disease Control, -

P055 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### **Environmental Sources of Zoonotic Enteric Parasites in Mongolia**

**Baasandavga, Uyanga** (2,3); Barnes, Amber (1,3); Davaasuren, Anu (3,4); Gonchigoo, Battsetseg (3); Grey, Gregory (1)

1: Duke University, Durham, North Carolina, United States - 2: National center for zoonotic diseases, Mongolia - 3: D43 One Health Team of the Institute of Veterinary Medicine, Ulaanbaatar, Mongolia - 4: The National Center for Communicable Diseases, MOH, Ulaanbaatar, Mongolia -

P056 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### **Community event-based Surveillance by using One Health approach in communities of livestock farmers**

**Smithsuwan, Punnarai** (1); Hinjoy, Soawapak (1); Wongkumma, Arthicha (1); Pinthip, Surachet (2); Kanchai, Khooraphat (3); Chairarnit, Kamon (3); Suphah, Phisit (4); Nakeesang, Apichai (5); Toanan, Wansane (6); Choomkasien, Pravit (1)

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P057 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### **The seropositive of influenza A (pH1N1) in Thai cat**

**Tangwangvivat, Ratanaporn** (1,2,3); Chaiyawong, Supassama (2,3); Nonthabenjawan, Nutthawan (2,3); Janetanakit, Taveesak (2,3); Prakairunnamthip, Duangduean (2,3); Amonsin, Alongkorn (2,3)

1: Coordinating Unit for One Health, Thailand - 2: Faculty of Veterinary Science, Chulalongkorn University - 3: Center of Excellences for Emerging and Re-emerging diseases in animals -

P058 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### **Risk of chronic Q-fever in patients with cardiac valvulopathy, after a large epidemic in the Netherlands: a one-year cross-sectional study**

**Lange, Marit de** (1); Scheepmaker, Arko (2); Hoek, Wim van der (1); Leclercq, Monique (2); Schneeberger, Peter (3)

1: National Institute for Public Health and the Environment, the Netherlands - 2: Bernhoven hospital, the Netherlands - 3: Jeroen Bosch Hospital, the Netherlands -

P059 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### **Characterizing ecological traits of wildlife hosts of zoonotic flaviviruses to identify geographical hotspots for sylvatic transmission**

**Pandit, Pranav Sudhir**; Doyle, Megan; Young, Cristin; Johnson, Christine  
University of California Davis, United States of America -

P060 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### **One Health in China—From SARS to H7N9**

**Lu, Jiahai**  
Sun Yat-sen University, One Health Center of Excellence for Research & Training, China -

P061 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Atlantic Bottlenose Dolphins (*Tursiops truncatus*) as A Sentinel for Exposure to Mercury in Humans: Closing the Loop

**Schaefer, Adam M** (1); Bossart, Greg D (2); Reif, John S (3)

1: Florida Atlantic University, United States of America - 2: Georgia Aquarium, United States - 3: Colorado State University, United States -

P062 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Insights Gained for Surveillance and Biosecurity from the 2015 High Pathogenicity Avian Influenza (HPAI) Outbreaks in the Midwestern U.S.

**Andreasen, Claire B**; Roth, James A  
Iowa State University College of Veterinary Medicine, United States of America -

P063 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Surveillance on Crimean-Congo Hemorrhagic Fever in Georgia

**Chakhunashvili, Giorgi**; Mamuchishvili, Nana; Babuadze, Giorgi; Tsereteli, David; Zakhshvili, Khatuna; Chanturia, Gvantsa; Imnadze, Paata

National Center for Disease Control and Public Health, Georgia -

P064 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### First study of Enterovirus typing by partial sequencing of VP1 gene in Georgia

**Dgebuadze, Magda**; Kutateladze, Tamar; Urushadze, Lela; Murckhvaladze, Mariam  
National Center for disease Control and public Health, Georgia -

P065 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Diversity and potential risk of dissemination of zoonotic pathogens associated with insectivorous bats in Georgia

**Urushadze, Lela**

National Center for Disease control and Public health, Georgia -

P066 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Monitoring of zoonotic agents along the food chain - a valuable risk management tool

**Lorenz, Klaus**; Pfefferkorn, Beatrice

Federal Office of Consumer Protection and Food Safety, Germany -

P067 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Territorial model of integrated epidemiological surveillance

Andryan, Armine

"Shirak" branch, National Center for Disease Control and Prevention SNCO, Ministry of Health, Gjumry, Republic of Armenia -

P068 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### The Canadian Food Inspection Agency strategy to face potential contamination of raw shellfish and associated illnesses

**Lucas, Annie**; Eloranta, Katie; White, John; Elmufiti, Mohamed

Canadian Food Inspection Agency, Canada -

P069 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Wildlife influences on the social determinants of health - key to climate change preparedness

**Stephen, Craig**; Reeder, Bruce

University of Saskatchewan, Canada -

P070 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### A One Health Approach Arbovirus Surveillance in the Atlantic Forest, Brazil

**Catenacci, Lilian Silva** (1,2,3,5); Ferreira, Milene (1); Fernandes, Debora (1); Martins, Livia (1); Deem, Sharon (3); Padda, Hannah (4); De Vleeschouwer, Kristel (5); Cassano, Camila (6); Oliveira, Leonardo (7); Canale, Gustavo (8); Cruz, Thito (1); Cruz, Ana Cecilia (1); Casseb, Samir (1); Vasconcelos, Pedro (1); Travassos da Rosa, Elizabeth (1)

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P071 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Characterizing the performance of avian influenza A(H9N2) surveillance from fecal samples and drinking water in live poultry markets

**Lau, Eric HY**; Zhang, Shengqiu; Leung, Connie; Cowling, Benjamin J; Wu, Joseph T; Peiris, Malik

The University of Hong Kong, Hong Kong S.A.R. (China) -

P072 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Implementation of One Health approach in Sciensano a new Belgian research centre for public and veterinary health

**Koenen, Frank Geert** (1); Kerkhofs, Pierre (1); Dierick, Katelijne (2); Sneyers, Myriam (2)

1: CODA-CERVA, Belgium - 2: WIV-ISP, Belgium -

P073 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Factors associated with willingness to test drinking well water for E. coli in rural Alberta.

**Hall, David Clement** (1); Munene, Abraham (1); Checkley, Sylvia (1); Wuite, Jamie (2); Neumann, Norman (3)

1: University of Calgary - 2: Alberta Agriculture and Forestry - 3: University of Alberta -

P074 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Investigation of Middelburgvirus, an African alphavirus, as cause of febrile and neurological disease outbreaks in horses, wildlife and humans following unusual high rainfall in South Africa, 2017

**Venter, Maria** (1); Fourie, Isabel (1); Steyn, Jumarie (1); Rakgotho, Mpho (1); Williams, June (1,2)

1: Centre for Viral Zoonoses, University of Pretoria, South Africa - 2: Paraclinical Sciences, Faculty of Veterinary Science -

P075 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### A One Health approach to detection of contamination in private well water systems in Western Canada

**Caffrey, Niamh** (1); Neumann, Norman (2); Scott, Candis (2); Banting, Graham (2); Checkley, Sylvia (1,3)

1: Faculty of Veterinary Medicine, University of Calgary - 2: School of Public Health, University of Alberta - 3: Provincial Laboratory for Public Health, Alberta -

P076 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Environmental Suitability and Predicted Distribution of Aedes Albopictus Mosquitoes in Canada and the United States: Assessing Arboviral Risks in North America

**Khan, Salah Uddin** (1,2); Ogden, Nicholas H. (2); Fazil, Aamir (2); Greer, Amy L. (1); Ng, Victoria (2)

1: Department of Population Medicine, University of Guelph - 2: National Microbiology Laboratory, Public Health Agency of Canada -

P077 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Formation of a national task force in response to the emerging infectious diseases in uganda: a case of the CCHF outbreak in Kiboga district.

**Namatovu, Carolyn Kisinga** (1); Ndumu, Deo. B. (1); Wejuli, Alfred (1); Kizito, Susan (2); Kagirita, Atek (3)

1: National Animal Disease Diagnostics and Epidemiology Centre (NADDEC)/MAAIF, Uganda - 2: Public Health Fellow, CDC-Uganda - 3: Central Public Health Laboratories, Uganda -

P078 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Investigation of Aedes mosquitoes as arbovirus vectors at sentinel sites in Gauteng, Limpopo, Mpumalanga and Kwazulu-Natal provinces, South Africa (2015-2017)

**Guarido, Milehna Mara** (1); Johnson, Todd (2); Rakgotho, Mpho (3); Fourie, Isabel (4); Smit, Aneliza (5); Braack, Leo (6); Almeida, A. Paulo G. (7); Venter, Marietjie (8)

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**P079 - OHS B01 - SURVEILLANCE AND EARLY DETECTION**

### Detection of novel reassortants of highly pathogenic avian H5 influenza strains in an outbreak situation

**Pohlmann, Anne**; Harder, Timm; Koethe, Susanne; Grund, Christian; Globig, Anja; Staubach, Christoph; Conraths, Franz J.; Beer, Martin

Friedrich-Loeffler-Institut, Greifswald - Isle of Riems, Germany -

**P080 - OHS B01 - SURVEILLANCE AND EARLY DETECTION**

### Linking Human and Animal Notifiable Zoonotic Disease Data in Washington State

**McConnell, Kate** (1); Buswell, Minden (2); Oltean, Hanna (3); Pappaioanou, Marguerite (1); Rabinowitz, Peter (1)

1: University of Washington School of Public Health, Seattle, Washington, USA - 2: Washington State Department of Agriculture, Olympia, Washington, USA - 3: Washington State Department of Health, Shoreline, Washington, USA -

**P081 - OHS B01 - SURVEILLANCE AND EARLY DETECTION**

### Mobile phone based surveillance for animal disease in rural communities: implications for detection of emerging zoonoses

**Thumbi, S M** (1,2); Njenga, M Kariuki (1,2); Otiang, Elkanah (2); Munyua, Peninah (3); Widdowson, Marc-Alain (3,4); McElwain, Terry F (1); Palmer, Guy H (1)

1: Paul G Allen School for Global Animal Health, Washington State University, US - 2: Center for Global Health Research, Kenya Medical Research Institute, Kenya - 3: Division of Global Health Protection, Centers for Disease Control and Prevention, Nairobi, Kenya - 4: Division of Global Health Protection, Centers for Disease Control and Prevention, Atlanta, Georgia, USA -

**P082 - OHS B01 - SURVEILLANCE AND EARLY DETECTION**

### A near real-time livestock-wildlife syndromic surveillance system for early detection and response to biological threats in Kenya

**Munyua, Peninah M** (1); Kemunto, Naomi (2); Oyas, Harry (3); Gakuya, Francis (4); Muturi, Mathew (3,5); Mwatondo, Athman (6); Bitek, Austine (7); kahariri, Samuel (3); Biggers, Keith (8); Beckham, Tammy (9); Chinyere, Ekechi (1); Mwangi, Thumbi (2); Njagi, Obadiah (3); Widdowson, Marc-Alain (1); Holmstrom, Lindsey (10); Njenga, Kariuki (2)

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**P083 - OHS B01 - SURVEILLANCE AND EARLY DETECTION**

### Seroprevalence and Risk Factors of Toxoplasma gondii Exposure in Small Ruminants in Ontario, Canada

**Meadows, Shannon L** (1); Shapiro, Karen (1,2); Packham, Andrea (2); Jansen, Jocelyn (3); Jones-Bitton, Andria (1); Menzies, Paula (1)

1: University of Guelph, Canada - 2: University of California, Davis - 3: Ontario Ministry of Agriculture and Food, and Rural Affairs -

**P084 - OHS B01 - SURVEILLANCE AND EARLY DETECTION**

### Evaluation for One Health in action – Enhancing animal disease surveillance systems in Africa

Lamielle, Gaël (1); **VonDobschuett, Sophie** (1); Aguanno, Ryan (1); Okuthe, Sam (1); Ruiz, Magali (2); Dhingra, Madhur (1); Bernard-Stoeklin, Sibylle (3); Bessin, René (1); Folorunso, Fasina (1); Mtui, Niwael (1); Sallu, Raphael (1); Kaboré, Youssouf (1)

1: Food and Agriculture Organization of the United Nation, Italy - 2: Solthis - 3: Santé Publique France -

**P085 - OHS B01 - SURVEILLANCE AND EARLY DETECTION**

### Microbial diversity analysis for pollution source tracking of a Michigan sub-watershed

**Wu, Huiyun** (1); Oun, Amira (2); Kline-Robach, Ruth (1); Xagorarakis, Irene (1)

1: Michigan State University, United States of America - 2: Department of Environmental Quality, State of Michigan, United States of America -

**P086 - OHS B01 - SURVEILLANCE AND EARLY DETECTION**

### Exploring the zoonotic risk in the general population, and among farmers and veterinarians in Western France: what are the prevalence and risk factors for Coxiella burnetii infection (Q fever)?

