10th One Health Bangladesh Conference

One Health Capacity Building for Health Security

ABSTRACT BOOK

26-28 November 2019

Radisson Blu Dhaka Water Garden

Dhaka, Bangladesh

Cover design
Shohag Datta

Date of Publishing
26 November 2019

Publisher
One Health Secretariat
Institute of Epidemiology, Disease Control & Research (IEDCR)
Mohakhali, Dhaka 1212, Bangladesh
Web: www.iedcr.gov.bd
Tel: +880-2-9898796, +880-2-9898691
Fax: +880-2-9880440
E-mail: info@iedcr.gov.bd

Printer

Preface

One Health Bangladesh and One Health Secretariat are going to organize 10th Annual Conference from 26 November, 2019. Theme of this year's conference is "One Health Capacity Building for Health Security." The purpose of the conference is to discuss and garner strong commitment for incremental investment for health security using one health approach.

The imprint of decade long One Health movement is clearly visible in Bangladesh with tangible progress in institutionalization, coordinated surveillance and response, workforce development, and food safety and security.

The vitality of global economy largely depends on the collective health of our human, animal and plants including the overall ecosystems. Death of about 300,000 people due to H1N1 pandemic in 2009, fatalities of more than 10,000 people due to Ebola, billions of dollars lost due to MERS-COV in South Korea and loss of 12 billion dollar due to SARS are only few examples of devastating power of health threats that does not respect political boundaries of the nations. The high burden of diseases due to uncontrolled physical growth of urban centres and climate change as demonstrated by the unprecedented upsurge of vector borne diseases in recent times has caused huge sufferings, losses and woes to individuals, families, communities, and nations.

The burden of emerging infectious diseases and threat of antibiotic resistances cannot be overstated. The capacities of health systems of a nation are critical for ensuring health security of nation as well as the world as exemplified by the outbreaks of Ebola in capacity compromised African nations. Weak health security capacities in any part of the world may threaten the global health system.

This health system encompasses the entire range of sectors and disciplines engaged in human, animal and ecosystems interface not merely the public health sector in the narrowest sense. Investment for human and physical capacity building remains far from adequate and staggeringly low in the developing world with scanty investment in animal and wild life health.

The conference invited submission of abstracts on six thematic areas and huge interest were generated among the scientists, researchers and professionals. We received large number of abstracts and selected either for oral or poster presentation. In addition, authorities of theme areas were invited to speak in the conference. This year panel of international scientists and panelists will discuss on six key areas and participants will be engaged for devising future directives for those areas.

The abstract book contains abstracts of oral, poster and key note presentations. We thank the reviewers, editing panel members and contributors. We also thank members of organizing committee and other sub committees for their tireless endeavors to make this conference a success. We express our gratitude towards World Health Organization (WHO), Food and Agricultural Organization (FAO), and Directorate General of Health Services (DGHS) for their technical support and cordial assistance. Special thanks go to the members of scientific sub-committee and souvenir publication sub-committee for their diligence for editing, compiling and publishing the abstract in the form of a book.

We express our sincere gratitude to all those who were instrumental for successful holding of the conference. We gratefully acknowledge the contribution of different institutions of the Government of Bangladesh and development partners for organizing the conference.

Nitish C Debnath
National Coordinator,
One Health Bangladesh &
Chair, Conference Organizing Committee

Meerjady Sabrina Flora
Director,
Institute of Epidemiology Disease Control and Research (IEDCR) &
Chair, One Health Secretariat Coordination Committee

Table of Contents

10th One Health Bangladesh Conference

26-28 November 2019
Radisson Blue Dhaka Water Garden

Committes and sub-committes of the Conference

1. Advisory Committee (Not according to seniority)

1.	Prof. Dr. Abul Kalam Azad, DG DGHS, MoHFW	Chairperson
2.	Major General (Dr.) Md Fashiur Rahman AMC – Director General, Directorate General Medical Service (DG DGMS)	Member
3.	Major General Md Mahbubur Rahman, DG, Drug Administration, MoHFW	Member
4.	Dr. Md Ainul Haque, Director General, Department of Livestock Services (DLS)	Member
5.	Mr.Mohammed Shafiul Alam Chowdhury, Chief Conservator of Forests. Bangladesh Forest Department, Bana Bhaban	Member
6.	Dr. Md Abdul Muyeed, Director General, Department of Agricultural Extension, Khamarbari, Farmgate, Dhaka	Member
7.	Kbd.Quazi Shams Afroz, Director General, Department of Fisheries, Matsya Bhaban, Ramna, Dhaka	Member
8.	Dr. Nathu Ram Sarker, Director General, Bangladesh Livestock Research Institute, Savar, Dhaka	Member

2. Organizing Committee (Not according to seniority)

1.	Prof. Dr. Nitish C Debnath, Director, Pet Hospital, CVASU	Chairperson
2.	Prof.Dr. Meerjady Sabrina Flora, Director, IEDCR, MoHFW	Co- Chairperson
3.	Dr. Abdul JabbarSikder, Director (Adm), DLS	Member
4.	Mr. Jahidul Kabir, CF, Wildlife, BFD	Member
5.	Kbd. Sabbir Ibne Jahan, Director, Plant Protection Wing, DAE	Member
6.	Prof. Dr. Sanya Tahmina, Director, CDC, & LD, CDC, DGHS	Member
7.	Dr. Md. Ainul Haque, Former DG,LRI,Mohakhali, Dhaka	Member
8.	Prof. Dr. Shah Monir Hossain, Former DG of Health Services	Member
9.	Prof. Dr. Tahmina Shirin, CSO, IEDCR	Member
10.	Dr. S M Bokhtiar, Director, SAARC Agriculture Center	Member
11.	Mollah Md Rezaul Karim, Director, Botanical Garden	Member
12.	Prof. Dr. Md Ahasanul Hoque, CVASU	Member
13.	Prof. Sharmin Choudhury, Director, One Health Institute, CVASU	Member
14.	Dr. Sheikh Azizur Rahman, Director, Extension, DLS	Member
15.	Prof. Dr Abul Faiz, Professor of Medicine & Former DG, DGHS	Member

16.	Kazi Shams Afroz, Director, Inland Fisheries, Department of Fisheries	Member
17.	Brig. Gen. Shahidullah, AMC, Dhaka	Member
18.	Prof. Dr. Iqbal Kabir, Director, Planning, DGHS	Member
19.	Dr. Minati Rani Saha, CSO, IEDCR	Member
20.	Dr. Begum Noor Jahan Toly, Chief, Epidemiology Unit, DLS	Member
21.	Prof. Dr. Mahmudur Rahman, former Director, IEDCR	Member
22.	Prof. Dr. Be-Nazir Ahmed, ASCEND	Member
23.	Prof. Dr. KBM Saiful Islam, Sher-E-Bangla Agriculture University, Dhaka	Member
24.	Mr. Mohammad Shamsul Azam, DCCF, Social Forestry Wing	Member
25.	Dr. Firdausi Qadri, Sr Scientist, icddrb	Member
26.	Dr. Iqbal Ansary Khan, PSO, IEDCR	Member
27.	Dr. A S M Alamgir, PSO, IEDCR	Member
28.	Dr. Bazlur Rashid PSO CDIL	Member
29.	Prof. Dr. Md. Jalal Uddin Sarder, RU	Member
30.	Krishibid Ashraful Islam Ranga	Member
31.	Dr. Md Abdul Matin, BAPA	Member
32.	Dr. Shahidul Islam, BAPA	Member
33.	Prof. Dr. Md. Khurshed Alam Bhuiyan,	Member
34.	Prof. Dr. Siddiqur Rahman, Department of Medicine, BAU	Member
35.	Prof. Dr M Bahanur Rahman, BAU, Mymensingh	Member
36.	Prof. Dr. Rafiqul Islam, Sr Consultant, FAO	Member
37.	Prof. Dr. Ashraf Ali, CVASU	Member
38.	Dr. Mohua Yesmin, LRI, Mohakhali, Dhaka	Member
39.	Dr. AHM Saiful Islam, Deputy Director, DLS	Member
40.	Mr. Md. Sayedur Rahman, Deputy Conservator Forests	Member
41.	Dr. AKM Ataur Rahman, DLS	Member
42.	Mr. Ramzan Ali, Deputy Director (Adm), DOF, Dhaka	Member
43.	Dr. TABM Mozaffar Goni Osmani, ULO, Epidemiology Unit, DLS	Member
44.	Dr. Munzur Mohammad Shahazada, NATP, DLS	Member
45.	Dr. Mahbubur Rahman, IEDCR	Member
46.	Dr. Ahmad Raihan Sharif, IEDCR	Member
47.	Prof. Syed Masud Ahmed, BRAC JPGSPH, BRAC University	Member
48.	Dr. Mohammad Mushtuq Husain, Advisor, IEDCR	Member
49.	Dr Nazneen Akhter, NSU Faculty Dhaka	Member
50.	Dr. Ashek Ahammed Shahid Reza, DS Consultant, IEDCR	Member
51.	Mr. Isteaque Uddin Ahmad, IUCN	Member
52.	Dr. El Sakka Al Hammam WHO	Member
53.	Dr. Eric Brum, TL, ECTAD, FAO	Member
54.	Dr. Shahidul Islam, BAPA	Member
55.	Ms. Neha Kapil, Unicef	Member
56.	Md. Abul Kalam, USAID	Member

57.	Krishibid Ashraful Islam Ranga	Member
58.	Dr. Ariful Islam, Eco Health Alliance	Member
59.	Dr Michael S Friedman, Country Director, US CDC, Bangladesh	Member
60.	Dr. Mehedi Hossian, KGF, BARC	Member
61.	Dr. Kazi Mohammad Hassan Ameen, WHO	Member
62.	Ms. Ariella Camera, USAID	Member
63.	Prof. Dr. Md. Khurshed Alam Bhuiyan, BSMRAU, Gazipur	Member
64.	Dr. K. Munisul Islam, icddr,b	Member
65.	Ms. Nadia Ali Rimi,icddr,b	Member
66.	Dr.Md. Nurul, Islam, TO, FETPV, CVASU	Member
67.	Dr. M. Salim Uzzaman, PSO, IEDCR	Member –Secretary

Responsibility:

- Plan and organize the One Health Conference program
- Maintain liaison with national and international agencies for the successful conference
- Coordinate and supervise sub-committees
- Co-opt member(s) as and when required

3. Reception, registration and invitation sub-committee

1)	Prof. Dr. Tahmina Shirin, IEDCR	Convener
2)	Dr. Kazi Mohammad Hassan Ameen, WHO	Member –Secretary
3)	Dr. Minati Rani Saha, IEDCR	Member
4)	Dr. Zakir Hossain Habib, IEDCR	Member
5)	Dr. Quazi Ahmed Zaki, IEDCR	Member
6)	Dr. Sharmin Sultana, IEDCR	Member
7)	Dr. Sultan Farida, IEDCR	Member
8)	Dr. Tanzila Naureen, IEDCR	Member
9)	Dr. Natasha Khurshid, IEDCR	Member
10)	Dr. Sudipta Sarkar, IEDCR	Member
11)	Dr. Saima-Binte-Golam Rasul, IEDCR	Member
12)	Dr. ASM Abdul Hannan, OHS/DLS	Member
13)	Dr. Mohua Yasmin, ULO, LRI	Member
14)	Dr. KabiunNesa, LRI	Member
15)	Dr. Faisol Talukder, Epi Unit, DLS	Member
16)	Dr.Tahmina Begum, ULO,LRI	Member
17)	Dr. Sonali Debnath, ULO,LRI	Member
18)	Dr. Mujaddeed Ahmed, Public Health Physician	Member
19)	Dr. Ashish Kundu, LRI	Member
20)	Dr. Tanima Islam, FETP Fellow, IEDCR	Member
21)	Dr. Shahjahan Siraj, Provita Chicks	Member
22)	Dr. Shusmita Dutta, IEDCR	Member
23)	Dr. Jinnat Ferdous, IEDCR	Member

Responsibility:

- Registration (prepare data base) and distribution of conference brochures
- Provide name-tags for the conference participants.
- Conference kit preparation (Provide file, pads, pen for the participants at registration) and distribution
- Collection and maintenance of accounts for registration
- Any activity related to invitation of chief & special guests
- Ensure banner and stands
- Co-opt member(s) as and when required

4. Souvenir publication, communication& publicity sub-committee

1)	Mr. Jahidul Kabir, CF, Wildlife, BFD	Convener
2)	Dr. Mohammad Mushtuq Husain, IEDCR	Member –Secretary
3)	Dr. Abu Syed Md AbdulHannan, DLS	Member
4)	Dr. M Salim uzzaman, IEDCR	Member
5)	Dr. Ahmad Raihan Sharif, IEDCR	Member
6)	Dr. Samsad Rabbani Khan, IEDCR	Member
7)	Dr. Md. Omar Qayum, IEDCR	Member
8)	Dr. Nurul Islam, Global Health Development	Member
9)	Dr. Ali Ahasan, Asstt Director, Epidemiology Unit, DLS	Member
10)	Dr. Mehedi Hossain, Former Director, DLS	Member
11)	Dr. Kulsum, Food Safety Project, FAO	Member
12)	Lt Col (Dr.) Omar Rashed Munir. AFMSD. Bangladesh Armed Forces	Member
13)	Dr. Mujaddeed Ahmed, Public Health Physician	Member
14)	Prof. Dr. Taohidul Islam, Department of Medicine, BAU	Member
15)	Dr. Md. Hemayatul Islam, Deputy Chief Veterinary Officer, RU	Member

Responsibility:

- Managing and ensure timely souvenir publication, communication & publicity
- Coordinate activities with the scientific sub-committee and reception, registration and invitation sub-committee.
- Timely design and distribution of souvenir, leaflets and registration materials
- Communicating with all One Health members and participants to keep them updated
- Advertisement on print and electronic media
- Co-opt member(s) as and when required

5. Conference scientific session management sub-committee

1)	Dr. Md. Ainul Haque, Director, LRI	Convener
2)	Dr. Abul Kalam Azad, USAID	Member –Secretary
3)	Prof. Rafiqul Islam, FAO, ECTAD	Member
4)	Dr. Mohammad Mushtuq Husain, IEDCR	Member
5)	Dr. Abu Syed Md Abdul Hannan, DLS	Member
6)	Dr. M Salim Uzzaman, IEDCR	Member
7)	KBM Saiful Islam, Sher-E-Bangla AU	Member

8)	Dr. Ahmad Raihan Sharif, IEDCR	Member
9)	Dr. Manjur Hossain Khan Jony, IEDCR	Member
10)	Dr. Anupam Sarker, IEDCR	Member
11)	Dr. Arifa Akram, IEDCR	Member
12)	Dr. Md. Omar Qayum, IEDCR	Member
13)	Ms. Nadia Ali Rimi, iccdr,b	Member
14)	Dr. Md. Abdus Samad, BLRI, Savar	Member
15)	Dr. Nurul Islam, Global Health Development	Member
16)	Col (Dr.) Md Mohshin, Asst Director General. DGMS	Member
17)	Col (Dr.) Md Saidur Rahman. AFMI	Member
18)	Dr. K. M. Mozaffar Hossain, Department of Animal Science, RU	Member
19)	Prof. Dr. Md. Jalal Uddin Sarder, RU	Member
20)	Dr. Mujaddeed Ahmed, Public Health Physician	Member
21)	Dr. Md. Kaisar Rahman, IEDCR	Member
22)	Dr. Shariful Islam, IEDCR	Member

Responsibility:

- Prepare conference schedule, themes & conference agenda
- Managing the scientific session including audio-visual function, maintaining presentation in designated laptop.
- Coordinate presentations and implementation of conference set-agenda systematically.
- Collect the PowerPoint files (for the computer presentation)
- Nominate/select chairperson and co-chair, rapporteur (and note taker) for the plenary-session work.
- Select chairand co-chair, time keeper for the paper- presentation session
- Decoration and management of conference hall including dais
- Co-opt member(s) as and when required

6. Scientific sub-committee

1.	Prof. Dr. Meerjady Sabrina Flora, Director, IEDCR	Convener
2.	Dr. Mahbubur Rahman, IEDCR	MemberSecretary
3.	Dr. Md. Ashraful Alam, PSO, IEDCR	Member
4.	Dr. ASM Alamgir, IEDCR	Member
5.	Dr. Noor E Alam Siddique, BLRI	Member
6.	Dr. Nazneen Akhter, NSU	Member
7.	Dr. TABM Mozaffar Goni Osmani, DLS	Member
8.	Dr. M Salim Uzzaman, IEDCR	Member
9.	Dr. Anupam Sarker, IEDCR	Member
10.	Lt Col (Dr.) Syed Abul Hassan Md Abdullah, DGMS	Member
11.	Dr. Md. Sohrab Hossain, Gazipur City Corporation	Member
12.	Dr. Natasha Khurshid, Managing Editor, NBPH, IEDCR	Member
13.	Dr. NahitunNaher, BRAC JPGSPH, BRAC University	Member
14.	Dr. Zobaidul Haque Khan, Eco Public Health Foundation	Member

15. Dr. Ariful Islam, Eco Health Alliance, IEDCR	Member
16. Dr. Abdus Samad, BLRI	Member
17. Dr. KaziMunisul Islam, icddr,b	Member
18. Dr. A F M Rakibul Hasan Bhuiyan, OHS, IEDCR	Member
19. Samiun Nazrin Bente Kamal, BRAC, JPGSPH	Member
20. Isha Bery, IEDCR	Member
21. Dr. Tanvir Hayder, IEDCR	Member
22. Dr. Humyra Shah, IEDCR	Member

Responsibility:

- Select panel for reviewers and finalize the abstract for the One Health conference.
- Coordinate activities with souvenir, publication & publicity sub-committee to organize and print abstracts
- Coordinate activities with conference scientific session management sub-committee
- Organize presentation date and time