**Pouquet, Marie** (1,2); Moret, Leïla (2); Beaudeau, François (1)

1: BIOEPAR, Oniris-INRA, Nantes, France - 2: Public Health Department, University Hospital, Nantes, France -

**P087 - OHS B01 - SURVEILLANCE AND EARLY DETECTION**

### Using satellite imagery and GIS data to help predict disease spread

**Randhawa, Nistara** (1); Mailhot, Hugo (2); Martínez-López, Beatriz (3); Mazet, Jonna A.K. (1)

1: One Health Institute, School of Veterinary Medicine, University of California - Davis, USA - 2: University of California - Davis, USA - 3: Center for Animal Disease Modeling and Surveillance, School of Veterinary Medicine, University of California - Davis, USA -

**P088 - OHS B01 - SURVEILLANCE AND EARLY DETECTION**

### Bats and viruses in Western Asia: a model for One Health surveillance using research coordination networks

Olival, Kevin J. (1); Alhmoud, Nisreen (2); Sidamonidze, Ketii (3); Urushadze, Lela (3); Epstein, Jonathan H. (1); Phelps, Kendra (1); Hamel, Luke (1); **Karesh, William** (1)

1: EcoHealth Alliance, United States of America - 2: Royal Scientific Society, Amman, Jordan - 3: R. Lugar Center, National Center for Disease Control, Tbilisi, Georgia -

**P089 - OHS B01 - SURVEILLANCE AND EARLY DETECTION**

### Using microbiome community structure analysis to characterize zoonotic microbial transmission at the human-macaque interface in Northeast Thailand

Grant, Erica T. (1); Kyes, Randall C. (2); Kyes, Pensri (2); Trinh, Pauline (1); Ramirez, Vickie (1); Schurer, Janna M. (1); **Rabinowitz, Peter** (1)

1: Center for One Health Research, University of Washington, Seattle, USA - 2: Department of Psychology, Center for Global Field Study, WaNPRC, University of Washington, Seattle, USA -

**P090 - OHS B01 - SURVEILLANCE AND EARLY DETECTION**

### Developing an Animal Exposure History Tool for Physicians-In-Training to Improve Detection of Zoonotic Disease

**Tin MPH, Alice H.** (1); Rabinowitz MD MPH, Peter (2)

1: Warren Alpert Medical School of Brown University, United States of America - 2: Center for One Health Research, University of Washington School of Medicine, United States of America -

P091 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Investigation of a Bonobo die-off Event of unknown origin at the “Lola ya Bonobo” Sanctuary IN Kinshasa, DRC, 2015-2016

**Kumakamba, Charles** (1); Belais, Raphael (2); Kisile, O (4); Nkawa, Frida (1); Ngay, Ipos (1); Gillis, Amethyst (1); Cranfield, Michael (3); Mbala, Placide (1); Makuwa, Maria (1); Mulembakani, Prime (1); Saylor, Karen (1); Muyembe-Tamfum, Jean-Jacques (5)

1: Metabiota Inc - 2: Lola Ya Bonobo, Kinshasa - 3: Mountain Gorilla Veterinary Project (MGVP), Goma, DRC - 4: Pathology Department of the University of Kinshasa, DRC - 5: Institut National de Recherche Biomedicale, Kinshasa, DRC -

P092 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

### Mapping the Distribution and Abundance of Major Zoonotic Diseases in South Tigray, North Wollo and Ab’ala (Afar), Ethiopia

**Menghistu, Habtamu Taddele**

Mekelle University, College of Veterinary Medicine, Mekelle, Ethiopia, Ethiopia -

## INTERVENTION STRATEGIES

P093 - OHS B02 - INTERVENTION STRATEGIES

### Should ecological approaches be used to manage the risk of Hendra virus spill-overs? - A report on two citizens’ juries

**Degeling, Chris** (1,2); Johnson, Jane (2,3); Annand, Ed (2); Taylor, Mel (3); Walsh, Michael (2,4); Ward, Michael (2); Gilbert, Gwendolyn (2,4)

1: University of Wollongong, Australia - 2: University of Sydney, Australia - 3: Macquarie University, Australia - 4: Marie Bashir Institute, Australia -

P094 - OHS B02 - INTERVENTION STRATEGIES

### Impact of nutrition therapy program on the global acute malnutrition in three counties- an experience in a war-torn lakes state of South Sudan.

**Daniel, Ebenezer Obi** (1); Amosu, Ademola M. (2); Ayeni, Gabriel Omoniyi (3); Olagbegi, Michael Oladapo (4)

1: Doctors with Africa-CUAMM, Lakes State South Sudan - 2: Babcock University Ilishan-Remo, Ogun state Nigeria - 3: Texila American University Guyana - 4: Rhodes University, South Africa -

P095 - OHS B02 - INTERVENTION STRATEGIES

### Brazilian initiative to guarantee the Human Right to Adequate Food with sustainable food production

Costa Polveiro, Richard (1); Bevenuto Mattar, Jéssica (2); Ferreira Tavares, Juliana (2); Torres Furtado Martins, Bruna (1); de Melo Tavares, Rafaela (1); Rodrigues Alves, Samuel (1); Scatamburlo Moreira, Maria Aparecida (1); Nero, Luis Augusto (1); **Pettan-Brewer, Christina** (3)

1: Department of Medicine Veterinary, Universidade Federal de Viçosa-Minas Gerais, Brasil - 2: Department of Nutrition and Health, Universidade Federal de Viçosa-Minas Gerais, Brasil 3: Department of - 3: Department of Comparative Medicine, School of Medicine, University of Washington, Seattle WA -

P096 - OHS B02 - INTERVENTION STRATEGIES

### One Health National Programme for rabies control and eradication 2017-2021

Nguyen, Hang Thuy (1); Padungtod, Pawin (1); Van Dang, Ky (1); Nguyen Ngoc, Tien (2); **Nguyen Thi Thanh, Huong** (3); Nguyen Tran, Hien (3)

1: Food and Agriculture Organization of the United Nations (FAO) Viet Nam - 2: Viet Nam Department of Animal Health - 3: National Institute of Hygiene and Epidemiology, Viet Nam -

P097 - OHS B02 - INTERVENTION STRATEGIES

### An integrated health delivery platform, targeting soil-transmitted helminths (STH) and canine mediated rabies, results in cost savings and increased breadth of treatment coverage for STH in remote communities in Tanzania

**Lankester, Felix John** (1); Davis, Alicia (2); Kinung’hi, Safari (3); Bunga, Catherine (3); Alkara, Shayo (4); Mzimhiri, Imam (4); Yoder, Jonathan (1); Cleaveland, Sarah (2); Palmer, Guy (1)

1: Washington State University, United States of America - 2: University of Glasgow, United Kingdom - 3: National Institute of Medical Research, Tanzania - 4: Global Animal Health Tanzania -

P098 - OHS B02 - INTERVENTION STRATEGIES

### Community Perceptions on Integrating Animal Vaccination and Health Education by Veterinary and Public Health Workers in the Prevention of Brucellosis among pastoral Communities of South Western Uganda

**Kansiime, Catherine** (1); Atuyambe, Lynn M (1); Guma, Victor (1); Mugisha, Anthony (1); Mugisha, Samuel (1); Asiimwe, Benon (1); Rwego, Innocent (1,2); Rutebemberwa, Elizeus (1)

1: Makerere University School of Public Health, Uganda - 2: University of Minnesota, St. Paul, MN, USA -

P099 - OHS B02 - INTERVENTION STRATEGIES

### Estimation of the cost of rabies to society in West and Central Africa and elaboration of the cost of rabies elimination in Africa

**Ndour, Andrée Prisca Ndjoug** (1,2); Mbaruku, Godfrey (1,3); Bada Alamedjji, Rianatou (2); Lechenne, Monique (1,4,5); Akakpo, Ayayi Justin (1,2); Bonfoh, Bassirou (1,6)

1: Afrique One ASPIRE - 2: Ecole Inter-Etats des Sciences et Médecine Vétérinaires (EISMV) de Dakar, Senegal - 3: Ifakara Health Institute (IHI), Tanzania - 4: Swiss Tropical and Public Health Institut (Swiss TPH), Switzerland - 5: Laboratoire de recherches zootechniques et vétérinaires de Farcha, Chad - 6: Centre Suisse de Recherches Scientifiques en Côte d’Ivoire (CSRS) -

P100 - OHS B02 - INTERVENTION STRATEGIES

### Describing and modelling livestock movements in northern Tanzania and the implications for the transmission of endemic zoonoses

Chaters, Gemma Louise (1); **Johnson, Paul** (1); Kao, Rowland (2); de Glanville, Will (1); Matthews, Louise (1)

1: University of Glasgow, United Kingdom - 2: University of Edinburgh, United Kingdom -

P101 - OHS B02 - INTERVENTION STRATEGIES

### Evaluation of a one health response to an outbreak of highly pathogenic avian influenza in the Western Cape province of South Africa

**van Helden, Lesley Susan** (1); Cousins, Thomas (2); Pentecost, Michelle (3)

1: Western Cape Department of Agriculture, South Africa - 2: Institute for Social and Cultural Anthropology, University of Oxford - 3: Department of Global Health and Social Medicine, Kings College London -

P102 - OHS B02 - INTERVENTION STRATEGIES

### First “Global Flipped Classroom in One Health”: From MOOCs to research on real world challenges

**Ruiz de Castaneda, Rafael** (1); Garrison, Amanda (1); Haeberli, Philippe (2); Crump, Lisa (3); Zinsstag, Jakob (3); Ravel, Andre (4); Flahault, Antoine (1); Bolon, Isabelle (1)

1: Institute of Global Health, Faculty of Medicine, University of Geneva, Switzerland - 2: Pôle de soutien à l’enseignement et l’apprentissage, University of Geneva (Switzerland) - 3: Swiss Tropical and Public Health Institute, University of Basel (Switzerland) - 4: Faculty of Veterinary Medicine, University of Montreal (Canada) -

P103 - OHS B02 - INTERVENTION STRATEGIES

### The first MOOC on Global Health at the Human-Animal-Ecosystem Interface: Two years of innovative activities since the International One Health Congress 2016

**Bolon, Isabelle**; Ruiz de Castaneda, Rafael; Flahault, Antoine

Institute of Global Health, Faculty of Medicine, University of Geneva, Switzerland -

P104 - OHS B02 - INTERVENTION STRATEGIES

### Assessment of IHR core capacities to prevent, detect and respond to zoonotic diseases in South Africa

**Ramkrishna, Wayne**; Ndala, Paul; Moonasar, Devanand

National Department of Health - South Africa, South Africa -

## P105 - OHS B02 - INTERVENTION STRATEGIES

**Brucellosis in northern Tanzania: insights into human disease prevalence, multi-species transmission processes and the design of sustainable interventions**

**Halliday, Jo** (1); Lukumbagire, Abdul-Hamid (2); Bodenham, Rebecca (1); Ashford, Roland (3); Buza, Joram (4); Crump, John (5); Kazwala, Rudovick (2); Maro, Venance (6); Mmbaga, Blandina (7); Mkenda, Nestory (8); Perrett, Lorraine (3); Rubach, Matthew (9); Sakasaka, Philoteus (7); Swai, Emanuel (10); Thomas, Kate (5); Viana, Mafalda (1); Whatmore, Adrian (3); Shirima, Gabriel (4); Haydon, Dan (1)

1: The Boyd Orr Centre for Population and Ecosystem Health, Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow, UK - 2: Sokoine University of Agriculture, Tanzania - 3: Animal and Plant Health Agency, Weybridge, UK - 4: Nelson Mandela African Institution for Science and Technology, Arusha, Tanzania - 5: Centre for International Health, University of Otago, Dunedin, New Zealand - 6: Kilimanjaro Christian Medical Centre, Moshi, Tanzania - 7: Kilimanjaro Clinical Research Institute, Moshi, Tanzania - 8: Enduleni Hospital, Ngorongoro Conservation Area, Tanzania - 9: Duke Global Health Institute, Duke University, Durham, North Carolina, USA - 10: Directorate of Veterinary Services, Dodoma, Tanzania -

## P106 - OHS B02 - INTERVENTION STRATEGIES

**The role of West African rodents in the transmission of zoonotic schistosomes: spillover or reservoir hosts?**

**Catalano, Stefano** (1); Léger, Elsa (1); Fall, Cheikh B. (2); Borlase, Anna (1); Diop, Samba D. (3); Sène, Mariama (4); Diouf, Nicolas D. (3,4); Bâ, Khalilou (5); Webster, Joanne P. (1)

1: Centre for Emerging, Endemic and Exotic Diseases (CEEED), Department of Pathobiology and Population Sciences, The Royal Veterinary College, University of London, Hatfield, United Kingdom - 2: Faculté de Médecine, de Pharmacie et d'Odontologie, Université Cheikh Anta Diop, Dakar, Senegal - 3: Institut Supérieur de Formation Agricole et Rurale (ISFAR), Université de Thiès, Bambey, Senegal - 4: Unité de Formation et de Recherche (UFR) des Sciences Agronomiques, d'Aquaculture et de Technologies Alimentaires (S2ATA), Université Gaston Berger, Saint-Louis, Senegal - 5: DepartmCentre de Biologie et de Gestion des Populations, Institut de Recherche pour le Développement, Campus ISRA-IRD Bel Air, Dakar, Senegal -

## P107 - OHS B02 - INTERVENTION STRATEGIES

**One health based Outbreak investigation of unknown diseases linked to consumption of raw wild boar meat in Guto Gida district, East Wollega of Western Ethiopia in 2017.**