7. Transport &Accommodation Sub-Committee

1) Dr. Iqbal Ansary Khan, IEDCR	Convener
2) Dr. Ahmad Raihan Sharif, IEDCR	Member –Secretary
3) Dr. Quazi Ahmed Zaki, IEDCR	Member
4) Dr. Mohammad Ferdous Rahman Sarker, IEDCR	Member

Responsibility:

- Organize transportation for the foreign guest as required
- Coordinate parking (at conference venue)
- Co-opt member(s) as and when required

8. Finance Committee

1) Dr. Md. Abul Kalam Azad, USAID	Convener
2) Dr. M Salim Uzzaman, IEDCR	Member –Secretary
3) Dr. Ashek Ahammed Shahid Reza, IEDCR	Member

Responsibility:

- Ensure financial support from all the partners
- Coordination with organizing committee and other subcommittees.
- Co-opt member(s) as and when required

9. Food & refreshment sub-committee

1. Dr. Ashek Ahammed Shahid Reza, IEDCR	Convener
2. Dr. Manjur Hossain Khan, IEDCR	Member –Secretary
3. Dr. Reefat Rubbi, IEDCR	Member
4. Dr. Ariful Islam, EcoHealth Alliance, IEDCR	Member
5. Dr Ferdous Rahman Sarker, IEDCR	Member
6. Dr. Nusrat Sharmin Popy, IEDCR	Member

7. Dr. Asif Iqbal, IEDCR	Member
8. Dr. Omar Qayum, IEDCR	Member
9. Dr. Farzana Islam Khan, IEDCR	Member
10. Dr. Shah Niaz Md. Rubaid Anwar, IEDCR	Member
11. Dr. Sudipta Sarker, IEDCR	Member
12. Dr. Sharmin Farzana, IEDCR	Member
13. Dr. Shafiul Islam, IEDCR	Member
14. Dr. Shusmita Datta, IEDCR	Member
15. Dr. Debasis Kumar Shaha, IEDCR	Member
16. Dr. Tanima Islam, IEDCR	Member
17. Dr. Md. Jahidur Rahman, IEDCR	Member
18. Dr. Ashis Kumar Kundu, IEDCR	Member

Responsibility:

- Ensure food and refreshments for all vip guest, journalist and participants
- Coordinate sittings arrangements for all vip guest, journalist and participants during meals
- Coordination with conference scientific session management sub-committee for time schedule of tea-breaks, lunch and dinner timings.
- Co-opt member(s) as and when required

10. Cultural sub-committee

1. Dr. Minati Rani Saha, CSO, IEDCR	Convener
2. Dr. Mohua Yeasmin, DLS	Member –Secretary
3. Dr. Asif Iqbal, IEDCR	Member
4. Dr.ASM Sabur, LRI	Member
5. Dr. Monalisa, IEDCR	Member
6. Dr. ArifaAkram, IEDCR	Member
7. Dr. Natasha Khurshid, IEDCR	Member
8. Dr. Shusmita Dutta, IEDCR	Member
9. Krishibid Ashraful Islam Ranga	Member
10. Dr. Md. Ashiqur Rahman, IEDCR	Member

Responsibility:

- Responsible for the overall cultural program at the conference
- Coordinate activities and timing with other committees & sub-committees.
- Co-opt member(s) as and when required

PROGRAM SCHEDULE

Day 1: 26 November 2019	
16:00 – 18:00	Annual General Meeting of One Health Bangladesh *(Only for life and general member of One Health Bangladesh)* Utsab Hall, Radisson Blu Dhaka Water Garden
	Inauguration ceremony
18:30 – 19:00	Registration
19:00 – 19:05	Welcome address: **Professor Dr Meerjady Sabrina Flora** Director, Institute of Epidemiology, Disease Control & Research (IEDCR) and Chair, One Health Coordination Committee
19:05 – 19:15	Key note presentation: **Professor Nitish Chandra Debnath** Chair, Organizing Committee of 10th One Health Conference & Professor, Chattogram Veterinary and Animal Science University (CVASU)
19:15 – 19:20	Speech by Guest of Honour: **Dr Bardhan Jang Rana** WHO Representative in Bangladesh (*on behalf of all development partners*)
19:20 -19:25	Speech by Guest of Honour: **Quazi Shams Afroz** Director General, Department of Fisheries
19:25 – 19:30	Speech by Guest of Honour: **Dr Shaikh Azizur Rahman** Director General, Department of Livestock Services (DLS)
19:30 – 19:35	Speech by Guest of Honour: **Mr Mohammed Shafiul Alam Chowdhury** Chief Conservator of Forest, Forest Department
19:35 – 19:40	Speech by Guest of Honour: **Dr. Md. Abdul Muyeed** Director General, Department of Agricultural Extension
19:40 – 19:45	Speech by Guest of Honour: **Professor Dr Abul Kalam Azad** Director General of Health Services
19:45 – 19:55	Speech by Special Guest: **Ms Habibun Nahar MP** Honourable Deputy Minister, Ministry of Environment, Forest and Climate Change
19:55 – 20:05	Speech by Special Guest: **Mr. Dhirendra Debnath Shambhu MP** Honourable Chairman, Standing Committee on Ministry of Fisheries & Livestock,

	Bangladesh National Parliament
20:05 – 20:20	Speech by Chief Guest: **Krishibid Dr Muhammad Abdur Razzaque MP** Honourable Minister, Ministry of Agriculture
20:20 – 20:35	Address by Chairperson: **Mr. Zahid Maleque MP** Honourable Minister, Ministry of Health and Family Welfare
20:35 – 21:30	Cultural Evening and Dinner

Day 2: 27 November 2019	
08:00 – 09:00	Registration
09:00 – 10:00	**Panel Discussion–I Are We Ready for Combating Emerging Infectious Disease Epidemics?** **Venue:** Ball room (1st floor) **Moderator:** Dr Guillaume Fournie, Senior Research Fellow, Royal Veterinary College (RVC), UK **Panellists** ▪ Prof Mahmudur Rahman, Consultant, Infectious Disease Division, icddr,b ▪ Dr Md Ainul Haque, Former Director General, Department of Livestock Services ▪ Dr Ishtiaq Uddin Ahmad, Former Chief Conservator of Forest, Forest Department **Rapporteurs** ▪ Dr Nawsher Alam, IEDCR ▪ Dr TABM Mozaffar Gani Osmani, DLS
10:00 – 10:30	**Tea Break**
10:30 – 12:00	**Panel Discussion–II One Health Approach for Rabies Control** **Venue:** Ball room (1st floor) **Moderator:** Prof. Dr Sanya Tahmina, Director, Disease Control and Line Director, CDC, DGHS **Speaker:** • Dr. Shukes Chandra Badhy, CDIL, DLS - Laboratory Diagnosis of Rabies in Cattle and Dog • Dr Umme Ruman Siddiqi, CDC, DGHS - Rabies Elimination Program in Bangladesh: Success and Challenges • Dr Eric Brum, ECTAD, FAO - The Epidemiological Principles of Rabies

	Control and the RACE against Rabies **Panellist:** Prof Dr Be-Nazir Ahmed, Country Lead, ASCEND Bangladesh **Rapporteurs** ▪ Dr Salmunnahar, CDC, DGHS ▪ Dr Kamrul Islam, CDC, DGHS	
12:00 – 13:00	**Poster session** • One Health Research, Practice, Policy and Governance for Addressing Infectious Diseases • Ecosystem Management towards Protecting Environmental Health and Natural Resources	
13:00 – 14:00	**Lunch and Prayer Break**	
14:00 – 15:00	**Parallel Session IA : One Health Research, Practice, Policy and Governance for Addressing Infectious Diseases** Venue: Antara Hall **Co-chairs** ▪ Dr Firdausi Qadri, Emeritus Scientist, icddrb ▪ Dr Md Taohidul Islam, Professor, Bangladesh Agricultural University **Rapporteurs:** ▪ Dr. Manjur Hossain Khan, IEDCR ▪ Dr. Md. Sohidul Islam, DLS	**Parallel Session IB : One Health Research, Practice, Policy and Governance for Addressing Infectious Diseases** Venue: Lohori Hall **Co-chairs** ▪ Professor Mohammad Abul Faiz, Former Director General of Health Services ▪ Prof Dr Md Ahasanul Hoque, Professor, CVASU **Rapporteurs:** ▪ Dr. Qazi Ahmed Zaki, IEDCR ▪ Dr Zinat Sobhan, DLS
14:00– 14:10	19-116: Zoonotic disease dynamics in South India- a topical study	19-46: Incidence and occupational risk factors of avian influenza A virus among a cohort of live bird market poultry workers, Bangladesh: 2012-2017
14:10 – 14:20	19-119: Molecular characterization of Giardia and Cryptosporidium in calves and children in Bangladesh	19-125: Cross Sectional Assessment of Aerosolization of Influenza A Viruses and Potential Transmission Risk for Live Bird Market Workers at the Animal-human Interface in Bangladesh
14:20 – 14:30	19-06: Molecular Epidemiological Analysis on the sources and	19-59: Continuing circulation of new reassortant clade 2.3.2.1a of highly

	diarrheagenecity of Shiga toxin-producing Eshcherichia coli and atypical Enteropathogenic E.coli	pathogenic avian influenza H5N1 virus in chickens in Bangladesh
14:30 – 14:40	19-35: Identifying diseases of farm deer and zoonotic risk prevailing in Bangladesh	19-97: The governance of one-health evidence in Bangladesh
14:40 – 15:00	Open Discussion	Open Discussion
15:00 – 15:30	**Tea break**	
15:30 -16:30	**Parallel Session IIA: Ecosystem Management towards Protecting Environmental Health and Natural Resources** Venue: Antara Hall **Co-chairs** ▪ Md Jahidul Kabir, Director, Sheikh Kamal Wildlife Center, Gazipur ▪ Xerses Sidhwa, USAID Bangladesh Country Office **Rapporteurs** ▪ Dr. Reefat Rubbi, IEDCR ▪ Dr. Faisol Talukder, DLS	**Parallel Session IIB: Ecosystem Management towards Protecting Environmental Health and Natural Resources** Venue: Lohori Hall **Co-chairs** ▪ Prof Md. Shahidur Rashid Bhuiyan, Department of Genetics and Plant Breeding, SAU ▪ Prof Shah Monir Hossain, Former DG, Health Service **Rapporteurs** ▪ Dr. Nusrat Sharmin, IEDCR ▪ Dr. AHM Shadat Hossain, DLS
15:30 – 15:40	19-128: 10 Years of Emerging Pandemic Threat (EPT) PREDICT Program to Prevent Viral Pandemics: Are we ready for Disease "X"?	19-19: Pesticide Exposure among Bangladeshi villagers
15:40 – 15:50	19-115: Tuberculosis at Wildlife-Livestock Interface– Creating Increasing Threat to Public Health and Wildlife Conservation in Bangladesh	19-89: Salt plug formation in the Sundarbans mangrove ecosystem impacts water quality
15:50 – 16:00	19-134: Prevalence and genetic diversity of coronaviruses and paramyxovirus in human at high-risk animal-human interfaces in Bangladesh	19-113: Epidemiology of Antimicrobial Resistance Patterns of *Staphylococcus spp.*, *E. Coli* and *Salmonella spp*. isolated from Rodents and Shrews in Chattogram, Bangladesh
16:00 –	19-126: Epidemiology and Molecular	19-121: Eco-epidemiological assessment

16:10	Characterization of group A Rota virus from Rhesus Macaques (*Macaca mulatta*) at wildlife-Human interface in Bangladesh	of antimicrobial resistance of Salmonella, Staphylococcus and Enterococcus from rhesus macaque at human-animal interfaces in Bangladesh
16:10 – 16:30	Open Discussion	Open Discussion
Day 3: 28 November 2019		
09:00 – 10:30	**Panel Discussion–III Coordinated Approach to Ensure Food Safety and Food Security** **Venue:** Ball room (1st floor) **Moderator:** Prof Robyn Alders, Senior Fellow, Chatham House, UK **Panellists** ▪ Dr Hiresh Ranjan Bhowmik, Former Director General, Department of Livestock Services ▪ Dr S M Mustafizur Rahman, Line Director, NNS, IPHN, DGHS ▪ Dr Md Saleh Ahmed, Postharvest Technology & Management Specialist, Department of Agricultural Extension ▪ Mr. A.K.M. Nurul Afsar, National Team Leader, Institutionalization of Food Safety in Bangladesh for Safer Food, FAO ▪ Dr. Benoy Kumar Barman, Senior Scientist, World Fish, Bangladesh Country Office **Rapporteurs** ▪ Dr. Zakir Hossain Habib, IEDCR ▪ Md Manik Mia, Department of Fisheries	
10:30 – 11:00	**Tea Break**	
11:00 – 12:10	**Parallel Session IIIA : Coordinated Approach to Ensure Food Safety and Food Security** Venue: Antara Hall **Co-chairs** ▪ Dr M A Matin, Vice President, BAPA ▪ Dr. Md. Giasuddin, Head, Animal Health Research Division, BLRI **Rapporteurs** ▪ Dr Monalisa, IEDCR ▪ Dr. Shusmita Dutta Chowdhury,	**Parallel Session IIIB : Intersectoral Engagement in Mitigating Antimicrobial Resistance (AMR)** Venue: Lohori Hall **Co-chairs** ▪ Dr Michael Friedman, Country Director, US CDC Bangladesh Country Office ▪ Prof Kazi Rafiqul Islam, Professor, Bangladesh Agricultural University **Rapporteurs** ▪ Dr. Sharmin Sultana, IEDCR

	IEDCR	▪ Dr. Rubaid Anwar, IEDCR
11:00 – 11:10	19-63: Antibiotic resistance in dairy cattle and farm environment having potential impact on food safety using one health approach	19-144: Antibiotic resistance surveillance in human: a step towards antibiotic containment in Bangladesh
11:10 – 11:20	19-13: Tackling AMR in developed nation (France) versus developing nation (Bangladesh)- A One Health Approach	19-03: Abundance of mobilized colistin resistance gene mcr-1 in genetically diverse commensal Escherichia coli in broiler chicken in Bangladesh
11:20 – 11:30	19-92: Prevalence and antibiotic susceptibility of Vibrio spp. isolated from raw shrimps in Bangladesh	19-15: Risk of multi-drug resistant Campylobacter spp. and residual antimicrobials in poultry farms and markets in the selected districts of Bangladesh
11:30 – 11:40	19-81: Susceptibility and resistance patterns of Escherichia coli to colistin isolated from common food animals at Sylhet division of Bangladesh: an approach to one health	19-74: Residue and potential ecological risk of veterinary antibiotics in poultry manure in Bangladesh: One Health perspective
11:40 – 11:50	19-132: Prevalence and Antimicrobial Susceptibility Pattern of Escherichia coli O157:H7 in calf and milk of Bangladesh: A Cross-Sectional Study	19-31: Mobilized colistin resistance (mcr) genes and tetracycline resistance (tet) genes in multidrug-resistant Escherichia coli circulating in poultry, food and human sources
11:50 – 12:10	Open Discussion	Open Discussion
12:10 – 13:10	**Poster session:** • Coordinated Approach to Ensure Food Safety and Food Security • One Health Approach to Control Vector Borne Diseases • Intersectoral Engagement in Mitigating Antimicrobial Resistance • Inter-professional Workforce Development for Achieving Health Security)	
13:10 – 14:00	**Lunch and Prayer Break**	

14:00 – 15:30	**Panel Discussion–III Inter-professional Workforce Development for Achieving Health Security** **Venue:** Room: Ball room (1st floor) **Moderator:** Vipat Kuruchittham, Executive Director, South East Asia One Health University Network **Panellists** ▪ Prof Dr Nitish Chandra Debnath, Professor, CVASU ▪ Prof Dr Meerjady Sabrina Flora, Director, IEDCR ▪ Dr A E M Mohiuddin Osmani, Joint Chief (Planning), Health Services Division, MoHFW ▪ Prof. Syed Masud Ahmed, Director, Centre of Excellence for Health Systems and Universal Health Coverage, BRAC University **Rapporteurs** • Dr Masum Billah, IEDCR • Dr Md Nurul Islam, GHD	
15:30 – 16:00	**Tea Break**	
16:00 – 17:00	**Parallel Session 4A: One Health Approach to Control Vector Borne Diseases** Venue: Antora Hall **Co-chairs** ▪ Prof Rafiqul Islam, FAO ECTAD ▪ Prof Khurshed Alam Bhuiyan, BSMRAU **Rapporteurs:** ▪ Dr Md Murshidul Ahsan, DLS ▪ Dr Arifa Akram Barna, IEDCR	**Parallel Session 4B: Inter-professional Workforce Development for Achieving Health Security & Others** Venue: Lohori Hall **Co-chairs** ▪ Major General (Dr) Md. Fashiur Rahman AMC – Director General, DGMS ▪ Neha Kapil, UNICEF Bangladesh **s:** ▪ Dr Sazeda Akter, CVASU ▪ Dr Anupam Sarker, IEDCR
16:00 – 16:10	19-11: Reliable identification of potential vector mosquitoes collected from Chittagong Bangladesh through morphotaxonomy and molecular DNA barcoding	19-75: Educational intervention and contents in veterinary education for prudent antibiotic use for one health in Bangladesh
16:10 – 16:20	19-147: Cost-Effectiveness of Dengue Vaccine Introduction in Dhaka City, Bangladesh	19-103: Introducing One Health concept and One Health practices among relevant student communities in Bangladesh

16:20 – 16:30	19-107: Viral etiology among the hospitalized encephalitis patient in Bangladesh	19-141: Behavioral risk practices and zoonotic disease emergence at high-risk communities in Bangladesh: An explorative qualitative study
16:30 – 16:40	19-49: "One Health" Approach for Combating Vector Borne Diseases in Bangladesh	19-72: Evidence of exposure to Brucella among humans and cows in Shahjadpur sub-district, a high milk-producing area in Bangladesh
16:40- 17:00	Open Discussion	Open Discussion
17:00 – 18:00	**Conference Recommendation and Closing**	