**Mekonta, Dechassa Tegegne** (1); Deressa, Benti (1); Havas, Karyn (2); Woldemichael, Kifle (1)

1: Jimma University, Ethiopia - 2: Cornell University, USA -

## P108 - OHS B02 - INTERVENTION STRATEGIES

**Generating evidence for one-health policies: An expert elicitation to assess the monetary impact of zoonotic diseases on society in Ethiopia**

**Mirkena, Tadele** (1); Mikecz, Orsolya (2); Cherenet, Thomas (3); Deressa, Asefa (4); Pica-Ciamarra, Ugo (2)

1: Food and Agriculture Organization of the United Nations (FAO), Ethiopia - 2: Food and Agriculture Organization of the United Nations (FAO), Rome - 3: Ministry of Livestock and Fisheries, Ethiopia - 4: Ethiopian Public Health Institute, Ministry of Health, Ethiopia -

## P109 - OHS B02 - INTERVENTION STRATEGIES

**A realist review of the impact of sterilisation in canine rabies control programs: What works, for whom and under what circumstances?**

**Collinson, Abi**; Dean, Rachel; Bennett, Malcolm; Stavisky, Jenny  
University of Nottingham, United Kingdom -

## P110 - OHS B02 - INTERVENTION STRATEGIES

**Global One Health Research, The Future**

**Van der Poel, Wim H.M.** (1); Zwietering, Marcel H. (2)

1: Wageningen University and Research, Netherlands, The - 2: Wageningen University, Netherlands, The -

## P111 - OHS B02 - INTERVENTION STRATEGIES

**Multi-Sectoral Involvement in Joint Cross-Border Disease Control Program in East Africa**

**Were, Willy Abwoka** (1); Matu, Martin (1); Mushi, Benedict (1); Makayotto, Lyndah (2); Lubwama, Bernard (3); Kagirita, Atek (3); Ndayikunda, Claudette (4); Mbagi, Vida (5); Sonoiya, Stanley (6); Schneidman, Miriam (7)

1: East, Central and Southern Africa Health Community, Tanzania - 2: Ministry of Health, Kenya - 3: Ministry of Health, Uganda - 4: Ministry of Health and Fight Against HIV, Burundi - 5: Ministry of Health, Community Development, Gender, Elderly & Children, Tanzania - 6: East African Community Secretariat, Tanzania - 7: The World Bank -

## P112 - OHS B02 - INTERVENTION STRATEGIES

**Building an Operational One Health Competency Based Education Framework**

**Macy, Katelyn Wuebbolt** (1); Dutcher, Tracey (2); Kircher, Amy (3); Pelican, Katey (1)

1: USAID-Funded One Health Workforce, Department of Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota - 2: Veterinary Services, APHIS, U.S. Department of Agriculture - 3: Food Protection and Defense Institute, University of Minnesota -

## P113 - OHS B02 - INTERVENTION STRATEGIES

**Causal inference and One Health interventions: the need for epidemiologic methods**

Meisner, Julianne (1,2); **Rabinowitz, Peter** (2,3)

1: Department of Epidemiology, University of Washington, United States of America - 2: Center for One Health Research, University of Washington, United States of America - 3: Department of Environmental and Occupational Health Sciences, University of Washington, United States of America -

## P114 - OHS B02 - INTERVENTION STRATEGIES

**Afrique One-ASPIRE: Bridging the gap in translation of One Health research to public policy in Africa**

**Adou, Djané Dit Fatogoma** (1); Alibu, Vincent Pius (2)

1: Centre Suisse de Recherches Scientifiques en Côte d'Ivoire, Côte d'Ivoire - 2: Makerere University Kampala, Uganda -

## P115 - OHS B02 - INTERVENTION STRATEGIES

**Educating children about One Health**

Vesterlund-Carlsson, Catrin (1); Engström, Lizbeth (2); Troell, Karin (1); Lindberg, Anna (1,2); Ferrari, Sevinc (1); **Strand, Tanja Maria** (1); Artursson, Karin (1)

1: National Veterinary Institute, Sweden - 2: Uppsala University, Sweden -

## P116 - OHS B02 - INTERVENTION STRATEGIES

**ONE HEALTH – A Practitioner's Viewpoint**

**Love, David Moody**

DM & J Love, Switzerland -

## P117 - OHS B02 - INTERVENTION STRATEGIES

**The growth and functioning of One Health Networks: A systematic analysis**

**S. Khan, Mishal** (1); Rothman-Ostrow, Peregrine (1); Spencer, Julia (2); Hasan, Nadeem (2); Sabirovic, Mirzet (2); Rahman-Shepherd, Afifah (2); Shaikh, Nabila (2); Dar, Osman (2)

1: London School of Hygiene & Tropical Medicine, United Kingdom - 2: Chatham House (the Royal Institute of International Affairs), United Kingdom -

## P118 - OHS B02 - INTERVENTION STRATEGIES

**Creating a network of emerging One Health leaders from Rwanda: Tufts-UGHE-UR One Health Fellowship Program**

**Amuguni, Janetrix Hellen** (1); Chase, Sharon (1); Trent, Sarah (2); Logan, Jenae (2); Henley, Phaedra (2); Ntawubizi, Martin (3); Gashumba, James (3); Kibuuka, Robert (3); Shyaka, Anselme (3); Binagwaho, Agnes (2); Kochevar, Deborah (1)

1: Cummings School of Veterinary Medicine at Tufts University, United States of America - 2: University of Global Health Equity, Rwanda - 3: University of Rwanda -

## P119 - OHS B02 - INTERVENTION STRATEGIES

**Strengthening capacity of bio-risk management in Central and Eastern Africa Using a One Health approach**

**Naigaga, Irene** (1); Wakabi, Timothy (2); Yawe, Agnes (3); Bokaako, Winnie (4); Kabasa, John David (5); Bazeyo, William (6)



1: One Health Central and Eastern Africa, Uganda  
 - 2: One Health Central and Eastern Africa, Uganda  
 - 3: One Health Central and Eastern Africa, Uganda  
 - 4: One Health Central and Eastern Africa, Uganda  
 - 5: Makerere University - 6: Makerere University -

P120 - OHS B02 - INTERVENTION STRATEGIES

## One Health @ University of Florida

**Munoz, Olga**, Agnelli, Sara; Gollakner, Rania; Mavian, Carla; Prosperi, Mattia; Salemi, Marco; Sabo-Attwood, Tara; Capua, Ilaria  
 University of Florida, United States of America -

P121 - OHS B02 - INTERVENTION STRATEGIES

## Students' leadership in breaking disciplinary silos

**Wakabi, Timothy Waiswa**, Naigaga, Irene; Alunguru, Elizabeth; Bikaako, Winnie; Nitumusima, Sarah; Nattimba, Milly  
 One Health Central and Eastern Africa, Uganda -

P122 - OHS B02 - INTERVENTION STRATEGIES

## Human Interactions with Bat Populations in Bombali, Sierra Leone: Implications for Zoonotic Disease Risk Mitigation among Bat Hunters and Residents with Household Infestations (USAID PREDICT-2)

**Euren, Jason** (1); Bangura, James (2); Gbakima, Aiah (2); Sinah, Marilyn (2); Yonda, Sylvester (2); Saylor, Karen (1)

1: Metabiota, United States of America - 2: UC Davis -

P123 - OHS B02 - INTERVENTION STRATEGIES

## Workforce planning using the OHS SMART tool in five One Health for Central and Eastern Africa (OHCEA) countries in Africa

**Wanzala, Sylvia Irene** (1); Macy, Katelyn (1); Yawe, Agnes (2); Naigaga, Irene (2); Rwego, Innocent (1); Bazeyo, William (2); Kabasa, John David (2); Errecaborde, Kaylee Myhre (1); Njajou, Omer (1); Vesterinen, Heidi (1); McMillen, Amy (1); Tzipori, Saul (3); Bender, Jeffery (1); Dutcher, Tracey Bruett (4); Pelican, Katherine (1)

1: University of Minnesota, United States of America - 2: One Health for Central and Eastern Africa - 3: Tufts University - 4: United States Department of Agriculture -

## PATHOGENESIS

P124 - OHS B03 B05 - PATHOGENESIS

## Immunopathological variations in brain tissues of mice and dogs infected with street and fixed strains of rabies virus

**Ahmad, Waqas** (1,2); Maolin, Zhang (2); Liu, Zengshan (2); Khan, lahtasham (1); Awais, Muhammad (1)

1: Section of Epidemiology and Public Health, College of Veterinary and Animal Sciences, Jhang Campus, Pakistan - 2: Key Laboratory of Zoonosis, Ministry of Education, College of Veterinary Medicine, Jilin University, China -

P125 - OHS B03 B05 - PATHOGENESIS

## Fluorescent Isothiocyanate Dextran evaluates the permeability of blood-brain barrier in rabies infected brain of mice

**Ahmad, Waqas** (1,2); Liu, Xinyue (2); Guan, Zhenhong (2); Duan, Ming (2); Maolin, Zhang (2); Khan, lahtasham (1); Awais, Muhammad (1); Ali, Muhammad Amjad (3)

1: Section of Epidemiology and Public Health, College of Veterinary and Animal Sciences, 12-Kilometer, Chiniot Road, Jhang, Pakistan - 2: Key Laboratory of Zoonosis Research, Ministry of Education, Institute of Zoonosis, College of Veterinary Medicine, Jilin University, Changchun 130062, China - 3: Department of Clinical Sciences, Faculty of Veterinary Sciences, BahauddinZakriya University, Multan, Pakistan -

P126 - OHS B03 B05 - PATHOGENESIS

## Screening and distribution of different genes related to cytoskeleton and neuronal transmitters in hippocampus under rabies infection

**Ahmad, Waqas** (1,2); Bin, Qiao (2); Guan, Zhenhong (2); Duan, Ming (2); Maolin, Zhang (2); Khan, lahtasham (1); Awais, Muhammad (1); Ali, Muhammad Amjad (3)

1: Section of Epidemiology and Public Health, College of Veterinary and Animal Sciences, Jhang, Pakistan - 2: Key Laboratory of Zoonosis Research, Ministry of Education, Institute of Zoonosis, College of Veterinary Medicine, Jilin University, Changchun 130062, China - 3: Department of Clinical Sciences, Faculty of Veterinary Sciences, BahauddinZakriya University, Multan, Pakistan -

## ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

P127 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

## Critical Evaluation of Maternal Health Program in Balasore District, Odisha (India)

**Dehury, Ranjit Kumar**

Goa Institute of Management Panaji, India -

P128 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

## Economic analysis of zoonotic diseases in Bangladesh

Ferdous, Jinnat (1,2); **Islam, Ariful** (1,2); Machalaba, Catherine (2); Feferholtz, Yasha (2); Hagan, Emily (2); Sharif, Ahmed Raihan (1); Berthe, Franck C.J. (3); Daszak, Peter (2); Karesh, William B. (2); Flora, Meerjady Sabrina (1)

1: Institute of Epidemiology, Disease Control & Research, Bangladesh, People's Republic of - 2: EcoHealth Alliance, NewYork, USA - 3: World Bank, Washington D.C., USA -

P129 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

## Preliminary insights on tuberculosis transmission between and among mahouts and captive elephants

**Abraham, David** (1); Kummannor Parameswaran Pillai, Venugopal (2)

1: Assistant Forest Veterinary Officer, Kerala Forests and Wildlife Department, India - 2: Associate Professor, Kottayam Government Medical College Hospital, Kerala, India -

P130 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

## National early infant diagnosis coverages and socio-health indicators: an ecological regression analysis of 33 low and middle-income countries.

**Adeyinka, Daniel Adedayo** (1,2); Olakunde, Babayemi (3); Morka, Mercy (1); Oladimeji, Olanrewaju (4,5); Adeyinka, Esther F (6); Ilesanmi, Oluwafunke (7); Ozigbu, Chamberline E (1,8)

1: University of Saskatchewan, Canada - 2: National AIDS & STIs Control Programme, Department of Public Health, Federal Ministry of Health, FCT Abuja, Nigeria - 3: National Agency for the Control of AIDS, Abuja, Nigeria - 4: Department of Public Health Medicine, College of Health Science, University of Kwazulu-natal, Durban, South Africa - 5: Centre for Community Health Care, Research and Development, FCT Abuja, Nigeria - 6: Obafemi Awolowo University, Ile-Ife, Nigeria - 7: World Health Organization (WHO), FCT Abuja, Nigeria - 8: University of South Carolina, Columbia, United States -

P131 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

## Anti-rabies vaccination campaign for pets in a community living below the poverty line in poor neighborhoods in Lubumbashi, Democratic Republic of Congo

**Abdallah, Ngona Idi** (1); Aline, Ngomb Kazad (2); Alain, Numbi Malale (1); Esther, Khang Imvar (2); Enoch, Mavanga (3); Nathalie, Nseye Kalala (4)

1: University of Lubumbashi, Congo, Democratic Republic of the - 2: Institut Supérieur des Techniques Médicales de Lubumbashi (Nursing High School), Lubumbashi, Congo, Democratic Republic of the - 3: State Veterinary Laboratory, Lubumbashi, Congo, Democratic Republic of the - 4: Lubumbashi Vaccine Office, Congo, Democratic Republic of the -

P132 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

## Multi-Sectoral prioritization of zoonotic diseases in Uganda, 2017: The perspective of One Health experts

**Sekamatte, Musa**

Ministry of Health, Uganda -

P133 - OHS B04 -  
ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### **Anthrax impacts on the health and livelihoods of impoverished communities**

**Aminu, O. Rhoda** (1,2); Forde, Taya (1); Biek, Roman (1); Zadoks, Ruth (1); Kiwelu, Ireen (3); Mkenda, Nestory (4); Mmbaga, Blandina (3); Mshanga, Deogratus (5); Ole Moko, Sabore (6); Shirima, Gabriel (2); Lembo, Tiziana (1)

1: University of Glasgow, United Kingdom -  
2: Nelson Mandela African Institution of Science and Technology, P.O. Box 447, Arusha, Tanzania -  
3: Kilimanjaro Clinical Research Institute, Box 2236, Moshi, Tanzania - 4: Endulen Hospital, Ngorongoro Conservation Area, Tanzania - 5: Tanzania Veterinary Laboratory Agency, Northern Zone, Box 1068, Arusha, Tanzania - 6: Endulen, Ngorongoro Conservation Area, Tanzania -

P134 - OHS B04 -  
ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### **Innovation of an improved tippy tap**

**Ninsiima, Lesley rose**; Luyiga, Annet Mary  
One health central and eastern Africa, Uganda -

P135 - OHS B04 -  
ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### **Evidence of exposure to Brucella among humans and cows in Shahjadpur sub-district, a high milk-producing area in Bangladesh**

Shanta, Ireen Sultana (1); Heffelfinger, James D (2); Kafi, Mohammad Abdullah Heel (1); Ahmed, Firoz (3); Sultana, Shabiha (1); Tiller, Rebekah (2); Kennedy, Erin D (2); Kadzik, Melissa (2); **Islam, Ausraful** (1); Ahmed, Syed Sayeem Uddin (4); Rahman, AKM Anisur (5); Giasuddin, Md. (6); Salzer, Johanna S (2)

1: icddr, People's Republic of Bangladesh -  
2: Centers for Disease Control and Prevention (CDC), Atlanta, USA - 3: Department of Microbiology, Noakhali Science and Technology University, Noakhali, Bangladesh - 4: Department of Epidemiology and Public Health, Sylhet Agricultural University, Sylhet, Bangladesh - 5: Department of Medicine, Bangladesh Agricultural University, Mymensingh, Bangladesh - 6: Bangladesh Livestock Research Institute, Savar, Dhaka, Bangladesh -

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ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### **Exploring agropastoral health seeking behaviour and attitudes towards animal vaccination in Arri, Northern Tanzania**

**Virhia, Jennika**

The University of Glasgow, United Kingdom -

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ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### **Epidemiology and evolution of zoonotic schistosomiasis in West Africa**

**Léger, Elsa** (1,2); Borlase, Anna (1,2); Fall, Cheikh B. (3); Diouf, Nicolas (4,5); Hamidou, Amina H. (6); Laskowski, Sara (1,2); Rupkus, Lucy (1,2); Morrell, Alice (1,2); Diop, Samba D. (5); Catalano, Stefano (1,2); Rollinson, David (7,2); Emery, Aidan (7,2); Rabone, Muriel (7,2); Sène, Mariama (4); Garba, Amadou (6); Webster, Joanne P. (1,2)

1: Centre for Emerging, Endemic and Exotic Diseases (CEEED), Department of Pathobiology and Population Sciences, The Royal Veterinary College, University of London, UK - 2: London Centre for Neglected Tropical Disease Research (LCNTDR), London, UK - 3: Faculté de Médecine, Pharmacie et Odontologie, Université Cheikh Anta Diop, Dakar, Senegal - 4: UFR des Sciences Agronomiques, d'Aquaculture et de Technologies Alimentaires (S2ATA), Université Gaston Berger de Saint-Louis, Senegal - 5: Institut Supérieur de Formation Agricole et Rurale (ISFAR), Université de Thiès, Bambey, Senegal - 6: Réseau International Schistosomoses Environnement Aménagement et Lutte (RISEAL), Niamey, Niger - 7: Department of Life Sciences, Parasites and Vectors Division, The Natural History Museum, London, UK -

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### **Cameroon One Health Response to HPAI (H5N1) Outbreaks (2016-2017)**

**Takanouo Toukem**, Doriane; Wade, Abel  
National Veterinary Laboratory (LANAVET) Annex in Yaounde, Cameroon -

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ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### **The genesis of one health activities and operationalisation in Tanzania: opportunities and challenges**

**Shirima, Gabriel Mkilema** (1); Buza, Joram (1); Nkya, Elingarami (1); Assenga, Justine (2); Bernard, Jubilate (2); Kunda, John (2); Kazwala, Rudovick (3)

1: NELSON MANDELA AFRICAN INSTITUTION OF SCIENCE AND TECHNOLOGY, Tanzania - 2: ONE HEALTH COORDINATION UNIT, TANZANIA - 3: SOKOINE UNIVERSITY OF AGRICULTURE, TANZANIA

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### **Promoting one health in the community**

**Baldrias, Loinda**

College of Veterinary Medicine, University of the Philippines Los Banos, Philippines -

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ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### **Sero-epidemiological study on human brucellosis and associated risk factors in occupationally exposed population of Punjab, India.**

**Kahlon, Ajaypal Singh** (1,3); Bedi, Jasbir Singh (1); Singh, Randhir (1); Gill, Jatinder Paul Singh (1); Kashyap, Neeraj (2)

1: School of Public Health & Zoonoses, Guru Angad Dev Veterinary and Animal Sciences University, Ludhiana, Punjab, India - 2: Department of Animal Genetics & Breeding, Guru Angad Dev Veterinary and Animal Sciences University, Ludhiana, Punjab, India. - 3: Department of Veterinary Pathology, Western College of Veterinary Medicine, University of Saskatchewan, Saskatchewan, Canada. -

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ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### **A multi-sectorial successful (One-Health) response to the 2016 HPAI-H5N1 outbreaks in domestic birds in Cameroon**

**Wade, Abel**

LANAVET, Cameroon -

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ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### **Investigating Zoonotic Parasites in Dogs in the Remote Northern Indigenous Community of Iqaluit, Nunavut, Canada.**

Julien, Danielle Arlaine **(1,2)**; **Sargeant, Jan Merrill** (1,2); Bunce, Anna (1,2); Sudlovenick, Enooqay (3); Imai, Rachel (4); Guy, Rebecca (5); Harper, Sherilee Lynn (1,2)

1: Department of Population Medicine, Ontario Veterinary College, University of Guelph, Canada - 2: Centre for Public Health and Zoonoses, Ontario Veterinary College, University of Guelph, Canada - 3: Department of Pathology and Microbiology, Atlantic Veterinary College - 4: Department of Pathobiology, Ontario Veterinary College, University of Guelph - 5: Public Health Agency of Canada, National Microbiology Laboratory at Guelph Ontario, Canada -

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ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### **Mycobacterium bovis infection in cattle and communal resource-constrained farmers living at the wildlife-livestock-human interface in South Africa**

Sichewo, Petronillah Rudo; Etter, Eric; **Michel, Anita**  
University of Pretoria, South Africa -

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ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### **Waste not, want not: Turning latrine waste into profit on northern Vietnamese rice farms**

**Pham-Duc, Phuc** (1); M. Schurer, Janna (2); Tran-Thi, Ngan (1); J. Lowe, Rachel (2); Vu-Van, Tu (1); E. MacDonald, Lauren (2)

1: Hanoi University of Public Health, Vietnam - 2: Department of Veterinary Microbiology, University of Saskatchewan, Saskatoon, -

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ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### **Strengthened Cross-Border Disease Surveillance is Valuable for Control of Disease Outbreaks in East Africa**

**Were, Willy Abwoka** (1); Matu, Martin (1); Mushi, Benedict (1); Makayotto, Lyndah (2); Lubwama, Bernard (3); Sonoiya, Stanley (4); Schneidman, Miriam (5)

1: East, Central and Southern Africa Health Community, Tanzania - 2: Ministry of Health, Kenya - 3: Ministry of Health, Uganda - 4: East African Community Secretariat, Tanzania - 5: The World Bank -

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ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### Building multi-sectoral One Health emerging infectious disease and zoonosis surveillance and response capacity in Indonesia: so much more than a training exercise

**Suseno, Pebi Purwo** (1); Sawitri, Elly (2); Syibli, Mohammad (1); Gozali, Ahmad (2); Nurhayati, Nurhayati (1); Jatikusumah, Andri (2); Saputro, Ratmoko Eko (2); Latuihamallo, Monica (2); Schoonman, Luuk (2); McGrane, James (2); Alders, Robyn (3); Prasetyowati, Endang Burni (4); Agustina, Lu'lu' (5)

1: Ministry of Agriculture, Indonesia - 2: FAO ECTAD Indonesia - 3: University of Sydney, Faculty of Science, School of Veterinary Science, Australia - 4: Ministry of Health, Indonesia - 5: Ministry of Environment and Forestry, Indonesia -

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### Knowledge, attitudes and behavioral practices of urban communities towards neglected zoonotic diseases in Addis Ababa, Ethiopia

**Stringer, Andrew** (1); Dessalegn, Ziyad (2); Abunna, Fufa (2)

1: NCSU, United States of America - 2: AAU, Ethiopia

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ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### One health implementation for the prevention and control of intestinal parasites in underprivileged communities near the Thai-Myanmar border

**Singhasivanon, Pratap** (1); Pawestri, Aulia Rahmi (2); Leetachewa, Sompob (3); Maneekan, Pannamas (1); Pinna, Chamnan (4); Moonsom, Saengduen (2)

1: Department of Tropical Hygiene, Faculty of Tropical Medicine, Mahidol University - 2: Department of Protozoology, Faculty of Tropical Medicine, Mahidol University - 3: Institute of Molecular Biosciences, Mahidol University - 4: Provincial Public Health Office, Tak Province -

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ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### Pesticide application practices and knowledge among local rice growers and community in mumumba valley of Nyagatare district-Rwanda

**Ndayambaje, Benjamin** (1); Amuguni, Hellen (2); Coffin-Schmitt, L Jeanne (2); Sibbo, Nancy (1); Van Wormer, Elizabeth (3); Ntawubizi, Martin (4)

1: University of Global Health Equity, Rwanda - 2: Tufts University, USA - 3: University of Nebraska-Lincoln, USA - 4: University of Rwanda, Rwanda -

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ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### Building Capacity in Trichinella Testing of Country Foods in Canada's North

**Scandrett, William Brad**; Konecsni, Kelly Alyson; Scheller, Cheryl Faye  
Canadian Food Inspection Agency, Canada -

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ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### Filling the healthcare professional gap in East Africa through a One Health focused education: the UGHE-UR-Tufts One Health Collaborative

Coffin-Schmitt, Jeanne (1); **Amuguni, Janetrix Hellen** (1); Trent, Sarah (2); Rouleau, Dominique (2); Henley, Phaedra (2); Logan, Jenae (2); Ntawubizi, Martin (3); Gashumba, James (3); Kibuuka, Robert (3); Binagwaho, Agnes (2); Shyaka, Anselme (3); Drobac, Peter (4)

1: Cummings school of Veterinary Medicine at Tufts University, United States of America - 2: University of Global Health Equity, Rwanda - 3: University of Rwanda - 4: The Skoll Institute -

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ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### Balzac: One Health in action in Bangladesh

Heymann, David L. (1); **Nitish, Debnath** (2); Consortium, Balzac (3)

1: Chatham House (the Royal Institute of International Affairs), United Kingdom - 2: FAO, Bangladesh - 3: Balzac Consortium -

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ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### Rural, East African, Poor, and Female – the fourfold climate change water-related liability for health

**Schuster-Wallace, Corinne J**; Watt, Susan  
McMaster University, Canada -

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ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### Attitudes and behaviors toward free-roaming dogs in marginalized urban communities in the Los Rios Region, Chile

**Mason, Meghan Rebecca**; Bayliss, Ruby  
St. Catherine University, United States of America -

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ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

### Using a user-friendly tool to promote utilization of One Health M&E Data to support decision making

**Wakabi, Timothy Waiswa**; Kagarama, Juvenal; Muta, Diana Njambi; Yawe, Agnes Nalugooti

One Health Central and Eastern Africa, Uganda -

## INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE

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### Dog bite cases in Veterinary Hospitals of Narayanganj of Bangladesh

Hossain, Mohammad Shahadat (1); Shahiduzzaman, Md. (1); Ahmed, Kabir Uddin (1); Parvin, Mahmuda (1); -, Anisuzzaman (2,3); **Islam, Ausraful** (4)

1: Ministry of Fisheries and Livestock, Bangladesh, Bangladesh, People's Republic of - 2: Department of Parasitology, Bangladesh Agricultural University, Mymensingh-2100, Bangladesh - 3: Center for Global Health, Technical University of Munich, Munich, Germany - 4: Program for Emerging Infections, Infectious Diseases Division, icddr,b, Mohakhali, Dhaka-1212, Bangladesh -

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### The Development of a One Health curriculum for Universities in Vietnam

**Phuc, Pham-Duc** (1); Thao, Nguyen-Thi-Bich (1); Trang, Le-Thi-Huyen (1); Fenwick, Stanley (2)

1: Hanoi University of Public Health, Vietnam - 2: Tufts University -

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### IN PURSUIT OF A SEROLOGICAL SCREENING TEST FOR MYCOBACTERIUM ULCERANS EXPOSURE