(The schedule may be changed due to unavoidable circumstances, please check www.iedcr.gov.bd One Health link for updated schedule)

Schedule (Tentative) for Poster Display

(the schedule may be changed due to unavoidable circumstances, please check www.iedcr.gov.bd One Health link for updated schedule)

Day 2: 27 November 2019

Time: 12:00 – 13:00

ID	Title	ID	Title
19-25	Evaluation of immune response of a heat killed Brucella abortus vaccine in guinea pig by ELISA	19-71	Pilot Experiments to Estimate Respirable Aerosols Produced During Poultry Slaughtering and Defeathering
19-47	Pathogenic E. coli in Drinking Water: Are They Human or Animal in Origin?	19-133	Live Poultry Exposure at the Human-Poultry Interface in Urban Bangladesh: Preliminary Results from a Cross-Sectional Cell-phone Based Survey
19-40	Bacteriological And Hematological Profiles In Balb/C Mice Experimentally Infected With Brucella Abortus Biovar 3	19-33	First Isolation, identification and genetic characterization of Brucella abortus biovar 3 in dairy cattle from some selected areas of Bangladesh
19-55	Knowledge on Nipah Virus Infection among Medical Students of Dhaka city	19-56	Ebola virus disease (EVD) - A retrospective study amongst 149 confirmed cases at Ebola Treatment Unit (ETU), Bong County, Liberia
19-78	One Health Application of Interoperable Technology: a feasibility of interoperability for Evidence-Based Decision-Making for Disease Surveillance and Control	19-09	One Health perceptions of Q fever among the animal science and veterinary students, South Australia
19-146	South Asia One Health disease surveillance network: regional Approach against Emerging infectious disease	19-111	Protective and immuno-efficacy of F-34 Stern strain Anthrax vaccine in mice model
19-41	Chemokine Receptor-5 (CCR5): a new hope in the immunoregulation of rhinovirus-induced severe refractive non-Th2 asthma exacerbation	19-140	An Outbreak Investigation of Anthrax Disease in Gangni, Meherpur District 2019
19-124	Rabies the deadly disease; How much we aware?	19-139	A Baseline Survey on Anthrax Disease in Sirajganj and Meherpur District, Bangladesh
19-45	Addressing governance challenges of preparedness and response to infectious threats and antimicrobial resistance through a sustainable, coordinated international network: SoNAR-Global	19-18	Leptospira epidemiology in dairy cattle of Bangladesh
19-66	Epilepsy like illness in pig rearing villages in Bangladesh, 2016	19-77	Antibacterial efficacy of Allium sativum and Zingiberofficinale against multi drug

			resistant (MDR) poultry pathogens
19-70	Vermicompost production and marketing system from different organic materials using of the earthworm to ensure soil health	19-130	Ecology of bat drinking behavior and antimicrobial resistant patterns of Salmonella spp., Staphylococcus spp. and Escherichia coli recovered from fecaldroppings of fruit bats and water in Bangladesh
19-24	Wild animal's tuberculosis (TB); a hidden source of spreading zoonotic TB	19-58	Epididymal spermatozoa ex-vivo: A potential source for preservation of male gametes for wildlife conservation
19-04	Changes in the reproductive system of the male mice immunized with a plasid DNA vaccine encoding GNRH-1 and T helper epitopes	19-106	The viral etiology of acute febrile illness of in Dhaka, Bangladesh in the year of 2017
19-95	Study of Prevalence and Associated Risk Factors of Anaplasmosis and Theileriasis in Cattle	19-90	Management of an outbreak of Babesiosis in a herd of sheep
19-23	Survey of Coxiellosis related to reproductive disorders in small ruminants	19-118	Immunogenicity of the local anthrax vaccine strain in animal models

Day 3: 28 November 2019

Time: 12:10 – 13:10

ID	Title	ID	Title
19-136	Prevalence of E coli and Salmonella spp. in Fresh Tomatoes at Different Market: A Cross-Sectional Study	19-99	Antimicrobial Resistance in acute Diarrhoeal cases at Bangladesh Institute of Tropical & Infectious Diseases (BITID) from April 2017 to April 2019
19-137	Prevalence of Vibrio cholerae in Pangasius fish with public practice and perception: A food safety concern	19-38	Surveillance and detection of antibiotic residues in poultry meat samples from Trishalupazila of mymensingh
19-43	ISOLATION, IDENTIFICATION AND ANITIBIOGRAM ASSAY OF SALMONELLA FROM CHICKEN EGGS	19-101	AMR and AMU perspective among physicians and veterinarians: opportunities of implementing ONE Health approach
19-14	Appraising meat quality of market broiler and ensuring consumer safety	19-17	Isolation, identification and antimicrobial resistance of Campylobacter spp. from the preputial swab samples of bulls
19-42	ISOLATION, IDENTIFICATION AND ANTIBIOGRAM STUDY OF ESCHERICHIA COLI FROM CHICKEN EGGS	19-57	Occurrence of antimicrobial resistance genes among shiga toxin-producing Escherichia coli isolated from sheep in rural Bangladesh
19-91	Cockroaches: A source of multidrug resistant pathogenic strains of Escherichia coli	19-62	Virulence determinants and antimicrobial resistance of E. coli in house flies (Musca domestica) captured from various

			environmental settings in Mymensingh, Bangladesh
19-51	Prevalence and risk factors of Campylobacter infection in broiler and cockerel flocks in Mymensingh and Gazipur districts of Bangladesh	19-28	Assessment of antibiotic residues and bacterial load in eggs collected from local markets of selected areas of mymensingh district
19-76	Investigation of anti-microbial activity of ash filtrates	19-52	Socio-demographic determinants of use and misuse of antibiotics in commercial poultry farms in Bangladesh
19-16	Microbial evaluation of fresh vegetables collected from different markets of Jamalpur, Netrokona and Kishoregonj districts	19-61	Prescribing antibiotic drugs for Bangladeshi patients: evidence from a scoping review
19-48	Detection and quantification of heavy metals and minerals in poultry feeds collected from local market of Sherpur	19-82	Prevalence of ESBL-producing multi-drug resistant E. coli, Salmonella and P. multocida in buffalo calves at Sylhet and Barisal division of Bangladesh
19-96	Assessing the food safety condition of the broiler shops and broiler meats at the live bird markets in Chattogram city	19-135	Antimicrobial resistance profile of bacteria causing pneumonia in goats brought to S AQuaderi Teaching Veterinary Hospital (SAQTVH), CVASU
19-94	Isolation and characterization of human pathogenic Vibrio cholerae from chicken	19-50	Antimicrobial resistance pattern of foodborne bacteria in wholesale chicken markets in Bangladesh
19-142	Detection of pathogens distribution, antibacterial susceptibility along with usage of antibiotics in mastitis in Chattogram: A food safety issue	19-53	Multi-drug resistant and extended spectrum β-lactamases producing Salmonella spp. in red meat of cattle
19-79	Development of estrus synchronization protocols using hormones in anestrus cows for improved reproductive performance	19-05	Irrational use of antibiotics and risk of bacterial resistance among Bangladeshi populaton:A scoping review
19-112	ASSESSMENT OF DAIRY FARMER’S HYGIENIC MILKING PRACTICES AND AWARENESS ON CATTLE MILK-BORNE ZOONOSES IN BAGHABARIGHAT MILK SHED AREAS OF BANGLADESH	19-29	screening of antibiotics residue in broiler and layer meat in Mymensingh of Bangladesh
19-22	Pathology of colibacillosis and molicular characterization of it’s pathogen	19-60	Isolation and molecular characterization of multi-drug resistant Salmonella typhimurium DT104 from selected dairy farm environments at Mymensingh.
19-37	Beneficial effects of probiotic and phytobiotic as growth promoter alternative to antibiotic for safe broiler production	19-114	Assessment of pet bird husbandry practices and antimicrobial resistant patterns of Escherichia coli and Staphylococcus spp. isolated from Budgerigar

19-44	Effect of meteorological factors on the density and distribution of tick vectors in Bangladesh
19-123	A Serological Survey of Rift Valley Fever and Q fever in sheep of Bangladesh
19-100	Entomological survey for identification of Aedes larval breeding site with abundance and distribution in Chattogram, Bangladesh
	(Melopsittacusundulatus) bird of Chattogram, Bangladesh
19-07	Carriage of coagulase positive methicillin-resistant Staphylococcus aureus & Staphylococcus psuedintermedius among dogs at teaching veterinary hospital in Bangladesh
19-109	Antimicrobial usage and resistance on commercial chicken farms in Chattogram (previously Chittagong), Bangladesh

Day One

Conference Key Note Speech

One Health Capacity Building for Health Security

Nitish C Debnath[1] and Meerjady Sabrina Flora[2]

[1]Chattogram Veterinary and Animal Sciences University (CVASU), [2]Institute of Epidemiology andDisease Control Research (IEDCR)

Emerging diseases pose critical threats to health security which must require multisectoral collaboration for effective mitigation. Bangladesh is one of the most rapidly growing economies in the world and it has unique interface between human, animal and environmental health. Bangladesh has managed to achieve many successes in health sectors including immunization and health care access to the rural area. However, the country has work to prepare for the next epidemic. The key One Health capacity building incudes workforce development, sensitive health surveillance, strong laboratory diagnostic capacity and rapid response capacity. Many countries are working to achieve international health standards and workforce capacities through the World Health Organization's (WHO) International Health Regulations (IHR), the World Organization of Animal Health's (OIE) Performance of Veterinary Services (PVS) Pathways Assessments, and the WHO-led Joint External Evaluation (JEE) which contributes to the Global Health Security Agenda. The JEE specifically calls out workforce development and highlights the importance of a One Health approach. Globally, there is a lack of standardization across One Health training programs. Many One Health focused trainings and programs incorporate a set of skills and knowledge requirements referred to as One Health Core Competencies (OHCCs). These competencies include management, communications, values and ethics, and teamwork. FETP and FETPV are providing an opportunity to develop the ready workforce for responding to any health emergency. Disease surveillance and rapid responding to a health emergency is crucial to avoid the pandemic and health threats. The four way linking between animal health and human health epidemiologist and laboratory experts are crucial for rapid detection of the outbreak. In the rapid changing environment of Bangladesh, we must set goal to achieve One Health capacity through academic programs in universities, professional trainings and Continuous Education involving all health professions to ensure the health security in Bangladesh.

Key words: Bangladesh, WHO, OIE, PVS, JEE

Day Two

Panel Discussion–I Are We Ready for Combating EID Epidemic/ Pandemics?

Guillaume Fournié
Royal Veterinary College, UK

Guillaume is a veterinarian and epidemiologist at the Royal Veterinary College, UK. His main research interest is understanding the way in which livestock production systems shape the emergence, spread, and maintenance of infectious diseases, with a particular focus on low and middle income countries. He is currently involved in projects focusing on avian influenza, antimicrobial resistance, foodborne pathogens, livestock diseases, and the role of live animal trade networks and production on the dynamics of zoonotic diseases. His research has been increasingly inter-disciplinary, involving collaborative work at the interface between epidemiology, virology, anthropology, economics and archaeology.

The world is experiencing major demographic and socioeconomic transitions. Rapid urbanisation and the emergence of a global middle class with new lifestyle expectations, environmental changes and intensification of livestock production contribute to the creation of new *risk environments*, promoting the emergence and dissemination of zoonotic health hazards. Indeed, the frequency of zoonotic disease outbreaks is increasing worldwide, and high-impact epidemics are now considered the “new normal.” These transformations are more pronounced in Asia, and especially in Bangladesh. While the country is experiencing a high economic growth and has achieved remarkable health advances in the last decades, is it currently equipped to face the increasing burden of zoonotic disease outbreaks?

The mitigation of zoonotic disease risks requires interventions to be tailored the local characteristics of the settings where these risks emerge. The interrelatedness of environmental, biological, economic, and social factors underlying those risks need to be addressed, or our ability to prevent and respond to these new zoonotic disease outbreaks will be limited. Our traditional approach to epidemic control now need to account for, and truly integrate, methods, practices and knowledge from a variety of fields and disciplines. Social sciences can help to increase our understanding of the way in which specific social, economic and cultural contexts shape the risk of disease transmission, and tore-direct the focus of behaviour change interventions from didactic programmes to addressing the factors constraining those behaviours. The rapid development of new technologies, including real-time sequencing, satellite imaging, and artificial intelligence provide us with new tools, making it possible to integrate multiple types of data to improve our understanding and prediction of epidemiological patterns. To achieve such a change in the way we characterise and mitigate zoonotic disease risks, we may need to re-think the way we train epidemiologists and microbiologists, as well as the policy-science interface. The presentation will draw on examples from research projects conducted in Bangladesh, including the BALZAC and the UKRI GCRF One Health Poultry Hub.

Panel Discussion–II One Health Approach for Rabies Control

Rabies Elimination Program in Bangladesh: Success and Challenges

Dr. Umme Ruman Siddiqi[1], Dr. Kamrul Islam[1], Dr. Mahmudullah[1], Dr. Rashed Ali Shah[1],Dr. Fazle Rabby[1], Dr. Afsana Akhter Jahan[1], Dr. Mujibur Rahman[1], H S M Tarif[1], Md. Kamruzzaman[1], Nadim Mahmud[1], Dr. Shakif-Ul-Azam[2], Dr. Abu Sufian[2], Dr. Ekramul Haq[1], Dr. Bholanath Bosak[3], Dr. Salmunnahar[1], Dr. Shotabdi Kar[1], Maruf Ahmed[1], Prof. Sanya Tahmina[1]

[1]Communicable Disease Control, Directorate General of Health Service (DGHS), [2]Department of Livestalk, Khamarbari, [3]Infectious Disease Hospital (IDH)

Globally approximately 59,000 humans die due to dog-mediated rabies every year. The disease is most prevalent in countries within Asia and Africa disproportionately affecting vulnerable populations. Rabies is endemic in Bangladesh where more than 2000 rabies related deaths occurred annually before 2010. In more than 95% cases dogs are responsible for disease transmission and there is estimated 1.6 million dogs which are mostly stray (83%) Considering the public health impact of human rabies, Communicable Disease Control unit of Directorate General of Health Services has taken the initiative and leading the National Rabies Elimination Program based on the National strategy and action plan adopted in 2013. Since rabies is a zoonotic problem, multi-sectoral engagement through One Health approach is one of the key policies to fight against rabies and accordingly CDC-DGHS has involved other stakeholders including Department of Livestock Services (DLS), Local Government, Non-Government organizations (NGOs) and Development partners (FAO). The One Health rabies elimination strategy aims at eliminating the disease from the dog population and stop transmission to human and animal by means of Mass Dog vaccination (MDV), preventing the disease in human populations by means of standard post-exposure prophylaxis (PEP) including vaccine and immunoglobulin along with immediate wound washing with soap and water for 15 minutes and education and education and awareness building. In 2018 about 2.8 million animal exposure cases received free PEP through national center (NRPCC) at IDH, Dhaka and 66 district rabies prevention centers at least one in every district Sadar hospitals. Until June 2019, minimum one round of MDV was accomplished in 40 of 64 districts and all district municipalities/city corporations with vaccination of about 1.3 million dogs with >70% coverage. Number of reported suspected rabies death at NRPCC has been reduced to 36 in 2018 compared to that of 160 in 2009. Capacity for laboratory diagnosis of animal rabies is now in place at CDIL. In conclusion, integrated and collaborative approach for implementation of strategic activities by all the stakeholders including ensuring standard PEP, effective implementation of MDV and strong surveillance mechanism is crucial to reach the national as well as SDG and global target of ‘Zero by 30’ for dog mediated rabies.

Key words: Rabies, Elimination, Post-Exposure Prophylaxis, Mass Dog Vaccination, One-Health.

Parallel Oral session-IA One Health Research, Practice, Policy and Governance for Addressing Infectious Diseases

ID: 19-116: **Zoonotic Disease Dynamics in South India- A Topical Study**

M. Raman, S. Thiyagarajan, R. Vijayakumar, G. Dhinakar Raj, Valentina Claudet
Tamil Nadu Veterinary and Animal Sciences University.

Email of corresponding author:raman.tanuvas@gmail.com

Introduction: Translational Research Platform for Veterinary Biologicals (TRPVB) is a partnership initiative between Department of Biotechnology, Government of India and Tamil Nadu Veterinary and Animal Sciences University, Chennai. Of the zoonotic diseases affecting humans, tuberculosis is one of the significant and biggest health issue in India with a disproportionately huge burden of more than 2 million cases complicated by totally drug resistant tuberculosis strains reported recently. Brucellosis is an important re-emerging zoonotic disease which is very often a under diagnosed disease condition in India. Currently *B. melitensis* remains the principal cause of human brucellosis worldwide including India. Recent studies indicated its prevalence in rural livelihoods involved in farming and animal breeding activities. Leptospirosis is a major neglected public health problem and is highly underreported in India.Lymphatic filariasis (LF) caused by *Wuchereriabancrofti* and *Brugiamalayi* is an important public health problem in India where about a third of the global population lives at risk of this disease.In India it's current control strategy was initiated through Global Programme for Elimination of LF (GPELF) by WHO from 1999 was calling for Elimination of LF as a public health problem by the year 2020, though it is yet to cover the majority of the population at risk residing in rural areas.