**Avumegah, Michael Selorm** (1,2); Athan, Eugene (1,2,3); O'Brien, Daniel P. (3,4); Shiell, Brian (5); Keyburn, Anthony (5); Michalski, Wojtek P. (5); Alexandersen, Soren (1,2,3)

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### Cutting costs by cutting DNA: Economic molecular tools for One-Health studies of ticks and tick-borne diseases associated with wild birds in Brazil

**Abreu, Daniel Paiva Barros de**; Faccini, João Luiz Horácio; McIntosh, Douglas  
Federal Rural University of Rio de Janeiro, Brazil -

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### A collaborative masters degree training program dealing with health challenges at the human/ animal interface

**Oosthuizen, Marinda C** (1); Dorny, Pierre (2); Matjila, Tshupo (1); Stevens, Mieke (2)

1: Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, Pretoria, South Africa - 2: Institute of Tropical Medicine, Antwerp, Belgium -

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### Q fever exposure risk set: application of multiple correspondence analysis (MCA)

**Woldeyohannes, Solomon Meseret** (1); Reid, Simon (1); Gilks, Charles (1); Baker, Peter (1); Perkins, Nigel (2)

1: School of Public Health, Faculty of Medicine, University of Queensland - 2: School of Veterinary Science, Faculty of Science, University of Queensland -

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### Detection and characterisation of coronaviruses in Australian wild birds

**Chamings, Anthony Neal** (1,2); Nelson, Tiffanie (1,2); Vibin, Jessy (1,2); Wille, Michelle (3); Klaassen, Marcel (4); Alexandersen, Soren (1,2,5)

1: Geelong Centre for Emerging Infectious Diseases, Geelong, Australia - 2: School of Medicine, Deakin University, Geelong, Australia - 3: WHO Collaborating Centre for Reference and Research on Influenza, Peter Doherty Institute for Infection and Immunity, Melbourne, Victoria, Australia - 4: Centre for Integrative Ecology, Deakin University, Geelong, Victoria, Australia - 5: Barwon Health, University Hospital Geelong, Geelong, Victoria, Australia -

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### Modelling multiple transmission routes of campylobacteriosis in Ontario using a One Health perspective.

**Cousins, Melanie Maryanne** (1,2); Fisman, David N. (3); Sargeant, Jan M. (1,2); Greer, Amy L. (1,2)

1: Dept. of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, CA - 2: Centre for Public Health and Zoonoses, University of Guelph, Guelph, ON, CA - 3: Dept. of Epidemiology, Dalla Lana School of Public Health, University of Toronto, Toronto, ON, CA -

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### Zoonotic disease research in Eastern Africa

**Kemunto, Naomi P** (1); Mogoa, Eddy (2); Osoro, Eric (1); Bitek, Austin (3); Njenga, M Kariuki (1); Thumbi, SM (1)

1: Paul G. Allen School for Global Animal Health, Washington State University, Pullman, USA, Kenya - 2: Faculty of Veterinary Medicine, University of Nairobi, Kenya - 3: Food and Agriculture Organization of the United Nations, Nairobi, Kenya.

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### The possible impact of the climate change on the Trans-Arax plague focus

**Manucharyan, Arsen**; Sahakyan, Levon "Reference Laboratory Center" branch, National Center for Disease Control and Prevention" SNCO, Ministry of Health, Yerevan, Republic of Armenia -

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### Epidemiology of Human Rabies Death in Vietnam 1994-2016

**Nguyen, Huong Thi Thanh**

National Institute of Hygiene and Epidemiology, Vietnam -

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### A Cross-Sectional Study Investigating Human Exposure to Dog Bites: Applying a One Health Philosophy to a Public Health Challenge in Rural and Urban communities in Ontario, Canada.

**Julien, Danielle Arlaine** (1,2); Sargeant, Jan Merrill (1,2); Filejski, Catherine (3); Harper, Sherilee Lynn (1,2)

1: Department of Population Medicine, Ontario Veterinary College, University of Guelph, Canada - 2: Centre for Public Health and Zoonoses, Ontario Veterinary College, University of Guelph, Canada - 3: Public Health Division, Ontario Ministry of Health and Long-Term Care, Toronto, Ontario, Canada -

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### Leptospirosis in Slaughter Livestock in Gauteng Province, South Africa: Isolation, Serological and molecular Studies.

**Dogonyaro, Banenat Bajehson** (1); dr van heerden, henriette (1); Wunder Jnr, Elsie Augusto (2); Ko, Albert Icksang (2); Casanovas-Massana, Arnau (2); Potts, Andrew David (3); Lotter, Christine (3); Katsande, Charles (4); Fasina, Folorunso Oludayo (1); Adesiyun, Abiodun (1)

1: University of Pretoria, South Africa - 2: Yale University School of Public Health, New Haven, Connecticut, USA. - 3: ARC-Onderstepoort Veterinary Research, Pretoria, South Africa. - 4: Gauteng Department of Agriculture and Rural Development, South Africa -

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### A model of inter-market livestock movement in northern Tanzania: exploiting routinely collected data to investigate infectious disease transmission

**Johnson, Paul Christopher Duncan** (1); Chaters, Gemma Louise (1); de Glanville, Will (1); Davis, Alicia (2); Yoder, Jonathan (3); Halliday, Jo (1); Lankester, Felix (3); Buza, Joram (4); Nyasebwa, Obed Malangu (5); Swai, Emanuel (5); Cleaveland, Sarah (1); Matthews, Louise (1); Kao, Rowland (6)

1: Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow, UK - 2: School of Geographical and Earth Sciences, University of Glasgow, UK - 3: Paul G. Allen School for Global Animal Health, Washington State University, USA - 4: Nelson Mandela African Institution for Science and Technology, Arusha, Tanzania - 5: Ministry of Agriculture, Livestock and Fisheries, Tanzania - 6: Royal (Dick) School of Veterinary Studies, University of Edinburgh, UK -

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### Where do bats go? Tracking bats sheds light on virus exposure pathways and guides surveillance

**Randhawa, Nistara** (1); Bird, Brian (1); VanWormer, Elizabeth (2); Sijali, Zikankuba (3); Kilonzo, Christopher (1); Msigwa, Alphonse (3); Ekiri, Abel (1); Samson, Aziza (3); Wolking, David J. (1); Smith, Woutrina A. (1); Martínez-López, Beatriz (4); Kazwala, Rudovick (3); Mazet, Jonna A.K. (1)

1: One Health Institute & Karen C. Drayer Wildlife Health Center, School of Veterinary Medicine, University of California - Davis, USA - 2: School of Veterinary Medicine and Biomedical Sciences, School of Natural Resources, University of Nebraska-Lincoln, USA - 3: Department of Veterinary Medicine and Public Health, Sokoine University of Agriculture, Morogoro, Tanzania - 4: Center for Animal Disease Modeling and Surveillance, School of Veterinary Medicine, University of California - Davis, USA -

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### Future One Health workforce preparation for effective prevention and control of emerging infectious diseases

**Moonsom, Saengduen**; Chavez, Irwin Fernandez; Singhasivanon, Pratap Faculty of Tropical Medicine, Mahidol University -

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### Assessment of Shiga Toxin-Producing Escherichia coli (STEC) in Private Well Waters in Western Canada with a One Health approach

Reynolds, Colin (1); **Checkley, Sylvia Lee** (2,3); Chui, Linda (3,4); Neumann, Norman F (1)

1: Environmental Health Sciences, School of Public Health, University of Alberta, Alberta, Canada - 2: University of Calgary, Faculty of Veterinary Medicine, Alberta, Canada - 3: Provincial Laboratory for Public Health, Alberta, Canada - 4: Department of Laboratory Medicine and Pathology, University of Alberta, Alberta, Canada -

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### Specifying EcoHealth Pathways of Zoonotic Disease Through a Unifying Biopsychosocial Ecological Framework and Geospatial Mapping

**Persad-Clem, Reema** (1); M, Karl (2)

1: University of California, Berkeley, United States of America - 2: Salisbury University, United States of America -

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### Surveillance of Zoonotic Viruses and Population Genetics of Confiscated Sunda Pangolins (*Manis javanica*) from Malaysia

**Lee, Jimmy** (1,2); Hughes, Tom (2); Lee, Mei Ho (2); Field, Hume (2); Lasimbang, Helen (1); Kumar, Vijay (3); Zambrana-Torrel, Carlos (2); Anthony, Simon J. (2); Sipangkui, Rosa (4); Ramirez, Diana (4); Japning, Jeffrine Rovie-Ryan (5); Sitam, Frankie Thomas (5); Epstein, Jonathan H. (2); Daszak, Peter (2)  
1: Faculty of Medicine and Health Sciences, University Malaysia Sabah, Kota Kinabalu, Malaysia - 2: EcoHealth Alliance, New York, USA - 3: Biotechnology Research Institute, University Malaysia Sabah, Kota Kinabalu, Malaysia - 4: Sabah Wildlife Department, Kota Kinabalu, Malaysia - 5: Department of Wildlife and National Parks, Kuala Lumpur, Malaysia

## AMR

### USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

P176 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### Epidemiology of Antimicrobial Resistance pattern of *Salmonella* spp. isolated from Small Mammals of Bangladesh

Hassan, Mohammad Mahmudul (1); **Islam, Ariful** (2,3); Rumi, Md Aftubuddin (1); Rahman, Md Kaisar (2,3); Uddin, Md Helal (1); Islam, Shariful (2,3); Samad, Mohammad A (4); Rostal, Melinda K (2); Hagan, Emily (2); Flora, Meerjady Sabrina (3); Epstein, Jonathan H (2)

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P177 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### Antimicrobial resistance of *Escherichia coli* associated with urinary tract infections and food poisoning at two main hospitals in Bujumbura, Burundi

**Claudette, Ndayikunda**

University of Burundi Faculty of Medicine, Burundi

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### Antibiotics Use on Small and Medium Scale Broiler Farms in West Java, East Java and South Sulawesi Provinces, Indonesia

**Isriyanti, Ni Made Ria** (1); Setyawan, Erry (2); Pangaribuan, Dameria Melany (1); Telussa, Rallya (2); Fitriastuti, Erna Rahmawati (1); Budi Utomo, Gunawan (2); Kompudu, Alfred (2); Harja, Adi (2); Nur Agustina, Irlia (1); Wagenaar, Jaap (3,4); Speksnijder, David (4); Schoonman, Luuk (2); McGrane, James (2)

1: Directorate General of Livestock and Animal Health Services, Ministry of Agriculture, Jakarta, Indonesia - 2: UN Food and Agriculture Organization (FAO) Emergency Centre for Transboundary Animal Diseases, Jakarta, Indonesia - 3: Department of Infectious Diseases and Immunology, Faculty of Veterinary Medicine, Utrecht University, Utrecht, The Netherlands - 4: Wageningen Bioveterinary Research, Lelystad, The Netherlands -

P179 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### Antibiotic residues in Raw Milk and locally produced dairy products in Ghana

**Mensah, Gloria Ivy** (1); Vicar, Ezekiel Kofi (2,3); Kankam, Daniel (4); Adjei, Vida Yirenyiwaa (1); Addo, Samuel Ofori (1); Saba, Courage Kosi Setsoafia (2); Addo, Kennedy Kwasi (1); Feglo, Patrick K. (3)

1: Noguchi Memorial Institute for Medical Research, University of Ghana, Legon, Accra - 2: Clinical Microbiology Department, School of Medical Sciences, University for Development Studies, Tamale, Ghana - 3: Clinical Microbiology Department, Kwame Nkrumah University of Science and Technology, Kumasi, Ghana - 4: School of Veterinary Medicine, University of Ghana, Legon/ Accra -

P180 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### Presence of *Salmonella* spp. And *Escherichia coli* in eggs, chicken meat and pork in Phnom Penh market city and Kandal market province in Cambodia

Soeung, Hynaren (1); Meng, Khoythor (1); Thorn, Putsopheakra (1); Kong, Lida (1); Sok, Koam (2); Yann, Sovankongkea (1); Hor, Sourloing (1); Kang, Kroesna (1); **Cheat, Sopal** (1)

1: Faculty of Veterinary Medicine, Royal University of Agriculture, Cambodia - 2: General Directorate of Animal Health and Production, Cambodia -

P181 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### Antimicrobial resistance profile of *Escherichia coli* and *E. coli* O157:H7 in raw milk produced and marketed in the Northern region of Ghana.

Vicar, Ezekiel Kofi (1,2); Acquah, Samuel E.K (1); Saba, Courage Kosi Setsoafia (1); Feglo, Patrick K. (2); **Mensah, Gloria Ivy** (3)

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### Prospective evaluation of Ceftriaxone use in medical and emergency wards of Gondar university referral hospital, Ethiopia

**Gebresillasse, Begashaw Melaku**

University of Gondar, Ethiopia -

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### Factors that drive antimicrobial use practices of beef cattle producers in Tennessee, United States

Ekakoro, John Eddie; Caldwell, Marc; Strand, Elizabeth B; **Okafor, Chika C**

College of Veterinary Medicine at the University of Tennessee, Knoxville, United States of America -

P184 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### Antimicrobial use practices of veterinary clinicians at a veterinary teaching hospital in the United States

Ekakoro, John Eddie; **Okafor, Chika C**

College of Veterinary Medicine at the University of Tennessee, Knoxville, United States of America -

P185 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### One Health and Antimicrobial Stewardship in the Pork Industry

**Fowler, Heather Nicole**

National Pork Board, United States of America -

P186 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### Use of a stochastic production frontier approach to examine the impact of GIN management in beef cow-calf herds in Canada.

**Rasmussen, Philip**; Hall, David; Gilleard, John; Windeyer, Claire; Wasmuth, James  
University of Calgary, Canada -

P187 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### Understanding disincentives to antibiotic use in Singapore's food fish farming: A qualitative study

**Lim, Jane** (1); Duong, Minh-Cam (1); Hsu, Li Yang (1); Tam, Clarence C (1,2)

1: National University of Singapore, Singapore -  
2: London School of Hygiene and Tropical Medicine -

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### Antibiotic-resistant pathogens in wastewater inside poultry slaughterhouses and their fate in in-house wastewater treatment plants

**Savin, Mykhailo** (1); Heinemann, Céline (1); Bierbaum, Gabriele (2); Dohlen, Sophia (1); Parcina, Marijo (2); Petersen, Brigitte (1); Sib, Esther (2); Kreyenschmidt, Judith (1)

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P189 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### Informing our knowledge on AMR through the use of risk assessments: a scoping review

**Caffrey, Niamh** (1); Invik, Jesse (1); Waldner, Cheryl (2); Ramsey, Dana (3); Checkley, Sylvia (1,4)

1: Faculty of Veterinary Medicine, University of Calgary - 2: Western College of Veterinary Medicine, University of Saskatchewan - 3: School of Public Health, University of Saskatchewan - 4: Provincial Laboratory for Public Health, Alberta -

P190 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### A critical evaluation in the implementation of antimicrobial resistance sustainable control plan in Brazil: what is being done, challenges and perspectives to control its effects

Torres Furtado Martins, Bruna (1); de Melo Tavares, Rafaela (1); Costa Polveiro, Richard (1); Rodrigues Alves, Samuel (1); Bevenuto Mattar, Jéssica (2); Ferreira Tavares, Juliana (2); Bressan, Josefina (2); **Pettan-Brewer, Christina** (3); Augusto Nero, Luís (1); Aparecida Scatamburlo Moreira, Maria (1)

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P191 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### Using a one health approach - understanding antibiotic resistance and coupling points across complex African landscapes

**Alexander, Kathleen A.**; Sanderson, Claire E.; Fox, John, T  
Virginia Tech, United States of America -

P192 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### Knowledge, attitudes and behavioral practices of antimicrobial usage and resistance within rural communities in central Ethiopia.

**Stringer, Andrew** (1); Argaw, Amare (2); Abunna, Fufa (2)

1: NCSU, United States of America - 2: AAU, Ethiopia -

P193 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### A scoping review of psycho-social factors influencing food animal producers' use of antimicrobials

**Moore, Megan Lesley**

University of Saskatchewan, Canada -

P194 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### Production animal antimicrobial use in New Zealand

Bryan, Mark; Fruean, Skye; Knupfer, Elena; **McCorkindale, Debra An**

VetSouth Limited Winton, New Zealand -

P195 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### Understanding the differences in antimicrobial use in dairy cows in New Zealand and in the UK

Bryan, Mark (1); Fruean, Skye (1); Knupfer, Elena (1); Reader, Jon (2); Hyde, Robert (3); Green, Martin (3); **McCorkindale, Debra An** (1)

1: VetSouth Limited Winton, New Zealand - 2: Synergy Farm Health, UK - 3: School of Veterinary Science, University of Nottingham -

P196 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### Analysis of antibiotic residues and metabolites in wastewater from Hospital, livestock and treated water in Kigali City, Rwanda

**Ndayambaje, Benjamin**

University of Nebraska-Lincoln, United States of America -

P197 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### ANTIMICROBIAL RESISTANCE PROFILES IN ESCHERICHIA COLI AND SALMONELLA SPP. ISOLATED FROM SLAUGHTER HOUSES IN CAMBODIA

**Chea, Rortana** (1); Sok, Koam (1); Tep, Bengthay (2); Osbjær, Kristina (3); Tum, Sothyra (1)

1: National Institute of Animal Health and Production Research Institute, General Directorate of Animal Health and - 2: Department of Public Health and Veterinary Public Health, General Directorate of Animal Health and Production Phnom Penh, Cambodia - 3: Emergency Centre for Transboundary Animal Diseases (ECTAD), Food and Agriculture of the United Nation -

P198 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### ANTIMICROBIAL RESISTANCE PROFILES IN SALMONELLA SPP. DETECTED IN DIARRHEAL CHICKEN IN CAMBODIA

**Lida, Kong** (1); Vouchsim, Kong (2); Bunthon, Chea (3); Sarim, Seng (4); Raveth, Por (4); Rithy, Seng (4); Kroesna, Kang (4); Vutey, Venn (4); Rortana, Chea (4)

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P199 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### Variation in airborne DNA concentrations of various antimicrobial resistance genes and livestock-related bacterial indicator organisms measured at residential level at 61 sites in a livestock dense area

**De Rooij, Myrna M. T.** (1); Schmitt, Heike (1); Janse, Ingmar (2); Swart, Arno (2); Heederik, Dick J.J. (1); Wouters, Inge M. (1)

1: Utrecht University, Institute for Risk Assessment Sciences, the Netherlands - 2: National Institute for Public Health and the Environment (RIVM), the Netherlands -

P200 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### Dairy calf treatment decisions by farm personnel compared to veterinary observations of clinical signs

**Sischo, William M.**; Moore, Dale A

Washington State University, United States of America -

P201 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### Our story of modelling antimicrobial resistance: broadening the scope, finding new tools and lessons learned.

**Murphy, Colleen** (1); Carson, Carolee (1); Marleau, Justin (2); Smith, Ben (1); Reid-Smith, Richard (1); Parmley, Jane (1)

1: Public Health Agency of Canada, Canada -  
2: Department of Biology, McGill University -

P202 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### Quantification, Antimicrobial Susceptibility Testing and Speciation of Vancomycin-Resistant Enterococci Isolated from Two Wastewater Treatment Plants using Different Treatment Processes

**Sanderson, Haley Ann** (1); Ortega-Polo, Rodrigo (2,3); Zaheer, Rahat (2); Brown, R. Stephen (1); Majury, Anna (1,4); McAllister, Tim A. (2); Liss, Steven N. (1,5)

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2: Agriculture Agri-Food Canada, Lethbridge Research and Development Center, Lethbridge, Alberta, Canada - 3: University of Lethbridge, Lethbridge, Alberta, Canada - 4: Public Health Ontario, Kingston, Ontario, Canada - 5: Ryerson University, Toronto, Ontario, Canada -

P203 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

### The role of benchmarking the use of antimicrobials at the farm level: the Dutch experience

Heederik, Dirk (1,5); Wagenaar, Jaap (2,5); Mouton, Johan (3,5); van Geijlswijk, Inge (4,5); **Sanders, Pim** (1,5)

1: Institute for Risk Assessment Sciences, Faculty of Veterinary Medicine, Utrecht University, Yalelaan 2, 3584 CM Utrecht, the Netherlands - 2: Department of Infectious Diseases and Immunology, Faculty of Veterinary Medicine, Utrecht University, Yalelaan 1, 3584 CL, Utrecht, the Netherlands - 3: Department of Medical Microbiology and Infectious Diseases, Erasmus MC, Wytemaweg 80, 3015 CN Rotterdam, the Netherlands - 4: Pharmacy Department, Faculty of Veterinary Medicine, Utrecht University, Yalelaan 106, 3584 CM Utrecht, The Netherlands - 5: Netherlands Veterinary Medicine Institute, Utrecht, The Netherlands -

## GENOMIC EPIDEMIOLOGY / EVOLUTION OF AMR TRANSMISSION

P204 - AMR 02 - GENOMIC EPIDEMIOLOGY / EVOLUTION OF AMR TRANSMISSION

### AMR Markers in Non-Pathogenic Bacteria Isolated From Food

**Mohajer, Sam**; Leclair, Daniel; Murphy, Johanna; Glencross, Jason; Koziol, Adam; Carrillo, Catherine; Blais, Burton  
Canadian Food Inspection Agency -

## PREVALENCE AND SURVEILLANCE OF RESISTANCE

P205 - AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE

### Epidemiology of Multidrug-resistance Tuberculosis in Bhutan: understanding the increasing burden, quality care and associated risk factors

**Zangpo, Tandin** (1); Dorji, Chencho (2); Nima, Gaki (3)

1: Medical Officer, Dechencholing BHU-I, Ministry of Health, Thimphu, Bhutan - 2: Medical Officer, Gidakom Hospital, Ministry of Health, Thimphu, Bhutan - 3: TB-Chest Specialist, Jigme Dorji Wangchuk (JDW) National Referral Hospital, Thimphu, Bhutan -

P206 - AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE

### Zoonotic E. coli as a Potential Driver of Antimicrobial Resistance in Pastoralist Communities of rural Western Uganda

**Asiimwe, Benon Byamugisha**

Makerere University, Uganda -

P207 - AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE

### Multidrug Resistance among Escherichia coli and Klebsiella Pneumoniae Isolated from Out-Patients in Pastoralist Communities of Kasese District, Uganda

**Iramiot, Jacob Stanley** (1,2); Kajumbula, Henry (1); Bazira, Joel (3); Rwego, Innocent (4); Asiimwe, Benon B (1)

1: Makerere University, Uganda1, Busitema University, Uganda 2 - 2: Makerere University, Uganda1 - 3: Mbarara University of Science and technology, Uganda 3 - 4: Department of Biosecurity, Ecosystem health and Veterinary Public Health, Makerere University College of Veterinary Medicine, Animal Resources and Biosecurity, P. O. Box 7062, Kampala, Uganda 4 -

P208 - AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE

### Spread of Escherichia coli carrying blaCTX-M and blaCMY-2 in Senegalese chicken farms through clones and plasmids

**Vounba, Passoret** (1); Arsenault, Julie (1); Bada-Alambédji, Rianatou (2); Fairbrother, John Morris (1)

1: Université de Montréal, Canada - 2: École vétérinaire de Dakar (Sénégal) -

P209 - AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE

### Antimicrobial Resistance of Shigatoxigenic E.coli to commonly prescribed antibiotics in diarrhoea patients from Kitale County Referral Hospital, Kenya

**Too, Rael Jepkinyor** (1); Ngari, Moses (2); Chebii, Jane (4); Kikui, Gideon Mutie (5); Wanzala, Peter (6); Githui, Willie Abela (3); Sang, Willie Kipkemboi (1)

1: Kenya Medical Research Institute (KEMRI)- Centre for Microbiology - 2: KEMRI- Centre for Geographic Medicine Research - 3: KEMRI- Centre for Respiratory Disease Research - 4: Kitale County Referral Hospital - 5: Jomo Kenyatta University of Agriculture and Technology - 6: KEMRI- Centre for Public Health Research -

P210 - AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE

### Near-equilibrium prevalence of antimicrobial resistance in an informal urban community

**Omulo, Sylvia** (1); Lofgren, Eric T. (1); Lockwood, Svetlana (1); Thumbi, Samuel M. (1); Bigogo, Godfrey (2); Ouma, Alice (2); Verani, Jennifer (3); Juma, Bonventure (3); Njenga, M Kariuki (1); Kariuki, Samuel (2); McElwain, Terry F. (1); Palmer, Guy H. (1); Call, Douglas R. (1)

1: Washington State University, Kenya - 2: Kenya Medical Research Institute - 3: Centers for Disease Control and Prevention -

P211 - AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE

### A comparison of antibiotic resistance trends of E. coli among bovine and human isolates in Washington State.

**Frisbie, Lauren** (1); Weissman, Scott (2); Trufan, Sally (1); Adler, Cheryl (4); Ramirez, Vickie (1); D'Angeli, Marisa (3); Rabinowitz, Peter (1)

1: Center for One Health Research, University of Washington - 2: Seattle Children's Hospital - 3: Washington State Department of Health - 4: Phoenix Central Laboratories -

P212 - AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE

### Antimicrobial resistance prevalence in Harbour seal (Phoca vitulina) pups and weaners stranded in the Netherlands and antibiotic treatment effect in their gut microbiome during rehabilitation

**Rubio-Garcia, Ana** (1); Rossen, John W. (2); van Zeijl, Jan H. (3); Rosema, Sigrid (4); Cobos, Silvia Garcia (4); Friedrich, Alex W. (4); Wagenaar, Jaap A. (1); Zomer, Aldert (1)

1: Utrecht University, The Netherlands - 2: Rijksuniversiteit Groningen, The Netherlands - 3: IZORE, The Netherlands - 4: University Medical Center Groningen, The Netherlands -

## NOVEL STRATEGIES FOR AMR INTERVENTIONS / PREPAREDNESS

P213 - AMR 05 - NOVEL STRATEGIES FOR AMR INTERVENTIONS / PREPAREDNESS

### The impact of national policies & programmes targeting antimicrobial resistance: A systematic review

**Lim, Jane** (1); Duong, Minh-Cam (1); Singh, Shweta R (1); Legido-Quigley, Helena (1,2); Hsu, Li Yang (1); Tam, Clarence C (1,2)  
1: National University of Singapore, Singapore - 2: London School of Hygiene and Tropical Medicine

## ALTERNATIVE APPROACHES TO TACKLING RESISTANT INFECTION

P214 - AMR 06 - ALTERNATIVE APPROACHES TO TACKLING RESISTANT INFECTIONS

### Barriers to, and enablers of, implementing antimicrobial stewardship programs in veterinary practices.

**Hardefeldt, Laura Yvonne** (1,2); Gilkerson, James R (1); Billman-Jacobe, Helen (1,2); Stevenson, Mark Anthony (1); Thursky, Karin (2); Browning, Glenn Francis (1,2)  
1: Asia-Pacific Centre for Animal Health, Melbourne Veterinary School, University of Melbourne, Australia - 2: National Centre for Antimicrobial Stewardship, Carlton, Victoria, Australia -

P215 - AMR 06 - ALTERNATIVE APPROACHES TO TACKLING RESISTANT INFECTIONS

### Non-antibiotic approaches at drying-off for treating and preventing intramammary infections in dairy cows: a systematic review and meta-analysis.