Methods: As per the vision and Mission of TRPVB, several vaccines, diagnostics and novel therapeutics had been developedsince its inception from 2012. Of this, diagnostic kits were developed against Tuberculosis, Brucellosis, Cystic Echinococcosis, Filariasis and Leptospirosis during the last 5 years of its existence. Using the above diagnostic kits developed,TRBVPhadinitiated screening of a total of936 human sera samples for the above zoonotic diseases in reputed National Medical Institutes such as Post Graduate Institute of Medical Education and Research (PGIMER), Chandigarh,Jawaharlal Institute of Postgraduate Medical Education & Research(JIPMER), Puducherry, NationalInstitute of Mental Health and Neuro Sciences(NIMHANS),Bangalore,National Institute of Epidemiology and King Institute of Preventive Medicine and Research,Chennai during the year 2014-2019.The 936 sera samples originated from targeted population and people with occupational hazard such as health workers, personnel working in the public abattoirs, field veterinarians, persons classified as pyrexia of unknown origin cases.

Results & Conclusion: At Translational Research Platform for Veterinary Biologicals, of the 690 samples screened for *Brucella* by cELISA only 20 samples were found to be positive. Similarly 7 samples were positive for Tuberculosis of the 72 sera samples screened using well defined recombinant protein coated ELISA & LF assay kits.Screening of 31 samples for Leptospirosis by Lateral flow assay kits & Latex Bead Agglutination method revealed 15 positive samples.Likewise screening of 143 sera samples for Cystic Echinococcosis using a purified native hydatid cyst fluid antigen coated lateral flow assay kits revealed 74 samples positive for Cystic echinococcosis in comparison with commercially available ELISA kits. Thus in total 936 human sera samplesprovided by the above said Indian National Medical Institutes were screened by the diagnostic assay / kits developed by TRPVB for prevalence of various zoonotic diseases affecting human and the results were discussed.

Key words: Man, zoonotic disease, dynamics, South India

Parallel Oral session-IA One Health Research, Practice, Policy and Governance for Addressing Infectious Diseases

ID 19-199: **Molecular Characterization of *Giardia*and *Cryptosporidium* in Calves and Children in Bangladesh**

Md. Robiul Karim[1], Farzana Islam Rume[2] ,S. H. M. Faruk Siddiki[1]

[1]Bangabandhu Sheikh Mujibur Rahman Agricultural University, [2]Patuakhali Science and Technology University
Email of corresponding author: vet_robiul@bsmrau.edu.bd

Introduction: *Giardia duodenalis* and *Cryptosporidium* species are zoonotic gastro-intestinal protozoa known to infect humans and livestock. They are among the most common causes of diarrhea in humans worldwide. The parasites are mainly transmitted via fecal-oral route. This study investigated the genetic diversity of these parasites in calves and children and elucidated their zoonotic potential in Bangladesh.

Methods: Four hundred fecal samples were collected from children (n=199) and calves (n=201) in Pabna, Sirajgonj and Gazipur and screened by nested PCR targeting β-giardin (*bg*), glutamate dehydrogenase (*gdh*) and triose phosphate isomerase (*tpi*) genes for *G. duodenalis* and 18S rRNA and glycoprotein 60 (*gp60*) genes for *Cryptosporidium*.

Results: The overall prevalence of *G. duodenalis* infection was 16.1% (32/199) and 5.5% (11/201) in children and calves, respectively. Similarly, the infection rate of *Cryptosporidium* species was 2.5% (5/199) in children and 10.5% (21/201) in calves. The prevalence of both *G. duodenalis* and *Cryptosporidium* infections varied insignificantly by age, sex and study areas in children and by study areas, sex, and breed groups in calves. However, calves younger than one month had significantly higher prevalence (50.0%) of *G. duodenalis* infection than older calves ($p< 0.01$). Multi-locus genotyping of human isolates of *G. duodenalis* showed the occurrence of the zoonotic assemblages A (50.0%, 16/32) and B (50.0%, 16/32). Similarly, analyses of bovine isolates of *G. duodenalis*revealed the presence of cattle specific assemblage E in 81.8% (9/11) and zoonotic assemblages A (A-I) and B, each in 9.1% (1/11). There was greater genetic variability among assemblage B (21 subtypes) as compared to assemblage A (8) and assemblage E (5). Among them, 14 isolates were novel, reported for the first time from this study, with 12 of them belonging to assemblage B and 1 belonging to each of the assemblages A and E. Genotyping of human isolates of *Cryptosporidium* showed the presence of *C. hominis* (2.5%). Four *C. hominis gp60* subtypes, IaA19R3, IaA23R3, IbA9G3 and IdA15G1, were observed. The characterization of 21 *Cryptosporidium* isolates of calves revealed the presence of *C. andersoni*(85.7%) and *C. bovis*(14.3%).

Conclusion: *G. duodenalis* and *Cryptosporidium* infections were widespread in children and calves in the study areas. The finding of zoonotic *G. duodenalis* assemblages A and B in calves indicates the possibility for zoonotic human infection.

Keywords: *Giardia duodenalis, Cryptosporidium,* nested PCR, genetic diversity, zoonotic transmission

ID: 19-06: **Molecular Epidemiological Analysis on the Sources and Diarrheagenicity of Shiga toxin-Producing *Escherichia coli*, and Atypical Enteropathogenic *E. coli***

Md. Shafiullah Parvej[1], Hiromi Nakamura[2], Md Ashraful Alam[1], Shono Mio[1], Mst. Nusrat Zahan[3], Eriko Kage-Nakadai[1], Md. Tanvir Rahman[4], Yoshikazu Nishikawa[1*]

[1]Osaka City University, [2]Osaka Institute of Public Health, [3]Sher-e-Bangla Agricultural University, [4]Bangladesh Agricultural University.
Email of corresponding author: *nisikawa@life.osaka-cu.ac.jp*

Introduction: Diarrheagenic *Escherichiacoli* (DEC)is one of the major public health concernsin developing countries while distinctive sources of infections are not completely understood yet.

Methods: To assess the sources and routes of transmission of DEC,1318 fecal samples obtained from cattle, poultry, and human patients were analyzed by molecular microbiological methods.

Results: In the preliminary screening by real-time PCR, the *virB*gene of enteroinvasive*E. coli* (EIEC) was predominant (41%) in human patients with positive correlation first with *afaB* of diffusely adhering *E. coli* (DAEC) and second with *aggR* of enteroaggregative *E. coli* (EAEC). In contrast, Shiga toxin genes *stx1* (57%) and *stx2* (40%) were prevalent among cattle samples. Genes (*eae*, *elt*, and *est*) of enteropathogenic *E. coli* (EPEC) and enterotoxigenic *E. coli* (ETEC) were detected among the three sample sources. Atypical enteropathogenic *E. coli* (aEPEC) strains(36 Japanese and 50 Bangladeshi) obtained from poultry fecal sampleswere analyzed. Clermont's phylogenetic typing showed that group A was more prevalent (58%, 50/86) than B1 (31%, 27/86). Intimin type β1was predominant in both phylogroups B1 (81%, 22/27) and A (70%, 35/50). However, about 95% of B1-β1 strains belonged to virulence group I, and 77% of them were Japanese strains, while 17% (6/35) of A-β1 strains did. When the data were combined with those of 142 previous strains from different sources, the minimum spanning tree formed five zones for porcine, poultry, healthy human, bovine and human patients, and the B1-β1 poultry strains. Sixty-eight percent of the poultry strains demonstrated resistance to ≥3 antimicrobial agents.

Conclusion: The noticeablefrequency of virulent DEC pathotypesin animals warrants precise attentiveness.

Keywords: Diarrheagenic *Escherichia coli,* virulence genes,diarrheic patients.

ID 19-35: **Identifying Diseases ofFarmDeer and Zoonotic RiskPrevailing in Bangladesh**

Sajeda Sultana[1,] Nazneen Sultana[2], Mahmuda Islam[2],S.M. SharifulHoqueBelal[2], Mohammad Abu Hadi**Noor Ali Khan**[2]

[1]*Sher e Bangla Agricultural University,*[2]*Bangladesh Agricultural University (BAU)*

Email of corresponding author: *hadi.khan@bau.edu.bd*

Introduction: Deer farming is a growing business and increasinginBangladeshduetodiversifiedlifestyleand fancy ecology associated with farming. Diseases are common constrain on successful deer farming. Data are scanty concerning the spectrum of diseases infarmdeer in Bangladesh. The present study is to identify causes of mortality of captive deer and their zoonotic perspective.

Methods: The mortality in three different deer farms (designated as farm A, B and C) between February 2018 to August 2019 were investigated with special emphasis to zoonotic etiology. Clinical sings ofinfected deer were investigatedand following death routine necropsy, histopathology, impression smears, isolation and identification of bacteria were carried out. PCR was carried out to safeguard the specific cause of infectivity.

Results: Farm A, B and C investigated was consisting of 87, 54, and 13 deer respectively. A total of 41 deer appeared dead during this investigation. Clinically deer of farm A and B showed acute illness characterized by high fever, recumbence, diarhhoea, reluctant to move, incoordination and death. Case fatality rates were 90% in thesefarms. Deer in these farms showed widespread congestion& hemorrhages at necropsy.Soft, discolored pulpy kidney and unclotted dark color blood was seen in the lumen of intestine in farm B deer. Deer in farm C showed progressive emaciation and anorexia. At necropsy multiple nodules wereseen in the lungs.Histopathological examination revealed severe pneumonia and coagulation necrosis in the liver of farm A deer; Pasteurellamultocida and Streptococci spp were isolated from their visceral organs. Widespread congestion and hemorrhages and necrosis were observed in the kidney, spleen, intestine, heart andlungs of farm B deer; Grams staining showed rod shaped Gram positive bacteria in their visceral organs. The bacteria were identified as Clostridium perfringensin PCR. Histopathological, bacteriological and PCR investigation revealed that the farm C deer was infected with M. tuberculosis.

Conclusion: The farm deer were died due to Pasteurellosis, enterotoximia and tuberculosis. The C. perfringens and M. tuberculosis are zoonotic pathogens and vet care free deer farming may pose serious zoonotic threat to other deer and farmers involved there in.

Keywords: Deer, Pasteurella, Enterotoxaemia, Mycobacterium,zoonosis

Parallel Oral session-IIBOne Health Research, Practice, Policy and Governance for Addressing Infectious Diseases

ID: 19-46: Incidence and Occupational Risk Factors of Avian Influenza A Virus Among A Cohort of Live Bird Market Poultry Workers, Bangladesh: 2012-2017

Md Zakiul Hassan[1], Sadia Afreen[1], Sharifa Nasreen[1], Abdullah Al Mamun[1], Mohammed Ziaur Rahman[1], Mustafizur Rahman[1], Stephen P Luby[3], Mohammad Abdullah Heel kafi[1], Shukanta Chowdhury[1], Tasnim Azim[1], A. Danielle Iuliano[2], Timothy M. Uyeki[2], Mahmudur Rahman[4], K Sturm-Ramirez[1, 2]

[1]icddr,b,[2]Centers for Disease Control and Prevention,[3]Stanford University, [4]Institute of Epidemiology, Disease Control and Research (IEDCR)

*Email of corresponding author:*zhassan@icddrb.org

Introduction: Live bird market (LBM) workers in Bangladesh with minimal use of personal protective measures may be exposed to avian influenza A viruses (AIV) from infected poultry. We followed LBM workers to estimate incidence of AIV detection and associated risk factors.

Methods: From February, 2012-September, 2017, we followed a cohort of workers from 16 LBMs in Dhaka, Bangladesh and collected potential AIV exposure data. We followed participants twice per week for illness associated with suspected AIV infection defined as fever and/or any respiratory symptom; we collected naso/oropharyngeal swabs from suspected cases. Samples were tested for influenza virus RNA by real-time RT-PCR and if positive for influenza A virus then subtyped for H1N1pdm09, H3, H5, H7 and H9 subtypes only. We estimated the incidence of detectable AIV RNA among LBM workers and calculated hazard ratios for risk factors of AIV detections using multivariable Cox's regression models.

Results: We followed 1152 LBM workers for 3905 person-years and identified 2560 suspected AIV cases. Of 2560 swabs tested, 84 (3.2%) had detectable AIVs (16 H5, 40 H9, 7 H5/ H9 co-detection with a seasonal strain and 21 A/unsubtypables). All AIV detections and A/unsubtypables were recorded between October-April, the AIV circulation period among poultry, whereas 80% (153/192) of the seasonal viruses (A/H1N1pdm09, H3 and influenza B) were detected between May September, during seasonal influenza epidemics in Bangladesh. The estimated incidence of AIV detection was 21/1,000 LBM worker-years. The annual incidence per 1,000 LBM worker for H5 was 4 (95% CI 3-7) and for H9 was 10 (95% CI 8-13). There was an increased risk of AIV detection among workers who were engaged in slaughtering, defeathering and eviscerating poultry (HR=3.31 95% CI 1.3-8.3, P=0.01). No significant risk of AIV detection was found among LBM workers engaged in live poultry transportation (p=.22); feeding (p=.24); cleaning feeding tray (p=.66), water container (p=.55) or feces from pen (p=.43); or collecting or transporting poultry feces (p=.17).

Conclusion: LBM workers frequently had detectable AIV in their swabs due to direct contact with AIV infected poultry. Risk factors linked with AIV detection such as slaughtering, defeathering, and eviscerating poultry could inform development of LBM interventions to reduce risk of poultry-to-human AIV transmission.

Key words: Avian influenza viruses, subtype H5N1, live bird market, poultry worker, Bangladesh

ID 19-125: **Cross Sectional Assessment of Aerosolization of Influenza A Viruses and Potential Transmission Risk for Live Bird Market Workers at Animal-human Interface in Bangladesh**

Mahbubur Rahman*[1,2], Punam Mangtani[3], Jacqueline M Cardwell[2], Md Ahasanul Hoque[4],Mahmudur Rahman[5],A S M Alamgir[1], Sudipta Sarkar[1], A K M Muraduzzaman[1],M Salimuzzaman[1], Md Abdus Samad[6], Mahmudul Hasan[6], MdGiasuddin[6], Guillaume Fournie[2], Dirk U Pfeiffer[7], Meerjady Sabrina Flora[1]

[1]Institute of Epidemiology, Disease Control and Research (IEDCR), [2]Royal Veterinary College (RVC), [3]London School of Hygiene and Tropical Medicine (LSHTM), [4]Chittagong Veterinary and Animal Sciences University (CVASU),[5]International Centre for Diarrhoeal Disease Research,(icddr,b);[6]Bangladesh Livestock Research Institute (BLRI), [7]CityUniversity of Hong Kong

E mail of Corresponding author: dr_mahbub@yahoo.com

Introduction: Influenza A virus (IAV) subtypes H5N1 and H9N2 are endemic among poultry in Bangladesh and poultry are frequently purchased at live bird markets (LBM). We assessed the presence of aerosolized IAVs at LBMs and potential occupational risk to LBM workers.

Methods:A cross-sectional study was conducted from January to May 2017 among702 randomly sampled asymptomatic workers at42 LBMs (selected probability proportional to market size) in Dhaka, Bangladesh. Nasal and throat swabsfrom workers and air samples collected at LBMs (using cyclonic and impactor air samplers)were tested for IAVsbyrRT-PCR; selected air samples (Ct value <38) were placed into viral culture.Acute and convalescent serum samples from workers were obtained for subsequent testing.

Results: MostLBMs were retail and three had separate slaughtering areas. None practiced market rest days or bannedpoultry overnight. Sixty percent(25/42) had air samples positive for Influenza A, 31% were positive for H5 and H9, 23.8% for H9 only, one for H5 only, and one was non-subtypeable. IAVswereisolated from 53% (16/30) of rRT-PCR positive air samples.Selling ducks was associated with influenza A in air samples [aOR 15.8 (95% CI:2.2-115.7, p=0.002), adjusted for season, solid waste disposal and cleaning frequency].Of 702 workers,93.3% were involved in slaughtering and 84.3% in defeathering. 10.8%of workershad IAV positive, H1 and H3 negative, respiratory specimens: 4% were positive for H5 and H9, 31.6% H9 positive, and 64.5% were negative for H5, H7,H9.Ducks were associated with IAV positive worker respiratory specimens [aOR 3.1 (95% CI: 1.0-9.5, p=0.044), adjusted for age, season, LBM type, presence of non-poultry birds, and use of defeathering machine].

Conclusion: Bangladesh LBM workers were exposed to aerosolizedviable influenza A viruses and IAV RNA was detected in respiratory specimens of some workers. Ducks were associated with aerosolization of influenza A virusesand influenza Avirus exposure ofLBM workers. Additional investigations includeserological testing of archived specimens to investigate workers' risk of AIV infection.Findings support policy directives for moving from emergency response to prevention of AIV spillover.

Key words:H5N1, H9N2, LBM

ID 19-59: **Continuingcirculation of New Reassortant Clade 2.3.2.1a of Highly Pathogenic Avian Influenza H5N1 Virus in Chickens in Bangladesh**

Mohammed Nooruzzaman, Congriev Kumar Kabiraj, TanjinTamanna Mumu, Md. MijanurRahman, EmdadulHaque Chowdhury and Mohammad Rafiqul Islam

Bangladesh Agricultural University. E mail of Corresponding author: khokondvm@yahoo.com

Introduction: In Bangladesh, highly pathogenic avian influenza (HPAI) virus of subtype H5N1 was first detected in chickens in February 2007. During the first few years, clade 2.2 viruses were circulating among poultry in Bangladesh before the introduction of clade 2.3.2.1a virus in 2011. The clade 2.3.2.1a virus further evolved through genome segment reassortments that started in 2013. Since2015, thereassortant clade 2.3.2.1a virus had been detected during surveillance in live bird markets (LBM) andwet lands. In 2017we detected the reassortant virus also from field outbreaks in chickens, ducks, goose and turkeys. Here we performed genetic characterization based on full genome sequencing of fiverecent H5N1HPAI viruses detectedin2018 (n=3) and 2019 (n=2).

Methods: This study was a part of our respiratory disease syndrome surveillance programme with the objective of pathogen search. Swab or tissue samples collected from layer flocks with respiratory symptoms were examined by a panel assay for different respiratory pathogens. Samples tested positive for H5N1 HPAI virus were subjected to sequencing of all genome segments. Phylogenetic analysis was performed for genetic characterization of the virus.

Results: A total of five samples turned out to be positive for H5N1 HPAI virus. Three samples were obtained from Sakhipurupazila, one in April 2018 and two in February 2019, and two other samples were obtained from Bhalukaupazila in April 2018. Phylogenetic analysis based on full length gene sequences of all eight gene segments revealed that these viruses were similar to the new reassortant of clade 2.3.2.1a H5N1 virus, which has been detected since 2015. This reassortant virusesacquiredPB2, PB1, PA, NP and NS genes from low pathogenic avian influenza viruses of non-H9N2 subtypes but retainedHA, NA and M genes of the old clade 2.3.2.1a virus, though with few mutations.

Conclusion: Continuing circulation of the new reassortant clade 2.3.2.1a virus with apparent replacement of the older genotype suggests relative fitness advantage of the new reassortant virus to poultry population.

Keywords: HPAI, H5N1, turkeys, clade 2.3.2.1, Bangladesh

ID 19-97: **The Governance of One-Health Evidence in Bangladesh.**

L.Vince[1],A.S.M.Alamagir[2], M.A.Rahman[2], M.N.Islam[3], S.Sarkar[2], N.C.Debnath[3], M.S.Flora[2], M.Salimuzzaman[2], M.A.**Hoque[3],** G.Ahmad[4], J.Parkhurst[5], G.Fournié[1], T.Barnett[4], D.Pfeiffer[1,6]

[1]The Royal Veterinary College, [2]Institute of Epidemiology Disease Control And Research(IEDCR), [3]Chittagong Veterinary and Animal Sciences University, (CVASU), [4]London School of Hygiene and Tropical Medicine, [5]London School of Economics and Political Science,[6]City University of Hong Kong.
E-mail of corresponsing author: lvince@rvc.ac.uk

Introduction: Evidence informed decision making in one-health policy is complex and central to one-health systems governance, yet few studies evaluate mechanisms of evidence use. In addition to research evidence, International health and development agenda, local priorities, experiential knowledge and political will affect one-health policy change. The objective of the study is to assess evidence use in one-health policy-making, and to provide recommendations for improved 1. access to evidence, and 2. evidence usability.

Methods: The study assesses the usage of research evidence in informing the health and agricultural policy making in Bangladesh. In-depth,semi-structured interviews (n = 52)were conducted (sept 2017 – may 2019) with government departments, scientific researchers and international stakeholders. Thematic analysis inspired by theory of knowledge and actor-network theory was performed in Nvivo 11 (qualitative analysis software).

Results: Evidence transfer occurred to i) researchers, ii) the public and iii) policy makers. Through i) thematic conferences, One-Health secretariat, technical advisory committees andpeer to peer discussionIi) project dissemination events, communications departments, and, the media. Iii) technical advisory committees, Briefings events, Media andInternational advice. Evidence use occurred in i) SOPs and protocols,ii) guideline formulation and iii) legislation. i) Government departments quickly used internal evidence, sharing externally was sometimes contentious. Independent evidence was reportedly used less. ii) Knowledge of the evidence informed policy primarily through key influencers, vital research evidence hascited in formulating policy;the mechanism of use is activated byexternal factors eg. International agenda, priority setting and funding. iii)Evidence used by Industry, media and international organisations to advocate for legislative change. Attitudes towards evidence use,Participants felt usage could be improved. Policy makers and technical expertsfelt good evidence usage involved linear change. Participants felt utilisation would be improved with a co-production approach.

Conclusion: Recommendations to improve 1. access to evidence. Strengthen the One-Health secretariat for dissemination of both governmental and independent evidence; Provide evidence synthesis platformsto improve access to evidence; provide support for thematic regional veterinary conferences.2. evidence utilisation;capability buildingprogramme(s) for evidence utilisation; develop co-production procedures for simultaneous knowledge development;refine equitable data sharing processes; formalise strategies at the science – media – policy interface.

Keywords: One-Health, Evidence, Policy, Research Impact, Knowledge Utilisation

Parallel Oral session-IIAEcosystem Management towards Protecting Environmental Health and Natural Resources

ID 19-128: **Ten Years of Emerging Pandemic Threat (EPT) PREDICT Program to Prevent Viral Pandemics: Are we ready for Disease "X"?**

Ariful Islam[1] Jonathan H Epstein[1], Melinda K Rostal[1], Emily Hagan[1], Mohammed Ziaur Rahman[2], Meerjady Sabrina Flora[3], Petar Daszak[1], Jonna K Mazet[4] and PREDICT Consortium

[1]EcoHealth Alliance New York, NY, USA; [2]Institute of Epidemiology Disease Control and Research (IEDCR), Mohakhali, Dhaka, Bangladesh;[3]International Centre for Diarrheal Disease Research, Bangladesh (icddr.b), Dhaka, Bangladesh; [4]One Health Institute, University of California Davis, California, USA.E mail of corresponding author: arif@ecohealthalliance.org

Background: The USAID Emerging Pandemic Threats (EPT): PREDICT program began in 2009, designed to prepare the public health community to combat disease threats at the first stage of their emergence through an early warning system for detecting novel zoonotic diseases in disease hotspots regions. PREDICT aimed to characterize viral diversity in key animal species; identify high risk interfaces where viral spillover is most likely to occur; and identify and assess novel viruses most likely to impact human health.

Methods: The PREDICT program, implemented in 24 countries in hotspot regions across Africa and Asia, inclusive of Bangladesh. Working in collaboration with the Government partners in a combination of longitudinal biological, ecological, and behavioral surveillance efforts to monitor spillover of viruses within key viral families. PREDICT surveillance consisted of the non-destructive sampling of wild animals, livestock and human. PREDICT tested 145000 animals and people samples using viral family-level PCR assays and Next generation sequencing on previously undescribed viruses. Both molecular and serological assays were used to determine spillover events. Results: We discovered 931 novel and 218 known viruses, including zoonotic diseases of public health concern such as a novel strain of Ebola Bombali, Ebola Zaire, Marburg virus, MERS and SARS-like corona viruses. We estimated the approximate viral diversity in the Indian flying fox (Pteropusgiganteus), a native frugivorous bat and the natural reservoir for Nipah virus. PREDICT responded 23 zoonotic disease outbreaks in 10 countries. We strengthened laboratory system and zoonotic disease detection in over 60 laboratories around the world. We developed the One HealthOne Health workforce by training more than 6000 people in over 24 countries.

Conclusion: The PREDICT program used a One Health approach building the capacity for detection and characterization of novel viruses and improved the understanding of the dynamics of zoonotic virus spillover, spread, evolution, and amplification of EIDs to inform prevention strategies and combat the risk of disease emergence. PREDICT strengthened workforce, laboratory capacity and improved our ability to prevent and respond unknown Disease outbreak like Disease X across the globe. Continue to develop next generation of One Health practitioners and sustain coordinated approach zoonotic surveillance is recommended.

Key words: Pandemics, Emerging, Novel, and virus

ID-19-115: **Tuberculosis at Wildlife-Livestock Interface– Creating Increasing Threat to Public Health and Wildlife Conservationin Bangladesh**

MohammadNizam Uddin Chowdhury[1, 4],SMSH Belal[3], Md. GA Chowdhury[2],Hatem Mohammad Zulkar Nine[1], Md. Jahidul kabir[1], Mihir Kumar Doe[1], Md. Abu HadiNur Ali Khan[3]

[1]Bangladesh Forest Department,[2]Central Disease Investigation Laboratory,[3]Bangladesh Agricultural University,

*Email of corresponding author:*nizamvet05@gmail.com

Introduction: Tuberculosis (TB) in wildlife is becoming one of the emerging challenges for wildlife conservation in South Asia including Bangladesh. Although Bangladesh is one of the high TB burdencountry according to World Health Organization(WHO)report 2018, butin wildlife mycobacterium infection and its impact is still overlooked and underexplored. Reviewing the present situation, the study was conducted to identify and explore diversity of mycobacterium strains circulating in wildlife population in Bangladesh. Other objective was to raise awareness of the impact of tuberculosis at the wildlife-livestock interface.

Method: The study was carried out among several species of dead wildlife in two important protected areas of Bangladesh i.e. Bangabandhu Safari Park, Bhawal National Park, Gazipur. In these protected areas there was evidence of unique ecological link between wildlife and livestock specially for feed and habit sharing.In study areas targeted disease surveillance system followed for a period of two yearsand throughout the period, post-mortem(pm)examination of a spotted deer (*Axixaxix*), two gaur (*Bos gaurus*), one giraffe (*Cervus Camelopardalis*) and one common eland (*Taurotragus oryx*)revealed disseminated granulomatous lesionin lungs and yellowish colouredmiliarytuberclein thoracic cavity.Tissue samples were collected aseptically fromall tuberculosis suspected cases in PM examinationand submitted to Central Disease Investigation Laboratory, Dhaka and Department of Pathology, Bangladesh Agricultural University, Mymensingh. In both laboratories,Ziehl–Neelsen (ZN) staining were carried out for preliminary microscopic examination and subsequently positive samples were subjected to PCR analysis for Mycobacterium strains identification.

Results: In microscopic examination acid fast bacilli were identified from spotted deer, gaur, giraffe and common eland. But *Mycobacterium bovis* confirmed in the sample of spotted deer and gaur by PCR analysis inboth laboratories and further genotypic characterization is under analysis.

Conclusion: Tuberculosis in wildlife is a diverse and complex issue that require close collaboration between professionals from wildlife health, livestock health and public health for management actions. A furthercollaborative research program under One Health approach is urgently warranted to address feasible solutions for prevention of tuberculosis at livestock-wildlife–human interface in Bangladesh; and protection of public health & wildlife conservation in Bangladesh.

Key words: Wildlife, Public health, Granulomatous lesion, Conservation.

ID 19-121: **Eco-epidemiological Assessment of Antimicrobial Resistance of *Salmonella, Staphylococcus*and*Enterococcus*from Rhesus Macaque at Human-Animal Interfaces in Bangladesh**

Md Kaisar Rahman[1,2], MA Samad[3], Shariful Islam[1,2], MdHelal Uddin[4], Aftubuddin Rumi[4], Melinda K. Rostal[1], Emily Hagan[1], Jonathan H. Epstein[1], Meerjady Sabrina Flora[2], Mohammad Mahmudul Hassan[4], Ariful Islam[1,2]

[1]EcoHealth Alliance, [2]Institute of Epidemiology, Disease control and Research (IEDCR), [3]Bangladesh Livestock Research Institute (BLRI), [4]Chittagong Veterinary and Animal Sciences University,

E mail of corresponding author: *kaisarrahman@ecohealthalliance.org*

Introduction: Antimicrobial resistance (AMR) is a global concern due to its impact on human and animal health. It is listed among the top 10 emerging public health threats. AMR bacteria can be transmitted between humans and animals. Environmental pollution of antimicrobials from human and animal waste has been linked to the detection of AMR bacteria within wildlife populations**.** The aim of thisstudy was to identify the ecology and characterizing the AMR profile ofSalmonella, Staphylococcus and Enterococcus spp. isolated fromrhesus macaques in human-animal interfaces.

Methods: Over the period of one year (2017), fecal samples were collected from 399individual rhesus macaques. The samples were cultured and bacterial isolates were identified by biochemical characteristics and PCR. Then antimicrobial susceptibility tests (AST) for 12 antimicrobials were conducted using the Kirby-Bauer Disc diffusion method on selective media.

Results: The overall prevalence of resistant organismswas 5% (n=18; 95%CI: 3-7)of*Salmonella spp*., 15% (n=61; 95%CI: 12-19) of *Staphylococcus spp*. and 61% (n=66; 95%CI: 51-70) of *Enterococcus spp*.in macaques. The odds of an animal having AMR *Salmonella* and *Staphylococcus* were significantly higher in macaques living in a peri-urban habitat respectively (OR: 6.6; 95% CI: 1-46) and (OR: 5.6; 95%CI: 1-26) as compared to other habitats The odds of an adult macaque having resistant *Enterococcus spp*. (OR: 3.8; CI: 1-12) was significantly higher than juvenile macaques having it. Antimicrobial susceptibility testing of *Salmonella spp*. indicated that among resistant samples, 89% wereresistant to tetracycline, 83% to azithromycin, 50% to sulfamethoxazole-trimethoprim, and44% to nalidixic acid. Among resistant *Staphylococcus spp*., we found that 93% were resistant ampicillin, whereas only 31% were resistant tomethicillinand 26% to clindamycin. We determined that 96% of resistant *Enterococcus spp*. wereresistant to streptomycin, 63% to tetracycline, 61% to erythromycin and 30% to linezolid.

Conclusion: Microorganisms in macaques were resistant to most of the commonly used antimicrobials in agricultural production. Implying transmission of AMR between human-livestock-macaque interfaces, this may be due to their interaction during feeding and drinking. Further study is needed to better understand the pathways of antimicrobial resistance in rhesus macaque and other wildlife.

Keywords: AMR, Salmonella, Staphylococcus, Enterococcus, Rhesus macaque

ID 19-126**Epidemiology and Molecular Characterization of Group A Rotavirus from Rhesus Macaques (Macaca mulatta) at Wildlife-Human Interfaces in Bangladesh**

Ariful Islam[1,2], Mohammad Enayet Hossain[3], Najmul, Haider[3], Melinda K. Rostal[1], Sanjoy Kumar Mukharjee[3], Mojnu Miah[3], Jinnat Ferdous[1,5], Mustafizur Rahman[3], Peter Daszak[1], Mohammed Ziaur Rahman[3], Jonathan H Epstein[1]

[1]EcoHealth Alliance, [2]Deakin University, [3]International Centre for Diarrheal Diseases Research, Bangladesh (icddr,b), [4]Royal Veterinary College, UK; [5]Institute of Epidemiology, Disease Control & Research (IEDCR),

E mail of corresponding author: arif@ecohealthalliance.org

Introduction: Rotavirus A (RVA) is an important cause of diarrhea in humans, especially children, and animals globally. Animal-to-human interspecies transmission is one of the evolutionary mechanisms driving rotavirus strain diversity in humans. This study aimed to detect and characterize RVA in rhesus macaques (Macaca mulatta) at wildlife-human interface in Bangladesh.

Methods: We collected fecal samples (N=454) from apparently healthy wild rhesus macaques from nine different sites of Bangladesh between February to March 2013. We used one-step rRTPCR followed by nucleotide sequence analysis of positive samples for the targeting two structural proteins, VP4 (P genotype), and VP7 (G genotype).

Results: Four percent of samples (95% CI 2-7%) were positive for RVA. We identified G3, G10, P[3] and P[15] genotypes which were associated as G3P[3], G3P[15] and G10P[15]. The phylogenetic relationship between animal RVA strains from this study and previously reported human strains indicates possible transmission between humans and macaques in Bangladesh.

Conclusion: To best of our knowledge, this is the first report of detection and characterization of rotaviruses in rhesus macaques in Bangladesh. These data will not only aid in identifying viral sharing between macaques, human and other animals, but will also improve the development of mitigation measures for the prevention of future rotavirus outbreaks.

Keywords: Genotyping, Group A Rotavirus, Macaca mulatta, Phylogenetic analysis, Rhesus macaque

Parallel Oral session-IIBEcosystem Management towards Protecting Environmental Health and Natural Resources

ID: 19-19: **Pesticide Exposureamong Bangladeshi Villagers**

Pritimoy Das[1], Hossain M S Sazzad[1], Mohammad Abdullah Heel Kafi[1],Mahmudur Rahman[2],Steve P Luby[3], Emily S Gurley[1,4]

[1]International Centre for Diarrhoeal Disease Research, Dhaka, Bangladesh[2]Institute of Epidemiology Disease Control and Research (IEDCR), [3]Stanford University, [4]Johns Hopkins Bloomberg School of Public Health.

Email of corresponding author: pritimoy@icddrb.org

Introduction: Pesticide use in Bangladesh increased over 13 times from 1977 to 2009. In 2008, 2009, and 2012, clusters of acute severe neurologic syndrome were suspected to have been caused by unintentional acute pesticide poisoning. There is a lack of systematically collected data in Bangladesh onbackground pesticide exposure levels.We aimed to assess biomarkers of pesticide exposure among individuals living in two rural farming villages near Dhaka where a previous outbreak occurred.

Methods: During 2013-2014, we conducted four cross-sectional assessments in two villages with1,938residents.Each time, we selected 80 participants from two villages (40×2) using a stratified (≤10 and >10years of age) random sampling technique, for a total of 320 villagers. We recordedexposure information using a questionnaire and collected urine samples which were analyzed by the U.S. CDC laboratory for commonly used pesticidemetabolites using semi-automated solid phase extraction method.We compared results to the United States National Health and Nutrition Examination Survey (NHANES)because it represents levels in a relatively un-exposed population and thus can serve as a reference group.

Results: Respondents median age was11 years (IQR 6-34years) with 53% male.Proportion of villagers with detectable concentration of pesticides in urine was highest for OPC metabolites- Parathion, Methyl parathion (100%), Chlorpyrifos; Chlorpyrifos methyl (97%) and Diazinon (68%). Metabolites of synthetic pyrethroids- Cyhalothrin, Cypermethrin, Deltamethrin, Permethrin was also highly detected (77%). Proportion of people with pesticide exposure was more found in winter and more in children. The creatinine corrected concentration(μg/g)of most pesticide metabolites in the urine exceeded reference levels (above the US NHANES 95thpercentile), suggesting that residents of these villages were exposed to much higher levels of pesticides metabolites in the environment than the comparison group.

Conclusions: Information from this study can be used for comparison in future pesticide biomonitoring studies or for reference levels in future outbreaks in rural Bangladesh.