**Francoz, David** (1); wellemans, Vincent (1); Ordonez Iturriaga, Alfredo (1); Roy, Jean-Philippe (1); François, Labelle (2); Lacasse, Pierre (3); Dufour, Simon (1)  
1: Université de Montréal, Faculté de médecine vétérinaire, Canada - 2: Valacta, Canada - 3: Agriculture Agri-Food Canada, Sherbrooke Research and Development Centre, Canada



## SCIENCE POLICY INTERFACE

P216 - SCIENCE POLICY INTERFACE

### Fostering One Health research and education in Pakistan

**Lida Anestidou, DVM, PhD**  
National Academies of Sciences, Engineering and Medicine, USA,  
**Audrey Thevenon, PhD**  
National Academies of Sciences, Engineering and Medicine, USA

P217 - SCIENCE POLICY INTERFACE

### Incorporating Sand Dynamics into Beach Water Quality Science and Policy

**Chelsea Weiskerger**  
Michigan State University, Department of Civil and Environmental Engineering,  
**Joao Brandao**, National Institute of Health,  
**Dr. Ricardo Jorge**, Portugal

P218 - SCIENCE POLICY INTERFACE

### Attacking the Hydra: Antimicrobial Stewardship in Primary Health Care

**Jason R. Vanstone**  
Saskatchewan Health Authority

P219 - SCIENCE POLICY INTERFACE

### Tuberculosis among captive elephants and mahouts: Implications to health policy

**Dr. David Abraham**  
Forest Veterinary Officer, Department of Forests and Wildlife, Kerala, India.

P220 - SCIENCE POLICY INTERFACE

### Epidemic clones of community-acquired methicillin-resistant Staphylococcus aureus in slaughter pigs, Cuba

**Michel Baez Arias** (1), Alexandra Collaud (2), Ivette Espinosa Castaño (1), Vincent Perreten (2).  
(1) National Centre of Animal and Plant Health (CENSA), San José de las Lajas, Mayabeque, Cuba, michel@censa.edu.cu; (2) Institute of Veterinary Bacteriology, Vetsuisse Faculty, University of Bern, Switzerland.

P221 - SCIENCE POLICY INTERFACE

### One Health -Easy to Say & Hard to Do – Using Progressive Project Management and Social Innovation to Implement One Health

**Dr. Adana Mahase-Gibson**,  
University of the West Indies, St. Augustine, Trinidad & Tobago. Collaborators:  
Prof. Chris Oura, University of the West Indies, St. Augustine, Trinidad & Tobago  
Prof. Craig Stephen, Canadian Wildlife Health Cooperative, Professor, Western College of Veterinary Medicine, University of Saskatchewan, School of Population and Public Health, University of British Columbia, Canada  
Dr. Keith William Gibson, Environmental Research Institute, Charlotteville, Trinidad & Tobago  
Dr. Chandra Degia, University of the West Indies, Mona, Jamaica  
Dr. Roderick K. King, Florida Institute for Health Innovation, Department of Public Health Sciences, University of Miami Miller School of Medicine, USA

P222 - SCIENCE POLICY INTERFACE

### AFTOSA: From Foot-and-Mouth Disease to One Health

**Ottorino Cosivi**  
Pan American Foot-and-Mouth Disease Center of the Pan American Health Organization, Rio de Janeiro

P223 - SCIENCE POLICY INTERFACE

### Establishment of a sustainable emerging disease surveillance program at a human/wildlife interface.

**Robert J. Fischer**  
US National Institutes of Health, Rocky Mountain Laboratories, Laboratory of Virology, Hamilton, MT; Kenneth Cameron, US Fish and Wildlife Service, Division of International Conservation, Falls Church, VA; Sarah Olson Wildlife Conservation Society, Wildlife Health Program, Bronx, NY; Trenton Bushmaker US National Institutes of Health, Rocky Mountain Laboratories, Laboratory of Virology, Hamilton, MT; Eeva Kuisma Wildlife Conservation Society, Wildlife Health Program, Bronx, NY; Christian Walzer Wildlife Conservation Society, Wildlife Health Program, Bronx, NY; Vincent J. Munster US National Institutes of Health, Rocky Mountain Laboratories, Laboratory of Virology, Hamilton, MT

P224 - SCIENCE POLICY INTERFACE

### A Case Study on One Health Approach in Addressing Antimicrobial Resistance in Cambodia

**Sokerya Seng** (1), Kristina Osbjør (1), Makara Hak (1 and Alessandro Patriarchi (2)  
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(2) Food and Agriculture Organization of the United Nations (FAO), Regional Office for Asia and the Pacific, Bangkok, Thailand

P225 - SCIENCE POLICY INTERFACE

### Exploring agropastoral health seeking behaviour and attitudes towards animal vaccination in Arri, Northern Tanzania.

**Jennika Virhia**  
The University of Glasgow, Scotland

## LATE BREAKERS

P226 - LATE BREAKERS

### Influenza at a wildlife - livestock interface: surveillance and transmission dynamics in traditional Mexican swine farms

**Mateus-Anzola, Jessica Paola** (1); Wiratsadaku, Anuwat (2); Rico-Chávez, Oscar (1); Ojeda-Flores, Rafael (1)  
1: Universidad Nacional Autónoma de México, Mexico - 2: Mahidol University, Thailand -

P227 - LATE BREAKERS

### Influenza A virus surveillance based on a socio-ecosystem approach in a wild bird-backyard poultry interface in Mexico

**Gaytán Cruz, Liliana**; Ojeda Flores, Rafael  
Universidad Nacional Autónoma de México, Mexico



P228 - LATE BREAKERS

### Mitigation and monitoring of risk of plague reemerging by development of new mapping method for natural FOCI

**Chubinidze, Svetlana;** Grdzeldize, Marina; Tsertsvadze, Nikoloz; Tsanova, Shota  
National Center for Disease Control and Public Health, Georgia -

P229 - LATE BREAKERS

### Enabling better surveillance and early detection of zoonotic diseases through online clinical decision support

**Walsh, Kieran**

BMJ, United Kingdom -

P230 - LATE BREAKERS

### A novel spotted fever group (SFG) Rickettsia species detected in Argasid ticks collected from toads in Brazil; cause for concern or simply symbiosis?

**Peixoto, Maristela Peckle;** Luz, Hermes; Faccini, João Luiz Horacio; McIntosh, Douglas  
Universidade Federal Rural do Rio de Janeiro, Brazil -

P231 - LATE BREAKERS

### Effects of land use practices on mosquito community abundance and diversity in Eastern Ontario

**Rakotoarinia, Miarisoa Rindra** (1); Lapen, David (2); Leighton, Patrick (1); Ogden, Nick (3); Ludwig, Antoinette (3); Guitard, Eric (4)  
1: Université de Montréal, Canada - 2: Agriculture and AgriFood Canada - 3: Public Health Agency of Canada - 4: University of Ottawa, Canada -

P232 - LATE BREAKERS

### Estimation of key Taenia solium transmission parameters across different epidemiological settings: implications for transmission modelling

**Dixon, Matthew A.** (1); Winskill, Peter (2); Walker, Martin (3); Harrison, Wendy E. (4); Schmidt, Veronika (5,6); Sarti, Elsa (7); Bawm, Saw (8); Basáñez, María-Gloria (1)

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P233 - LATE BREAKERS

### A comparison of goat breeds and routes of infection as a challenge model for Rift Valley Fever Virus

**Kroeker, Andrea** (1); Smid, Valerie (1); Truong, Thang (1); Embury-Hyatt, Carrisa (1); Collignon, Brad (1); Lindsay, Robbin (2,3); Babiuk, Shawn (1,4); Weingartl, Hana (1,5)

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P234 - LATE BREAKERS

### Human seroprevalence to eleven zoonotic pathogens in the US Arctic, Alaska

**Bruce, Michael George** (1); Mierny, Karen (1); Parkinson, Alan (1); Hurlburt, Debby (1); Klejka, Joe (2); Berner, Jim (3); Stoddard, Robyn (1); Handali, Sukwan (1); Wilkins, P (1); Kersh, Gil (1); Fitzpatrick, Kelly (1); Drebot, Mike (4); Priest, Jeff (1); Pappert, Ryan (1); Petersen, Jeanine (1); Teshale, Eyasu (1); Hennessy, Tom (1)

1: CDC, United States of America - 2: Yukon Kuskokwim Health Corporation - 3: Alaska Native Tribal Health Consortium - 4: Public Health Agency of Canada -

P235 - LATE BREAKERS

### Development of pre-pandemic influenza vaccine against highly pathogenic H5 strains

**Lu, Yao** (1,2); Liu, GuanQun (1,3); Landreth, Shelby (1,3); Gaba, Amit (1); Brownlie, Robert (1); Zhou, Yan (1,2,3)

1: Vaccine and Infectious Disease Organization-International Vaccine Center (VIDO-InterVac) - 2: Department of Veterinary Microbiology, Western College of Veterinary Medicine - 3: Vaccinology & Immunotherapeutics, School of Public Health, University of Saskatchewan, Canada -

P236 - LATE BREAKERS

### Diversity of mcr-4 harbouring Escherichia coli isolates from food and livestock in Germany

**Hammerl, Jens Andre;** Shamoun, Dina; Schmoeger, Silvia; Grobbel, Mirjam; Tenhagen, Bernd-Alois; Kaesbohrer, Annemarie  
German Federal Institute for Risk Assessment, Germany -

P237 - LATE BREAKERS

### Klebsiella plasmids and their relevance for the transfer of antimicrobial resistance determinants

**Hammerl, Jens Andre;** Carl, Gaby; Jäckel, Claudia; Grobbel, Mirjam; Käsböhrer, Annemarie

German Federal Institute for Risk Assessment, Germany -

P238 - LATE BREAKERS

### Identification of Aedes albopictus (Skuse, 1894) in Kinshasa/ RDCongo.

**Fasine, Sylvie Mukalimungele** (1); Manzambi, Emile Makima (1); Wat'senga, Francis Tezzo (1); Ahuka, Steve Mundeke (1,2); Muyembe, Jeanjacques Tamfumu (1,2)

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P239 - LATE BREAKERS

### Operationalizing One Health approach in Uganda: challenges and opportunities

**Buregyeya, Esther** (1); Nsamba, Peninah (2); Naigaga, Irene (3); Kabasa, John David (2); Bazeyo, William (1,3)

1: Makerere University School of Public Health, Uganda - 2: Makerere University College of Veterinary Medicine, Animal Resources and Biosecurity - 3: One Health Central and Eastern Africa (OHCEA) -

P240 - LATE BREAKERS

### What is the cost of snakebite envenoming? A One Health approach to the economic impact assessment of snakebite based on primary data collection and multi-method analysis

Babo Martins, Sara (1); Chappuis, Francois (2); Ray, Nicolas (3); Alcoba, Gabriel (2); Ochoa, Carlos (3); Bolon, Isabelle (1); **Ruiz de Castañeda, Rafael** (1)

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P241 - LATE BREAKERS

### Comparison of the Effectiveness of Colistin Monotherapy and Colistin-meropenem Combination Therapy in the Treatment of Nosocomial pneumonia Caused by Carbapenem resistant Acinetobacter baumannii

**Poosirianusorn, Naphat;** Nakseannun, Atima; Katip, Wasan; oberdorfer, Peninah  
Chiang Mai University, Thailand -

P242 - LATE BREAKERS

### Effect of antibiotic de-escalation for treatment gram negative bacterial infections with extended-spectrum-β-lactamase-producing organism at Maharaj Nakorn Chiang Mai Hospital

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P243 - LATE BREAKERS

### A new global medical concept - one health - Romania

**Predoi, Gabriel** (1); Barbuceanu, Florica (2); Manolescu, Nicolae (3); Cinca, Sabin (4); Raita, Stefania (1); Furnaris, Florin (1); Balint, Emilia (1)

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P244 - LATE BREAKERS

### Sero-prevalence of Brucellosis and risk factors associated with past infection in the General Rural Population of Punjab, India