Keywords: Pesticides, Pesticide Exposure, Outbreak, Bangladesh

ID: 19-89: **Salt Plug Formation in the Sundarbans Mangrove Ecosystem Impacts Water Quality**

Dinesh Chandra Shaha, Jahid Hasan, ShaidaAkter, RabinaAkther Lima, Salman Ahmed

Bangabandhu Sheikh Mujibur Rahman Agricultural University.

E-mail of the corresponding author :dinesh@bsmrau.edu.bd

Introduction: The SundarbanMangrove Ecosystem (SME) is the world's largest coastal wetland in the Southwestern part of Bangladesh. At its upstream extent, the Pasur River Estuary (PRE) connects with the Ganges, the principal freshwater source for the SME. However, due to construction of the Farakka barrage in the Ganges in 1975, the freshwater discharge in the dry season reduced to post-Farakka mean flows of 0 m^3 sec^{-1} in 2012 from a pre-Farakka mean flow of 190 m^3 sec^{-1} in 1973.Consequently, salt water intrusion in the Pasur River has received substantial attention in recent years due to climate change and decreased river discharges resulting from an upstream barrage. However, earlier work typically omitted the details of vertical salinity distribution in the SME. Here we investigated the influence of river discharge patterns on the formation of salt plug in the SME and water quality parameters.

Methods:Vertical salinity and water sample data were collected using a conductivity-temperature-depth profiler from Harbaria to Batiaghata in the dry and wet seasons in 2014, 2018 and 2019.

Results: The longitudinal vertical salinity during the dry season shows salt plug, a salinity maximum zone within estuary, around Chalna. An export of saline water from the Shibsa River estuary to the Pasur estuary through Chunkhuri channel created salt plug and persisted for several months. This salt plug was essentially isolated the upper reaches of the estuary from bay water and prevented the seaward flushing of riverine waters. Therefore, the dissolved oxygen level dropped < 5.0 mg L^{-1} in the salt plug area in the dry seasons. Ammonium concentration ranged between 0.13 to 3.21 mgL^{-1} and nitrate concentration between 0.01 and 0.07 mgL^{-1}. Cadmium, copper and Iron concentration exceeds many folds from the acceptable limit.

Conclusion: This work will provide an ecological baseline for the SME and serves as a basis for an interdisciplinary approach linking the physical phenomena with chemical and biological properties.

Keywords: Sundarbanmangrove ecosystem, salt plug, nutrients, Farakka barrage, heavy metals

ID 19-113: **Epidemiology of Antimicrobial Resistance Patterns of *Staphylococcus* spp., *E. Coli* and *Salmonella* spp. Isolated from Rodents and Shrews in Chattogram, Bangladesh**

Md. Aftabuddin Rumi[1,2], Ariful Islam[3,4], Md. Kaisar Rahman[3,4], Shariful Islam[3,4], Md Helal Uddin[2], Meerjady Sabrina Flora[4], Jonathan H Epstein[3], Mohammad Mahmudul Hassan[4]

[1]Department of Livestock Services,[2]Chittagram Veterinary and Animal Sciences University,[3]EcoHealth Alliance,[4]Institute of Epidemiology Disease Control and Research (IEDCR),

E mail of corresponding author: miladhasan@yahoo.com

Introduction: Antimicrobial resistance (AMR) is a significantthreat to human and animal health worldwide. A considerable number of antibiotics already developed resistance against particular bacteria. As small mammals are known to transmit the bacteria to humans and animals, hence they could transmit the antibacterial resistant gene.This research aimed to determine the epidemiology of antimicrobial-resistant patterns in *Staphylococcus* spp., *E. coli,* and *Salmonella* spp. isolated from wild rodents and shrews in Chattogram, Bangladesh.

Methods: FromJanuary to Jun 2017, we captured 200 wild small mammals consisted of 42 mice (*Mus musculus*), 73 Rat (*Rattus rattus, Bandicotabengalensis,Bandicotaindica*) and85 houseshrews (*Suncusmurinus*) from 30 different locations of Chattogram district. We collected oral and rectal swab samples from small mammals and tested using standard bacteriological tests for isolation and identification and performed antibiogram for 14 differenttypes of antimicrobials by following Kirby-Bauer disc diffusion method.

Results: The overall prevalence of *Staphylococcus* spp. was 26.50% (95% CI= 0.20-0.33) (n=53), *E. coli*. was 56.0% (95% CI= 0.49-0.63) (n=112), and *Salmonella* spp. was 49.5% (95% CI= 0.43-0.56) (n=99). Significant differences were found between species (p=0.01)and the location of the sample collected (p=0.02). The antibiogram result revealed that *Staphylococcusspp.* showed 100% resistant to Oxacillin, Oxytetracycline, Cefixime, and Metronidazole followed by Ceftriaxone (64.10%), Ciprofloxacin (60.38%), Doxycycline (83.02%), Gentamycin (41.5%), Sulphamethoxazole and Trimethoprim (69.81%). Furthermore, *E. coli* isolates presented 100% resistant to Ampicillin, Erythromycin, and Metronidazole followed by Ampicillin (97.32%), Ciprofloxacin (72.32%), Azithromycin (91.08%), Gentamycin (38.39%). Moreover, *Salmonella* spp*.,* exhibited 100% resistant to Ceftriaxone, Ampicillin, Doxycycline, Cefixime, Amoxicillin, Erythromycin and Metronidazole followed by Ceftriaxone (77.78%), Gentamycin (56.56%) and Azithromycin (80.81%).

Conclusion: Our study reveals that thehigh percentage ofmulti-drug resistance bacteria in free-ranging small mammals' species with more thanthreeantibiotics.Therefore, further study and attention needed for the proper use of antimicrobial in food animals and agricultural products to reduce transmission of resistant bacteria through small mammals from the environment to the livestock and human.

Keywords: Antibiotics, Resistance,Bacteria, andsmall mammals

ID 19-134: **Prevalence and Genetic Diversity of Coronaviruses and Paramyxoviruses in Human at High-Risk Animal-Human Interfaces in Bangladesh**

Shusmita Dutta Choudhury[1,2], Ariful Islam[2,3]*, Josefina Abedin[1,2], Emily Hagan[2], Shahnaj Shano[1,2], Nafis Rahman[1,2], Romana Shermin[1,2], Md. Ziur Rahman[4], Tahmina Shirin[1], Jonathan H Epstein[2], Peter Daszak[2] and Meerjady Sabrina Flora[1]

[1]*Institute of Epidemiology, Disease Control and Research (IEDCR),* [2]*EcoHealth Alliance,* [3]*Deakin University,* [4]*International Centre for Diarrhoeal Disease Research (icddr,b).*

E mail of corresponding author: arif@ecohealthalliance.org

Introduction: Coronaviruses and paramyxoviruses are important viral families that account for a significant number of human, and animal diseases. Over the last decades, the emergence of coronaviruses and paramyxoviruses causes an increased incidence of zoonotic transmission among animal and human hosts that have been arisen a major public health concern globally. This study aimed to detect and characterize of known and novel coronaviruses and paramyxoviruses in humans at the high-risk animal-human interfaces in Bangladesh.

Methods: We interviewed a questionnaire for behavioral risk assessment and collected biological specimens from 612 participants in communities of Dhaka, Madaripur, and Dinajpur districts from October 2017 to October 2018, twice (dry and wet season). We collected samples from participants who had a history of domestic and wild animal contacts. We tested oral, rectal swabs and blood using consensus PCR targeting RNA-Dependent RNA Polymerase (rdrp) gene for coronaviruses and Polymerase (pol) gene for paramyxoviruses. Positive PCR products were confirmed by sequencing.

Result: Overall coronaviruses were detected in 10 (95% CI: 0.7-2.9) and paramyxoviruses in 6 (95% CI: 0.3-2.1) participants. Coronavirus identified 3 in influenza-like illness (n=239), 1 in fever of unknown origin (n=78), and 6 in apparently healthy participants (n=295). One measle case has been detected from participants having a history of fever of unknown origin. Parainfluenza virus detected 3 (n=239) and 2 (n=295) in ILI cases and apparently healthy participants, respectively. Coronavirus and paramyxovirus were not associated with age and gender of the participants; however, the viruses were associated with dry season ($p= <0.001$). Based on BLASTN search and clade analysis, suggest that HCoV-229E, HCoV-OC43, and HCoVHKU1, measles genotype D8, and parainfluenzavirus genotypes -1, 2 and 3 are circulating in the study areas. However, we did not find any novel coronavirus and paramyxovirus in the studied human population.

Conclusion: This study demonstrates diverse strain of coronavirus and paramyxovirus circulating in the communities. Measles virus is circulating in the study area, highlighted for the vaccination coverage. However, using One Health approach, continued surveillance is recommended to better understand the diversity of viruses at human-animal interfaces that may reduce the risk of disease spillover, amplification, and spread.

Keywords: Epidemiology, Molecular characterization, Paramyxovirus, Coronavirus, Bangladesh.

Day Three

Panel Discussion–III Coordinated Approach to Ensure Food Safety and Food Security

Moderator: **ROBYN ALDERS, AO, bsC(vET) HONS I, BVSC HONS I, DIPVETCLINSTUD., PHD.**

Robyn Alders is a Senior Scientific Advisor with the Chatham House Centre on Global Health Security, Chair of the Kyeema Foundation, an Honorary Professor with the Development Policy Centre within the Australian National University and an Adjunct Professor in the Department of Infectious Disease and Global Health, School of Veterinary Medicine, Tufts University. For over 30 years, she has worked closely with family farmers in sub-Saharan Africa, SE Asia and Australia and as a veterinarian, researcher and colleague, with an emphasis on the development of sustainable infectious disease control in animals in rural areas in support of food and nutrition security.

Robyn's current research and development interests include domestic and global food and nutrition security/systems, health security, One/Planetary Health, gender equity and Science Communication.

In May 2002, Robyn was the recipient of the Kesteven Medal, awarded by the Australian Veterinary Association and the Australian College of Veterinary Scientists in recognition of distinguished contributions to international veterinary science in the field of technical and scientific assistance to developing countries. In January 2011, she was invested as an Officer of the Order of Australia by the Governor General of Australia for distinguished service to veterinary science as a researcher and educator, to the maintenance of food security in developing countries through livestock management and disease control programs. In February 2017, Robyn was the recipient of the Inaugural Mitchell Global Humanitarian Award which recognises Australians and others supported by Australian aid who have made an outstanding contribution to the cause of international development.

***Panellists**:*

- Dr Hiresh Ranjan Bhowmik, Former DG, DLS
- Dr S M Mustafizur Rahman, NNS, IPHN
- Dr Md Saleh Ahmed, Postharvest Technology & Management Specialist, DAE Bangladesh
- Mr. A.K.M. Nurul Afsar, National Team Leader, Institutionalization of Food Safety in Bangladesh for Safer Food, FAO
- Dr. Benoy Kumar Barman, Senior Scientist, World Fish

Sustainable, Safe and Ethical Food Systems through a One Health Lens

Robyn Alders

Australian National University, and Centre on Global Health Security, Chatham House, UK

The number of people living with chronic hunger has risen for the third consecutive year to over 820 million in 2018, while incomes for men and women smallholder farmers are not increasing in line with SDG2 targets. The current overall direction our food systems is considered by many to be unhealthy, environmentally unsustainable and inequitable. The world is waking up to the challenge of feeding a growing global population, but can we bring about deep enough change and fast enough to meet the SDGs? What disruptive changes are emerging and what do these mean for the roles of government, business and civil society in transforming food systems?

Food systems are among the most important and complex of human responsibilities and underpin civilisation as we know it. A disconnect between food systems and human needs has failed to eliminate undernutrition, resulted in epidemics of over-nutrition and related non-communicable diseases, inequitable smallholder/family farmer incomes and contributed to growing inequity within and between countries. Locally and globally, the majority of food systems lack resilience in the face of environmental degradation (e.g. diminishing biodiversity and soil and water quality), climate change and market fluctuations.

Key policy challenges relating to sustainable food systems recently identified during a livestock and aquaculture policy project implemented in collaboration with Bangladesh included: the existence of many policies that were not implemented effectively, inadequate monitoring and evaluation of implementation and a general lack of engagement with stakeholders during policy development and implementation.

A realignment of food systems, to provide sufficient, safe and nutritious food within planetary boundaries is urgent. Numerous initiatives and responses are emerging including alternative foods and production systems, country-led nutrition programmes, global platforms, changing consumer behaviour and new business models. Emerging technological frontiers offer numerous possibilities. Many solutions are at hand, but what is needed to bring about sufficient change quickly enough? How do we integrate the necessary political, institutional and technical innovation to drive the required systemic transformation?

Key words:SDG, livestock, aquaculture

Parallel Oral session-IIIACoordinated Approach to Ensure Food Safety and Food Security

ID 19-63: **Antibiotic Resistance in Dairy Cattle and Farm Environment Having Potential Impact on Food Safety UsingOne HealthApproach**

Md. AbdusSobur, Md. Saiful Islam,S.M. LutfulKabirand Md. Tanvir Rahman

Bangladesh Agricultural University,

E-mail of Corresponding author: tanvirahman@bau.edu.bd

Introduction: Antibiotic resistance is a global crisis. One health components, dairy cattle and farm environment are directly linked with the production of safe food of animal origin. Dairy farm environment may carry antibiotic resistance bacteria that can end up into food chain. The present study was carried out to determine load of total bacteria, *Escherichia coli* and *Salmonella* spp. in dairy farm and its environmental components and detection of their virulence and antibiogram under a One Health approach.

Methods:A total of 240 samples of six types (cow dung – 15, milk – 10, milkers' hand wash – 10, soil – 10, water – 5, and vegetables – 10) were collected from four dairy farms. Total count was done by spot dilution method. Isolation and identification of *E. coli* and *Salmonella* spp. were performed based on cultural, and PCR. Virulence and antibiotic resistant genes were detected by PCR and antibiogram by disk diffusion method.

Results: The mean total bacterial count, *E. coli* and *Salmonella* spp. count in the samples ranged from 4.54±0.05 to 8.65±0.06, 3.62±0.07 to 7.04±0.48, and 2.52±0.08 to 5.87±0.05 log colony-forming unit/g or ml, respectively. Out of 240 samples, 180 (75%) isolates of *E. coli* and 136 (56.67%) isolates of *Salmonella* spp. were recovered through cultural and molecular tests. Among 180 *E. coli* isolates, 47 (26.11%) were found positive for the presence of all the three virulent genes, of which *stx1* was the most prevalent (13.33%). Only three isolates were identified as enterohemorrhagic *E. coli*. Isolated *E. coli* and *Salmonella* spp. were found resistant to azithromycin, tetracycline, erythromycin, oxytetracycline, and ertapenem and susceptible to gentamycin, ciprofloxacin, and imipenem. Among the four antibiotic resistance genes, the most observable was *tetA* (80.51-84.74%) in *E. coli* and *Salmonella* spp. and *SHV* genes were the lowest one (22.06-25%).

Conclusion: Antibiotic resistant bacteria were frequently detected in various farm environment components. Present findings suggest that milk and vegetables originating from dairy farm and surrounding agriculture land carry antibiotic resistant pathogenic *E. coli* and *Salmonella* spp. that can be transmitted to consumers through food chain and requires a one-health approachto combat the threat.

Keywords: one-health, antibiotic resistance genes, dairy farmenvironment, virulence, food chain

ID 19-13: **Tackling AMR in Developed Nation (France) Versus Developing Nation (Bangladesh): A One Health Approach**

Tasnuva Ahmed[1,3], Mounia Eygue[1], Guillaume Martin[1], Gladys Pangga[1,4], and Nathalie Ruvoen[2]

[1] Man-Imal[2]Oniris - Ecole Nationale Vétérinaire, Agroalimentaire et de l'Alimentation, [3] International Centre for Diarrhoeal Disease Research, (icddr,b) [4]University of the Philippines.

E-mail of corresponding author: *tasnuva.ahmed@icddrb.org*

Introduction: Antimicrobial Resistance (AMR) is a serious threat to public health, requiring concerted action across countries and sectors. HereAMR regulations and measures implemented in France and Bangladesh werecompared to gain insight on the situation in developed and developing nations respectively.

Methods: A multidisciplinary group of international students (Human and Veterinary doctors, Agricultural engineer etc.)of Man-ImalMaster,conductedanextensive search on Google Scholar and PubMed to find relevant information and compare the current situation in those countries.

Results: European Union (EU) started acting against AMRsince the early 2000s by launching several action plans. Significant measures implemented at French level werestrengthening surveillance, research on AMR, promoting diagnosis, vaccination and regulating the sales of antimicrobials(AMs).These measures resulted in a significant decrease in AMs consumption in human health sector,29% at health care facilities and 19% outside between 1999-2006. In 2006, EU countries banned used of AMs as growth promoters in livestock. The veterinary sector also noted a decrease of 37% in the sales of AMs between 2012-2016. Similarly, Government of Bangladesh also passed bill on banning AMs use as growth promoter in 2010 along with development of National Action Plan against AMR. However, several reports have revealed poor implementation of the rule and lack of regulatory data to quantify the antimicrobials used in both human medicine and livestock. Recently, Bangladesh has formed Antimicrobial Consumption Monitoring Taskforce but monitoring system is underdevelopment. Hence, no information on AM sale and consumption could be retrieved. Previous studies revealedthat unqualified personnel sold a major portion of AMs to patients and farmers as over-the-counter.

Conclusion: France, as a developed nation, has developed national regulations to fight against AMR and has been successful so far in implementing the rules. In contrast, Bangladesh has national policies, action plans however lack of monitoring, training and regulatory actions have led to increased threat of AMR in the region.