Mangtani, Punam (1); **Berry, Isha** (1,2); Beauvais, Wendy (1); Holt, Hannah (3); Kulashri, Amit (4); Bharti, Satinder (4); Sagar, Vivek (4); Nguidop-Djommo, Patrick (1); Bedi, Jasbir (5); Kaur, Manmeet (4); Guitian, Javier (3); Grover, Gagandeep (6); Gill, JPS (5); Kumar, Rajesh (4)

1: London School of Hygiene and Tropical Medicine, London, UK - 2: Dalla Lana School of Public Health, University of Toronto, Toronto, Canada - 3: Royal Veterinary College, London, UK - 4: School of Public Health, Postgraduate Institute of Medical Education and Research, Chandigarh, India - 5: Guru Angad Dev Veterinary and Animal Sciences University, Ludhiana, India - 6: Directorate of Health & Family Welfare, Govt. of Punjab, Chandigarh -

P245 - LATE BREAKERS

### Proprotein convertase subtilisin/kexin type 9 interacts with hepatitis C virus NS5A protein and inhibits viral replication

**Li, Zhubing** (1,2); Liu, Qiang (1,2)

1: University of Saskatchewan, Canada - 2: Vaccine and Infectious Disease Organization-International Vaccine Centre, Canada -

P246 - LATE BREAKERS

### A qualitative inquiry to understand the drivers affecting uptake of health promotion intervention to reduce zoonotic infections and non-prescribed veterinary antibiotics use in peri-urban small holder dairy farms in India

**Chauhan, Abhimanyu Singh** (1); Lindahl, Johanna (2,3,4); Grace, Delia (2); Kakkar, Manish (1)

1: Public Health Foundation of India, India - 2: International Livestock Research Institute, Kenya - 3: Zoonosis Science Laboratory, Uppsala University, Sweden - 4: Department of Clinical Sciences, Swedish University of Agricultural Sciences, Sweden

P247 - LATE BREAKERS

### Understanding the Role of Porcine Reproductive and Respiratory Syndrome Virus Minor Glycoproteins in Porcine Immune Response

**Asavajaru, Akarin** (1); Uhlemann, Eva (2); Van Kessel, Jill (1); Strom, Stacy (1); Dmitriev, Oleg (2); Gerdt, Volker (1)

1: Vaccine and Infectious Disease Organization (VIDO) - International Vaccine Center (InterVac), University of Saskatchewan, Canada - 2: Department of Biochemistry, College of Medicine, University of Saskatchewan, Canada -

P248 - LATE BREAKERS

### Exploring effective therapeutic options against Extensively Drug Resistant (XDR) S. Typhi infections

**Khan, Erum**; Saeed, Dania; Shaheen, Ghazala; Shahid, Asima; Hasan, Rumina; Shakoor, Sadia

Aga Khan University, Pakistan -

P249 - LATE BREAKERS

### Estimation of the incidence of human brucellosis infection in Punjab, India, using a reversible catalytic mathematical model fitted to sero-prevalence data

Berry, Isha (1); Wynnycky, Emilia (1); Beauvais, Wendy (1); Holt, Hannah (2); Guitian, Javier (2); Kumar, Rajesh (3); Mangtani, Punam (1); **Nguidop Djomo, Patrick** (1)

1: London School of Hygiene and Tropical Medicine, United Kingdom - 2: Royal Veterinary College, London, UK - 3: School of Public Health, Postgraduate Institute of Medical Education and Research, Chandigarh, India -

P250 - LATE BREAKERS

### Peri-urban dairy farming in emerging livestock systems and transmission potential of brucellosis to occupational risk groups and the general population in West and Central Africa: A tale of two countries

**Nguidop Djomo, Patrick** (1); Musallam, Imadidden (2); Ndjoung Ndour, Andrée Prisca (3); Mouiche Moulom, Mohamed Moctar (4); Yempabou, Damitoti (3); Ngong, Cha'Ah Crystella (4); Nguend Mbock, Jacques (5); Thioub, Daouda (6); Akakpo, Ayayi Justin (3); Diop, Sylvie Audrey (6); Mangtani, Punam (1); Guitian, Javier (2)

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P251 - LATE BREAKERS

### Therapeutic failure as a challenge to overcome in the zoonotic transmission of sporotrichosis in Brazil

**Abreu, Daniel Paiva Barros de**; Gomez, Marisol Alvim; Makita, Mário Tatsuo; Bonci, Mário Mendes; Baroni, Francisco de Assis Federal Rural University of Rio de Janeiro, Brazil -

P252 - LATE BREAKERS

### Bat cells persistently infected with Middle East respiratory syndrome (MERS) coronavirus: a molecular model to study spill over

**Banerjee, Arinjay** (1); Subudhi, Sonu (1); Rapin, Noreen (1); Falzarano, Darryl (2); Misra, Vikram (1)

1: University of Saskatchewan, Canada - 2: Vaccine and Infectious Disease Organisation-International Vaccine Centre (VIDO-InterVac) -

P253 - LATE BREAKERS

### Altered Translation Regulation Promotes miR-122-independent Replication of Hepatitis C Virus Genomes.

**Panigrahi, Mamata**; Wilson, Joyce University of Saskatchewan, Canada -

P254 - LATE BREAKERS

### Toxoplasma gondii exposure in free-ranging wolverine (Gulo gulo): serostatus and risk factors

**Sharma, Rajnish** (1); Harms, Jane (2); Jung, Tom (2); Kukka, Piia (2); Parker, Sarah (3); Bachand, Nick (1); Al-Adhami, Batol H (4); Gajadhar, Alvin A (1); Jenkins, Emily (1)

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P255 - LATE BREAKERS

### Responsible antimicrobial usage in practice – putting the “Action” back in National Action Plans in Bangladesh

**Rahman, Mohammad Habibur** (1); Sultana, Sayeda Papia (2); Smith, Ingrid (3); Lejeune, Jeffrey T (4); Crafter, Sally (5); Rahman, Md. Sayedur (6); Debnath, Nitish C (1); Brum, Eric (1)

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P256 - LATE BREAKERS

### Stressors in persistently infected bats may influence the severity of the disease and/or increase virus shedding

**Subudhi, Sonu** (1); Paranjape, Neha (1); Rapin, Noreen (1); Davy, Christina (2); Donaldson, Michael (2); Misra, Vikram (1)  
1: University of Saskatchewan, Saskatoon, Canada  
2: Trent University, Peterborough, Canada -

P257 - LATE BREAKERS

### Genotypic characterization of salmonella spp. Isolated from wild animals in 3 selected wildlife holding centres in north central Nigeria

**Oludairo, Oladapo Oyedeji** (1); Kwaga, Jacob K. P. (2); Kabir, Junaid (2); Abdu, Paul A. (2); Gitanjali, Arya (3); Perrets, Ann (3); Cibir, Veronica (4); Lettini, Antonia Anna (4)  
1: University of Ilorin, Nigeria; 2: Ahmadu Bello University, Zaria, Nigeria; 3: OIE Salmonella Reference Laboratory, National Microbiology Laboratory, Public Health Agency of Canada, Guelph, ON, Canada; 4: Salmonella Reference laboratory, Istituto Zooprofilattico Sperimentale delle Venezie Viale dell'Università, Legnaro (PD), Italy

P258 - LATE BREAKERS

### Rabies burden in developing countries: nigeria perspective

**Aiyedun, Julius Olaniyi** (1); NWOHA, Rosemary I. O. (2); Oludairo, Oladapo Oyedeji (1)

1: University of Ilorin, Nigeria; 2: Michael Okpara University of Agriculture, Umudike, Nigeria"

P259 - LATE BREAKERS

### Health education strategies in enhancing rabies control and prevention in Nigeria.

**Nwoha, Rosemary I. O** (2); Aiyedun, Julius Olaniyi (1); Oludairo, Oladapo Oyedeji (1)

1: University of Ilorin, Nigeria; 2: Michael Okpara University of Agriculture, Umudike, Nigeria"

P260 - LATE BREAKERS

### One Health In Practice: Viet Nam's Five Year Strategic Plan For One Health Approaches To Zoonotic Diseases

**Dao, Thu Trang** (1); Payne, David Goodman (1); Coghlan, Ben (2); Vu, Van Minh (3); Nhu, Van Thu (4); Pham, Duc Phuc (5); Sims, Leslie David (6)

1: Vietnam One Health Partnership for Zoonoses, Vietnam; 2: Burnet Institute; 3: Ministry of Agriculture and Rural Development, Vietnam; 4: National Institute of Animal Science, Vietnam; 5: Vietnam One Health University Network (VOHUN); 6: Asia Pacific Veterinary Information Service (APVIS)

P261 - LATE BREAKERS

### Phenotypic characterization and antibiogram of salmonella spp. Isolated from captive wildlife and humans in two zoos and a park in north central nigeria

**Oludairo, Oladapo Oyedeji** (1); Kwaga, Jacob K. P. (2); Kabir, Junaid (2); Abdu, Paul A. (2); Gitanjali, Arya (3); Perrets, Ann (3); Cibir, Veronica (4); Lettini, Antonia Anna (4)

1: Univrsity of Ilorin, Nigeria; 2: Ahmadu Bello University, Zaria, Nigeria; 3: OIE Salmonella Reference Laboratory, National Microbiology Laboratory, Public Health Agency of Canada, Guelph, ON, Canada; 4: Salmonella Reference laboratory, Istituto Zooprofilattico Sperimentale delle Venezie Viale dell'Università, Legnaro (PD), Italy"

P262 - LATE BREAKERS

### Qualitative Approach to Developing a One Health Intervention Strategy for Zoonosis Risk Mitigation in Southern China

**Li, Hongying** (1); Zhu, Guangjian (1); Zhang, Yunzhi (2); Zhang, Libiao (3); Hagan, Emily (1); Chmura, Aleksei (1); Shi, Zhengli (4); Martinez, Stephanie (1); Qasmieh, Saba (1); Francisco, Leilani (1); Daszak, Peter (1)

1: EcoHealth Alliance, United States of America; 2: Yunnan Institute of Endemic Diseases Control and Prevention, China; 3: Guangdong Institute of Applied Biological Resources, Guangdong Academy of Sciences, China; 4: Wuhan Institute of Virology, Chinese Academy of Sciences, China

P263 - LATE BREAKERS

### Attitudes Towards Wildlife Trade and Disease Risk in China

**Li, Hongying** (1); Chmura, Aleksei (1); Ma, Chenyue (2); Gabriel, Grace (3); Daszak, Peter (1)

1: EcoHealth Alliance, United States of America; 2: International Fund for Animal Welfare, China; 3: International Fund for Animal Welfare, Asia

P264 - LATE BREAKERS

### Epidemiology of brucellosis in Nigeria

**Oludairo, Oladapo Oyedeji**; Aiyedun, Julius Olaniyi  
University of Ilorin, Nigeria

P265 - LATE BREAKERS

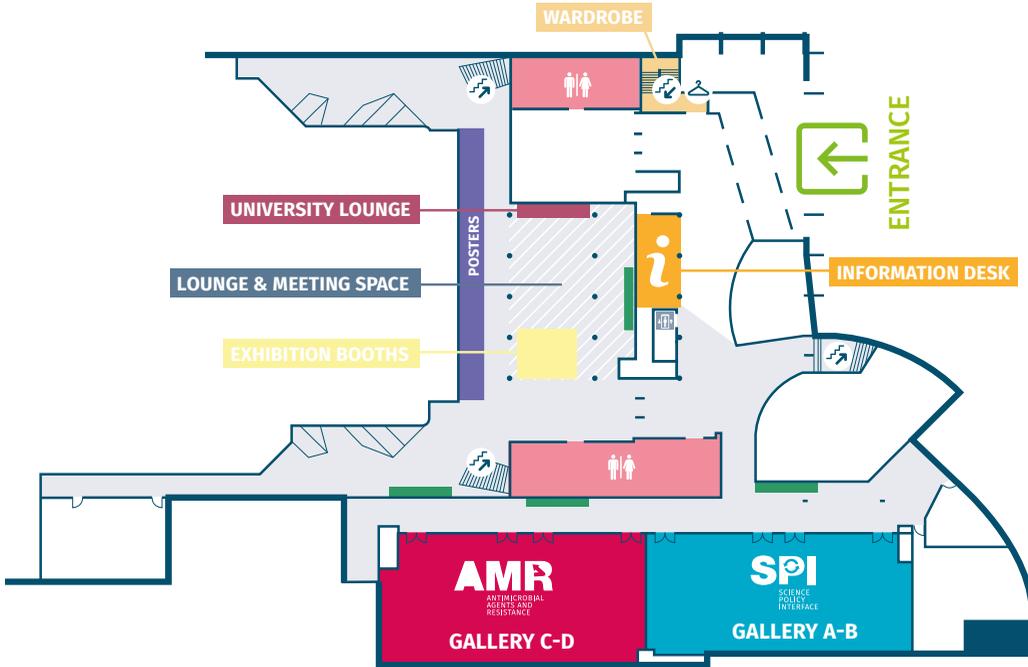
### One Health approach to the prevention and control of mycobacterial infections in Tanzania: Lessons learnt and future perspectives

**Katale, Bugwesa Zablou**; Mbugi, Erasto V; Keyyu, Julius D; Fyumagwa, Robert D; Rweyemamu, Mark M; van Helden, Paul D; Dockrell, Hazel M; Matee, Mecky I  
Southern African Centre for Infectious Disease Surveillance (SACIDS)



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