Key words: AMR, multidisciplinary, Man-Imal, Bangladesh, France, OneHealth

ID 19-92: **Prevalence and Antibiotic Susceptibility of *Vibrio*Spp. Isolated from Raw Shrimps in Bangladesh**

Ripon Sarker, KHM Nazmul Hussain Nazir,Muhammad Tofazzal Hossain*

Bangladesh Agricultural University,

E-mail of Correspondent author: tofazzalmh@yahoo.com

Introduction: Among more than 70 identified *Vibrio* species, *V.parahaemolyticus, V. cholerae*, *V. alginolyticus*and *V. vulnificus* are of major concern as they are pathogenic to human and fish as including shrimps. Vibriosis is important concern due to huge loss of shrimp industries throughout the world. The present research work was conducted for the detection of *Vibrio species* from raw shrimp with their prevalence and antibiotic susceptibility.

Methods: A total of 146 samples (Shrimp=100, Water=23 and Mud=23) were collected from shrimp farm areas of Satkhira, Khulna, and Bagerhat districts and subjected to bacterial isolation and identification by cultural, morphological and biochemical properties. Confirmatory diagnosis was performed by multiplex PCR using species-specific primers designed from *groEL* gene. Antibiotic sensitivity test of selected isolates were also performed using 17 commercially available antibiotics.

Results: Among 146 samples, 128 were suspected for the presence of *Vibrio* spp. on the basis of culture and finally 122 isolates were confirmed as *Vibrio* by PCR using genus specific *groEL* gene primers which produced a positive band at 1117 bp. Out of 122 PCR positive isolates, 88 were confirmed as *V.parahaemolyticus*(60.3%), 7 were as *V. cholerae* (4.8%), 13 were as *V. alginolyticus*(9%) and 6 were as *V. vulnificus* (4%) by multiplex PCR.All the tested isolates of *V. Parahaemolyticus, V. cholerae, V. alginolyticus*and *V. vulnificus* were found sensitive to Levofloxacin and Norfloxacin; and found resistant to Amoxycillin, Cefixime, Moxifloxacin, Lincomycin and Cefuroxime which is the indication of presence of multidrug resistant *Vibrio* spp. in shrimp farm areas.

Conclusion: It might be concluded that multidrug resistant *Vibrio* species is not only a threat for the shrimp farms but also a big threat to human health.

Keywords: Shrimp,*V. Parahaemolyticus, V. cholerae, V. alginolyticus, V. vulnificus.*

ID 19-81: **Susceptibility and Resistance Patterns of *Escherichia Coli* to Colistin Isolated from Common Food Animals at Sylhet Division of Bangladesh: An Approach to One Health**

TaslimaAkter[1], Juned Ahmed[1], Shampa DebNath[1], PranthoMalakarDiptho[1], IffatAra[1], MahfuzRahman Adnan[1], AsmaulHusna[1],Mohammad Al Mamun[1], Nahid Arjuman Banu[1], Bashu Deb Paul[1],Md. MahfujurRahman[1]Mohammad Rafiqul Islam[2]andMdMasudurRahman[1]

[1]Sylhet Agricultural University, [2]Livestock Division, Bangladesh Agricultural Research Council

E-mail of corresponding author:rahmanmm.dpp@sau.ac.bd, mmrahman.sau@gmail.com

Introduction: Antibiotics are a blessing to both animal and human that has saved millions of lives. Now-a-days antimicrobial resistance is becoming a growing global threat.*E. coli* spreads antimicrobial resistance from animals to humans and vice versa. Colistin is a last-resort antibiotic and resistance to colistin in food animals might be alarming. Therefore, the study was conducted to determine the susceptibility and resistance patterns of *E. coli* to colistin isolated from common food animals at Sylhet Division of Bangladesh.

Method:A total of 400 meat samples of chicken, cattle, sheep and buffalo (50 samples from each) were randomly collected from two districts of Sylhet division.*E. coli* was isolated and identified by using cultural and biochemical tests. The susceptibility and resistance patterns of isolated *E. coli*to colistin were determined by disk diffusion method according to CLSI guidelines.

Results: In case of Sylhet district, the percent positive cases of*E. coli* in chicken, cattle, sheep and buffalo were 64%, 58%,70% and 28%, respectively and in Moulvibazar district the percent positive cases were 70%, 40%,56% and 20%, respectively.*E. coli* isolated from chicken in Moulvibazardistrict and from cattle, sheep and buffalo in both of the districts shown 100% susceptibility to colistin. Whereas, *E. coli* isolated from chickensin Sylhet district shown 6.25% resistance and 93.75% susceptibility to colistin. Overall, in Sylhet division, 2.98% *E. coli*isolates from chicken were found resistant to colistin and 97.01% were susceptible. On the other hand, all of the isolates (100%) from cattle, sheep and buffalo in Sylhet division shown susceptibilityto colistin.

Conclusion: The current study demonstrated a spacious continuity of the susceptibility and resistance profile of *E. coli* isolates to colistin. *E coli* isolates of food animals were sensitive to reserve antibiotic colistin except few cases in chicken. The results of the study might be helpful to providevaluable guidelines on the use of reserve antibiotics in food animalsand thereby to achieve the goal of One Health approaches in Bangladesh.

Key words: *E. coli*, Antibiotic resistant, Colistin, Food animals, Bangladesh.

ID 19-132: **Prevalence and Antimicrobial Susceptibility Pattern of *Escherichia coli* O157:H7 Isolated from Calf and Milk inBangladesh**

Mohammad AsheakMahmud[1],MdShajalalSagor[1], MdSujan Mia[1], MdNureAlamSiddiky[1], Muhammad Sazzad Hossain[1],Ruhena Begum[1], MdRezaul Karim[1], MdZakaria Mia[2],Md Giasuddin[1], Mohammed A. Samad[1]

[1]Bangladesh Livestock Research Institute (BLRI), [2]Jagannath University,

Email of corresponding author email: samad_blri@yahoo.co.nz

Shiga toxin-producing *Escherichiacoli* (*E. coli*) O157:H7 has been emerged as a global public health threat. A cross sectional study was done to assess the prevalence and pattern of antimicrobial resistance of *E. coli* O157:H7 in calf and cow milkofSavar&Dhamrai;Chashara and NarayanganjSadar&Shahjadpursub district of Bangladesh. A total of 290 samples comprising 210 calf rectal swabs and 80 cow milk were collected from October 2017 to August 2018.In preliminaryscreening by real time PCR,overall 20% (n=58; CI: 15.80-24.98) samples were positive for *E. coli* O157:H7 –in which24.76% (n=52; 95%CI: 20.1-31.9) were calf samples and 7.5% (n=6; 95%CI: 2.78-12.22) were milk samples. The highest prevalence was found in Dhamrai (75%) followed by Narayanganj, Saver and Shahjadpur.However, the prevalence rate was found higher in household farm (30%) compared to commercial farm (20.83%). After screening, 15%(n=8) of the positive samples were cultured in selective and differential media to obtain pure isolate. Positive isolates were reconfirmed using slide agglutination test followed by Vitek-2 application (bioMérieux, France) as well as with real time PCR.The isolates (n=8) were tested forantimicrobial susceptibility testing against twenty different antibiotics belongs to fourteen different classes.Following disk diffusion test, all the isolates were found 100% sensitive to seven antibiotics including amoxicillin/clavulanic acid, chloramphenicol, cefixime, ceftriaxone, cefotaxime, cefepime and nitrofurantoin. Nevertheless, the isolates showed resistance to at leastone of the remaining antibiotics including tetracycline, nalidixic acid, azithromycin, streptomycin,trimethoprim/ sulphamethoxazole, gentamycin, imipenem, kanamycin, levofloxacin, norfloxacin, colistinsulphate, ciprofloxacin, and doxycycline.The highest percentage of resistance werefound to streptomycin 38%(n=3; 95%CI: 13.68-69.43), followed by azithromycin 25%(n=2; 95%CI: 7.0-59.07), nalidixic acid 25%(n=2; 95%CI: 7.0-59.07), and tetracycline 25%(n=2; 95%CI: 7.0-59.07). However, 37.5% (n=3; 95%CI: 13.68-69.43) isolates were found multi-drug resistance and none of the isolates were found resistant to all antibiotics. Prevalence of *E. coli* O157:H7 in milk is a great public health hazard thatindicate poor hygienic practices during milking, handling as well as poor biosecurity practices at farm level.

Keywords: *E. coli* O157:H7, PCR, vitek -2, multi-drug resistance, disk diffusion

Parallel Oral session-3BIntersectoral Engagement in Mitigating Antimicrobial Resistance

ID 19-144: **Antibiotic Resistance Surveillance in Human: A Step Towards Antibiotic Containment in Bangladesh**

Dr. Zakir Hossain Habib, Dr. Saimabinte Golam Rasul, Dr. Ahmed NawsherAlam, Prof. Dr. Tahmina Shirin, Dr. M. Salim Uzzaman, Dr. ASM Alamgir, Dr. AshekAhammed Shahid Reza , Dr. Iqbal Ansari Khan, Dr. Ashraful Alam, Dr. NazmunnaharBably, Prof. Dr. Meerjady Sabrina Flora

Institute of Epidemiology Disease Control and Research (IEDCR).

Introduction: The widespread overuse and misuse of antimicrobial agents to combat infectious diseases in human as well as animal~~s~~, plant~~s~~ and agricultureis associated with the development of resistance to these drugs, which has emerged as a major problem globally. For the containment of Antimicrobial Resistance (AMR), surveillance is an important strategy. Accordingly a surveillance is being conducted in the country since 2017 by Institute of Epidemiology, Disease Control and Research (IEDCR) to find out the status of AMR in the country and develop antibiogram periodically according to observe sensitivity pattern.

.**Methods:** Nine sentinel sites representing different geographical areas of Bangladesh are included in this surveillance. Ten priority pathogens has been selected for five clinical conditions namely urinary tract infection, diarrhoeal diseases, wound infection, pneumonia and septicaemia. Six types of samples-urine, stool, wound swab or pus, sputum, blood, and endotracheal aspirate are being collected from selected cases and tested for culture and sensitivity in the respective microbiology departments following SOP (Standard Operating Procedure).

Results: Till the end of September, 2019 total 14669 samples has been processed. Among them 26% yielded growth. *Klebsiella pneumoniae* was the highest pathogen isolated from sputum (48%) and endotracheal aspirate (35%) whereas *E.coli* (60%)*,* Pseudomonas (44%), *Salmonella spp*. (58%) and *Vibrio cholera* (47%) was the highest isolated pathogen from urine, wound swab, blood and stool samples respectively. Imipenem showed highest sensitivity to *Klebsiella pneumoniae* (75%), *E.coli* (90%), *Proteus spp.* (69%) *Pseudomonas aeruginosa* (52%) and *Salmonella spp. (*99%) while Ciprofloxacin (81%) showed highest sensitivityfollowed by Azithromycin (80%) to *Vibrio cholerae*.

Conclusion: This countrywide AMR Surveillance is first of its kind in Bangladesh and the data generated from this surveillance representing the whole country will help to prepare an antibiogram as well as a standard treatment guideline for infectious diseases.

Key words: AMR, surveillance, antibiotic, sensitivity

.

ID: 19-03: **Abundance of Mobilized Colistin Resistance Gene *Mcr-1*in Genetically Diverse Commensal *Escherichia Coli*in Broiler Chicken in Bangladesh**

S. Ahmed[1], T. Das[2], M. Z. Islam[1,2,3,4], A. Herrero-Fresno[1], **P. K. Biswas***[2] and J. E. Olsen[1]

[1]University of Copenhagen, [2]Chattogram Veterinary and Animal Sciences University,[3]Joslin Diabetes Center,[4]Harvard Medical School,

Email of corresponding author: biswaspk2000@yahoo.com

Introduction: In spite of the importance of colistin as a last-resort antibiotic for the treatment of human infection caused by carbapenem resistant *Enterobateriaceae*, this antimicrobial is still used in intensive broiler production in Bangladesh. Prevalence, distribution and genetic reasons for colistin resistance in *Escherichia coli*population in broiler chicken are, however, still unknown. Resistance to colistin in *Escherichia coli* can be due to mutations in the chromosome or, as reported very recently, plasmid-mediated transferable genes called mobilized colistin resistance (*mcr*) genes. The objective of this study was to investigate genetic diversity of commensal *E.coli* strains in broiler poultry in Bangladesh along with the prevalence of five *mcr*(*mcr-1* to *mcr-5*) genes in them.

Methods: A prospective cohort study was conducted to explore the occurrence and genetic diversity of colistin-resistant commensal *E. coli* from broiler chickens throughout the production period. We isolated 1200 *E. coli* strains from 60 pooled fecal samples of 20 broiler farms at three-time points in the production (day1, day15 and day28). A multiplex PCR targeting five *mcr* genes (*mcr-1* to *mcr-5*) was used to screen their presence in the strains isolated. We measured the genetic diversity of 1200 commensal *E. coli*by repetitive extragenic palindromic (REP)-PCR fingerprinting. Detail genomic characterization and phylogenetic comparison was performed by whole genome sequencing (WGS) of 32 strains randomly selected among the dominant REP-types of the *mcr*-positive isolates.

Results: The results revealed that 25% (95% CI, 23-28%) of the isolates obtained were positive for the mcr-1 gene. The minimum inhibitory concentration (MIC) values of colistinsulphate to the mcr-1 positive *E. coli* strains varied from 2 to 128 mg/L. As many as 367 unique profiles were seen in the isolates by REP-PCR with a high ecological diversity index (Shannon diversity index, H', of 5.3). By genome analysis, 42 acquired antimicrobial resistance genes (ARGs) were detected in the 32 *E. coli* strains.

Conclusion: There is high abudance of commensal *E.coli* strains carrying the *mcr-1* gene in poultry in Bangladeshand the strains are genetically diverse, suggesting a massive horizontal spread of the gene rather byclonal expansion.

Keywords: *Antimicrobial Resistance, Colistin, Mcr, Poultry*

ID 19-15: **Risk of Multi-Drug Resistant *Campylobacter* Spp. and Residual Antimicrobials in Poultry Farms and Markets in the Selected Districts of Bangladesh**

SucharitBasu Neogi[1], Md. Mehedul Islam[2], SK Shaheenur Islam[3], A.H.M. Taslima Akhter[4], Md. MahmudulHasan Sikder[5], Shinji Yamasaki[1] and **S. M. Lutful Kabir**[2]

[1] Osaka Prefecture University,[2]Bangladesh Agricultural University, [3]Epidemiology Unit, Department of Livestock Services, [4]Institute of Public Health, [5]Bangladesh Agricultural University,

E mail of Corresponding author: lkabir79@gmail.com

Introduction: Understanding potential risks of multi-drug resistant (MDR) pathogens from the booming poultry sector is a crucial public health concern, particularly for developing countries. *Campylobacter* spp. are among the most important zoonotic pathogens associated with MDR infections in poultry and human. This study systematically examined potential risks and associated socio-environmental factors of MDR *Campylobacter* spp. in poultry farms and live bird markets (LBMs) of the selected districts (Gazipur and Tangail)of Bangladesh.

Methods: Microbial culture and PCR-based methods were applied to examine the occurrence and MDR patterns of *Campylobacter* spp. at hatcheries (n = 33), broiler farms (n = 122) and LBMs (n = 69). Antimicrobial residues in broiler meat and liver samples (n = 50) were detected by advanced chromatographic techniques. A questionnaire based cross-sectional survey was conducted on socio-environmental factors.

Results: In poultry farms, *Campylobacter* spp. was primarily found in broiler cloacal swabs (21/49, 43%), followed by water (8/24, 33%) and broiler meat (8/28, 29%). Remarkably, in live bird markets, *Campylobacter* spp. was detected in higher prevalence in broiler meat (14/26, 54%), which could have an association with bacterial contamination in water sources (11/21, 52%) and floor (9/21, 43%). Majority isolates of the predominant species, i.e., *Campylobacter jejuni* (33/47, 70%) and *Campylobacter coli* (14/24, 58%), were observed to be MDR, showing resistance to amoxycilin, tetracycline and erythromycin, and additionally ciprofloxacin, norfloxacin, streptomycin, and azithromycin. Residual antimicrobials, including oxytetracycline, ciprofloxacin and enrofloxacin, were detected in majority of broiler liver (79%) and meat (62%) samples; and alarmingly, 33% and 19%, respectively, with concentration above acceptable limit. Inadequate personal and environmental hygiene, unscrupulously use of antimicrobials, improper waste disposal, and lack of health surveillance and quarantine facilities of diseased birds were distinguishable anthropogenic risk factors, with local diversity and compound influences on MDR pathogens.

Conclusion: The observed large-scale occurrence of MDR *C. jejuni* and *C. coli* and residual antimicrobials in poultry value chain reflects an alarming situation for public health in Bangladesh. Potential contamination sources of MDR *Campylobacter* and the combined influences of diverse socio-environmental risk factors, noted in this study, would aid in developing interventions to minimize the increasing risks of poultry-associated MDR pathogens under 'One Health' banner that includes poultry, human and environment perspectives.

Keywords: Poultry farms, live bird markets, *Campylobacter*, multi-drug resistant, residual antimicrobials

ID 19-74: **Residue and Potential Ecological Risk of Veterinary Antibiotics in Poultry Manure in Bangladesh: One Health Perspective**

Yusuf Ali Sarker, Bishan Lal Das Chowdhury and **Mahmudul Hasan Sikder***

Bangladesh Agricultural University,

Email of corresponding author:drmsikder@bau.edu.bd

Introduction: The residue of Veterinary antibiotics (VAs) is becoming an obstinate health hazard and environmental problem in all over the world. However, residual levels of antibiotics and distribution are still obscure. Here, we systematically analyzed the usage pattern, occurrence, concentration and potential ecological risks of VAs residue in manure in Bangladesh.

Methods:A questionnaire survey was conducted to understand farmer's and prescriber's perspective on VAs in poultry production and in manure.

Results: All respondent farmers were multidrug users and only a quarter had residual knowledge (35.49%). However, most farmers (86.08%) didn't respect the withdrawal period. Sixteen different patterns of antibiotics of seven classes mostly (86.84%) critically important for human medicine was used. These farms used poultry manure in the agricultural field and fish pond (91.96%) and rest of 8.04% in the biogas plant. We applied both identification (TLC) and quantification (HPLC) methods to screen four antibiotics namely ciprofloxacin (CIP), enrofloxacin (ENR), oxytetracycline (OTC) and doxycycline (DOX) in 120 poultry manure sample. Occurrence and concentration (mean±SD) of CIP, ENR, OTC and DOX are 40.83% and 28.81±20.85 mg/kg, 8.33% and 17.72±9.48 mg/kg, 23.33% and 16.50±11.48 mg/kg, 17.50% and 11.75±10.69 mg/kg respectively. The Hazard Quotient (HQ) value of OTC is 61.11, which resembles potential ecotoxic (since HQ>1considered potential ecotoxic).

Conclusion:Overall, this work explores the perspective of VAs residue in farmers and prescribers and builds a foundation for the potential adverse effect of VAs residue in antibiotics resistance phenomenon and in the human food chain, and understanding the ecological risk of VAs that contributes to One Health.

Keywords: Veterinary antibiotics, Poultry manure, Risk evaluations, Ecological risk, One health

ID: 19-31: **Mobilized Colistin Resistance (*Mcr*) Genes and Tetracycline Resistance (*Tet)* Genes in Multidrug-Resistant *Escherichia Coli* Circulating in Poultry, Food and Human Sources**

Tridip Das[1]*, Md Zohorul Islam[1,2], Eaftekhar Ahmed Rana[1], Avijit Dutta[1], Shahana Ahmed[3], Probir Deb[1], Avijit Das[1], Himel Barua[1], Paritosh Kumar Biswas[1]

[1]Chattogram Veterinary and Animal Sciences University,[2]Harvard Medical School,[3]University of Copenhagen,

*Email of corresponding author:*das.vet671@gmail.com

Background: The antimicrobial resistance (AMR) is rapidly spreading not only in pathogenic but also in commensal bacteria. Consequently, the later becomes a reservoir pool for resistance genes, contributing to their transfer to other zoonoticpathogens over time. A cross-sectional survey was conducted to investigate the AMRpatterns along with the presence of the mobilized colistin resistance (*mcr*)genes and three selected *tet* genes in commensal *Escherichia coli*circulating in poultry, poultry farm environment, street foods and human patients.

Methods: A total of 530 samples were investigated. Of them 150 (cloacal swabs) were from live broiler, 150 from different matrices (litter, feed, water and soil) at poultry farm environments, 78 from street foods and 152 (stool samples) from human patients suffering from clinical illness. All the *E. coli* isolates obtained from the survey were tested for their susceptibility to a panel of nine antimicrobials.Univariate and multivariate logistic regression analyses were performed to identify risk factors associated with the presence of colistin- and tetracycline-resistant*E. coli*.

Results: In total, 313 E. coli isolates were obtained from all collected samples. Of them, 98% (95% CI 95%-99%) were found to be MDR with 58% (95% CI 52%-63%) showing resistance to colistin and 98% (95% CI 96%-99%) to tetracycline. MIC values of colistin against the isolates ranged from 4 to 64 mg/L. Except for human patients, 20% colistin-resistant isolates of other sources of isolation had the mcr-1 gene. Among the tetracycline-resistant isolates 45%, 12% and 5% had the tetA, tetB and tetC genes, respectively. Despite a diverse isolation source, the identity and similarity percentages of the sequences of the mcr-1 gene of the isolates showed a clonal relationship among them. After multivariable analysis, the variable ‘antibiotic use’ was identified as a risk factor for the occurrence of colistin (Odds Ratio (OR) 2.55; 95% CI 1.22-5.32; P=0.01)) and the occurrence of tetracycline-resistant E. coli (OR 2.09; 95% CI 1.02-4.27; P<0.04) in live broilers.

Conclusion: The presence of MDR commensal *E. coli* with the acquisition of the *mcr-1* gene in non-human sources and the *tet-A* gene in both non-human and human sources are quite high in Bangladesh.

Keywords: Antimicrobial resistance, *Escherichia coli*, *mcr-1* gene, *tet* genes, One Health

Panel Discussion–IVDevelopment of One Health Workforce by UniversityNetworks in Southeast Asia

Dr. VipatKuruchittham

Dr. Vipat (Pat) Kuruchittham is the Executive Director of Southeast Asia One Health University Network (SEAOHUN) Secretariat working to develop a resilient and competent One Health workforce by leveraging education, research, and training provided by university networks in Southeast Asia. Dr. Kuruchittham has worked to improve population health in several capacities since 1999. He worked as health informatician, monitoring and evaluation (M&E) professional, researcher, and trainer at leading organizations including U.S. CDC, WHO, and UNDP. He also taught at the College of Public Health Sciences, Chulalongkorn University and worked with the Thailand Ministry of Public Health to strengthen its national malaria control and elimination program. Additionally, he worked to promote the harmonization of Southeast Asian higher education systems when serving as Deputy Director of SEAMEO RIHED (Southeast Asian Ministers of Education Organization Regional Centre for Higher Education and Development). He holds a Ph.D. in Health Systems Engineering with a minor in public health and MSIE in Decision Science and Operations Research from the University of Wisconsin – Madison.

E mail address of the author: vipat@seaohun.org

One Health (OH) workforce development is fundamental for any country to effectively respond to all hazards and emerging threats. With support from the U.S. Agency for International Developmentand its One Health Workforce projects, the Southeast Asia One Health University Network (SEAOHUN) has fostered a regional network of 72 universities in Cambodia, Indonesia, Lao PDR Malaysia, Thailand, and Vietnam working collaboratively to enhance the capacity of OH workforce with cross-sectoral competencies to prevent, detect, and respond to infectious disease threats. Soon SEAOHUN will expandour network to comprise eight additional universities in Myanmar and the Philippines, that have agreed to partner with SEAOHUN to build the next generation of One Health leaders.Our key target audiences are national trainers, faculty members, and in-service and pre-service health professionals in Southeast Asia. For graduates and health professionals to thrive in the 21st century, equipping them solely with technical skills is insufficient. The next generation of the OH workforce needs to acquire core competencies or soft skills (e.g., communication, collaboration, critical thinking, and creativity) in addition to their technical skills to work together across disciplines to solve complex issues of OH. Our approach on capacity building is to apply learner-centered activities when teaching One Health and to thus transform students from passive to active learners. We also actively support the training of students from multiple disciplines together, so that they can understand the principles of One Health and the One Health approach to disease prevention and control, and this allows them to exchange their perspectives and share experiences.Moreover, universities as producers of OH workforce would be able to support surge capacity of government when required during emergency situations and provide policy makers with evidence-based information to make informed decisions on competing priorities.In summary, SEAOHUN’s work is to build the next generation of skillful and competent One Health professionals in Southeast Asia to make the world safer from infectious disease threats.

Parallel Oral session-IVAOne Health Approach to Control Vector Borne Diseases

ID 19-11: **Reliable Identification of Potential Vector Mosquitoes Collected from Chittagong Bangladesh through Morphotaxonomy and Molecular DNA Barcoding**

AMAMZ Siddiki[1], MS Sarker[1], MS.Mazumder[2], AB Bhuiya[2], K Basher[3], MA Hossain.[1]

[1]*Veterinary and Animal Sciences University (CVASU),* [2]*University of Chittagong,*[3]*Jahagirnagar University.Email of corresponding author:* *zsiddiki@gmail.com*

Introduction: Mosquitoes are important vectors for a wide variety of pathogens and parasites.Identificationof different mosquito species are crucial for their eventual control. We have used the classical morphometry and modern molecular methods like DNA barcoding approach for reliable identification ofmosquitoes that were collected from different locations of Chittagong Metropolitan area of Bangladesh.

Methods:A total of 20 randomly collected specimens were included in this study. Different morphological features of head, clypeus, vertex, antenna, maxillary palp, thorax, wings, legs and abdomen of the mosquitoes were examined using three-dimensional microscopy.

Results: The morphological characteristics of the mosquitoes observed under stereo binocular microscope in the laboratory shown high similarity with the *Aedesaegypti* species. Total DNA was extracted from all of the 20 samples using commercial kits and specific primers were used for amplification of partial COI genes for molecular characterization.PCR products were then sequenced and further bioinformatics analyses were accomplished. Sequence similarity based BLASTnand phylogenetic analyses (MEGA 6) of the sequence indicated similarity with three different species namely *Aedesaegypti, Culexpipiens* and *Aedesalbopictus*. The findings were compatible with the morphological data and reliably characterized the mosquito species.

Conclusion: The study showed the feasibility of using molecular tools for their characterization. Further study about the origin and vector potential of these mosquitoes will enhance our capacity to improve existing vector surveillance and control program.

Keywords: Mosquito, Vector, Chittagong, Morphology, DNA barcoding

ID 19-147: **Cost-Effectiveness of Dengue Vaccine Introduction in Dhaka City, Bangladesh**

Sabbir Haider

Directorate General of Health Services.

Email of corresponding author: sabbir_doc@yahoo.com; dr.sabbir@gmail.com

Introduction: Dengue infection is one of the major public health threats in Bangladesh, especially in the capital city Dhaka. In 2019, Dengue causes massive outbreak in Bangladesh specially in the Dhaka city where the casualty were more. In recent years dengue vaccine was launched in the market to prevent this infection. Several countries introduce dengue vaccine in their health system.This study aimed to evaluatecost-effectiveness andto analyze financial feasibility for introducing dengue vaccination in Dhaka city, Bangladesh.

Methods: We conducted a cost-effectiveness analysis using Markov model from the government perspective. The model was limited to second infection and compared dengue vaccination with no vaccination during20-yeartime horizon with a 1 year cycle length. Cost, epidemiological and vaccine parameters were obtained fromliterature review. We measured utility by converting disability adjusted life years (DALYs) weight into quality adjusted life years (QALY). The cost and outcomes values were adjusted using 3% discount rate. One-way, threshold,and probabilistic sensitivity analyses were employed to observe model uncertainty. Budget impactanalysis was performedbased on the governmental perspective for 5 years to introduce the vaccine for 9-15 years age group.

Results: The incremental cost-effectiveness ratio (ICER)values of dengue vaccine introduction in Dhaka city wereUSD 397/QALY and USD 394/QALY in deterministic and probabilistic approaches, respectively.The total budget for introducing vaccination in the Dhaka city among the target group was USD115 million in first year and USD207million for 5 years. Vaccine coverage wasthe most sensitive parameter to have an impact on theICER. Probability of vaccination was 90% cost-effective at the willingness to pay of USD 600.

Conclusion: We found dengue vaccination was cost-effective and ICER isone-fourth GDP of Bangladesh. However, the budget impactwas relatively high, as it was about 4.43% of total budget for spending on health in Bangladesh in the first year and will be less than 0.9% from second year and onwards. Policy makers of Bangladesh can think and take initiative to introduce the dengue vaccine in national immunization program.

Key Words: Dengue; Cost-effectiveness; Dengue vaccine

ID 19-107: **Viral Etiology among the Hospitalized Encephalitis Patient in Bangladesh**

Sharmin Sultana[1], A K M Muraduzzaman[1], ASM Alamgir[1], Md.Tanbirul Islam[2], Kishorkumar Paul[3], AhmedNawsher Alam[1], Manjur Hossain Khan Jony[1],Arifa Akram[1],Tahmina Shirin[1],Meerjady Sabrina Flora[1]

[1]Institute of Epidemiology, Disease Control and Research (IEDCR),[2]World Health Organization(WHO),[3]International Centre for Diarrhoeal Disease Research(icddr,b).

E-mail of Corresponding Author:dr.sharmin1579@yahoo.com, dr.sharmin@iedcr.gov.bd

Introduction: Acute encephalitis syndrome (AES), a quite common neurological emergency, requires immediate hospitalization, and often associated with disability or death.By using the acute encephalitis syndrome surveillance platform an attempt was made to explore the viral etiology of encephalitis. The objectives wereto identify the viral causes of encephalitis from AES surveillance platform in Bangladesh

Methods: A total of 644 cases were enrolled following AES case definition from January 2018 to June 2018. Of them CSF was collected from 239 cases. Cerebrospinal fluid (CSF) were collected from 62suspected cases within 7 days of onset of illness and where adequate amount is available for the test.Detection of viral pathogens was done by commercially available FTD Neuru 9 Multiplex real-time PCR kit (TaqMan® technology).

Results: Out of 62 CSF tested. 32(51.61%) specimens were positive for different viruses. HPV-B19 was most common virus for viral encephalitis (43.75%) followed by HAdV (12.5%), EBV(6.25%) and single case positive for, EV, HPeV and HSV-1(3.12%) among the positive cases. In addition mixed infections likeHAdV with HPV- B19 and HAdV and HCMV (6.25%), HAdV with HSV-7, HAdV with HSV-1, HAdV and EV, HAdV and EBV, EBV and HPV- B19 and were also detected (3.12% for each group).

Conclusion: Strengthening of surveillance platform for encephalitis is very much essential to find out the trend of viral encephalitis, which will reduce misuse of antibiotics as well as contribute to develop management guideline for viral encephalitis**.**We need to continue the surveillance to detectviral infections and based on the findings we can generate data for the policy maker to develop strategy for prevention, control and management of those encephalitis cases.

Key words: AES, CSF, surveillance

ID 19-49: **"One Health" Approach for Combating VectorBorne Diseases in Bangladesh**

Md. Zakir Hassan[1], Mohammad Rafiqul Islam[2]

[1]Bangladesh Livestock Research Institute, [2]Bangladesh Agricultural Research Counci.

Email of corresponding author: zhtitas@gmail.com,**zakir.vet@blri.gov.bd**

Introduction: Vector borne diseases (VBDS) are group ofinfectious diseases which aretransmitted to human and animal by crawling or flying insects usually mosquitoes,sandflies, ticks, mites.Annually, above 7 million deaths occur due to VBDs identically, malaria, dengue, trypanosomiasisby vector transmission. Travel, trade, unplanned urbanization, deforestation,and climatic change are the main risk factor for VBDs. There are 38,844 reported case and 29 deaths occur up to August, 2019 due to Dengue outbreaks in Bangladesh. For combating VBDs aims is to reduce the burden and threat through One Health approach, notably locally adapted sustainable vector control strategy.

Methods: Prevention of VBDs by targeting vectors is the first and best approach. Through,WHO, global vector control response comprises four stages to reducing mortality and incidence for achieving SDG 2030.Stage one-Strengthening inter and intra-sectoral action and collaboration-Introductionof training facilities,mass vaccination and allocation of sufficient fund and policy against the threat. Stage two-Engage and mobilize communities- Public awareness and emergency health service could be effective through engage and mobilize communities. Moreover, expert advocacy and partner coordination is necessary.Stage three- Enhance vector surveillance monitoring and evaluation of interventions-Initiation of national vector surveillance program including veterinary entomologist, health expert, environment specialist with proper diagnostic capacity. Proper monitoring evaluation, reporting, co-ordination with neighboring countries and research also mandatory for control program. Stage four-Scale up and integrate the tools and approaches-Ensuring the vector control programs are well fitted for the community.

Results: Millions of people have already benefited from vector control program with major reduction of malaria and leishmanisis,chikungunya, notably in Indian subcontinent. Bangladesh is one of the best examples for controlling recent dengue outbreaks by One Health approach through involving health expert, laboratory personal, researcher, policy maker,local government, media and public awareness.

Conclusion: Finally, active collaboration with immediate reporting and action through One Health approach can combat the VBDs successfully.

Keywords: One health, Vector, transmission, Dengue

Parallel Oral session-IVBInter-professional Workforce Development for Achieving Health Security

ID 19-75: **Educational Intervention and Contents in Veterinary Education for Prudent Antibiotic Use for One Health in Bangladesh**

Mahmudul HasanSikder[1], Mohammad Mahmudul Hassan[2], Md. Mizanur Rahman[3]

[1]Bangladesh Agricultural University, [2]Chittagong Veterinary and Animal Sciences University, [3]Bangabandhu Sheikh Mujibur Rahman Agricultural University.

Email of corresponding author: drmsikder@bau.edu.bd

Introduction: Widespread antimicrobial use and concomitant resistance have led to a significant threat to One Health. As inappropriate and overuse of antibiotics based on insufficient knowledge are one of the major drivers of antimicrobial resistance (AMR), education about prudent antibiotic usage (AMU) aimed at both the prescribers and the stakeholders is important. We conducted a study to evaluate the educational effectiveness, day-one-skills target, and contents that are directed to train ~1000 veterinary graduates at ten veterinary schools for prudent antibiotic usages in Bangladesh

Methods:A structured questionnaire was used to evaluate the current curriculum, contact hours and teaching methods where 10 percent of students and faculty of each school participated. We also assessed the contents of AMR and perception on AMR.

Results:The curriculum of all schools ensure antibiotics resistance, AWaRe categorization by WHO, guidelines for prudent AMU and causes of AMR and measures to prevent AMR. The contents of AMR is mostly in Microbiology and Pharmacology course and about 4-12% questions are focused on AMR and AMU. Most schools follow didactic lectures with few demonstration classes where one recently introduced Problem Based Learning (PBL) in a semester. Students undergo clinical rotation during the internship which varies 6 months-1 years. Evaluation of the graduates' prescriptions pattern in digestive system diseases in dairy animal and in bacterial or viral disease in poultry suggest only 25% prescribers follow AWaRe categorization and withdrawal period suggestions.

Conclusion: Our study suggests that introduction of better teaching methods is obligatory to meet day one skills that could lead to a better understanding of AMR and AMU to ensure One Health in Bangladesh.

Keywords: Educational intervention, AMR, AMU, Day one skills, One health

Introducing One Health Concept and One Health Practices among Relevant Student Communities in Bangladesh

Easrat Jahan Esha[1], Seemanta Das[1], Tahia Logno[1], Meherjan Islam[1], Sabrin Fahmi[1], Shariful Shaikat[1], Ankon Das[1], SH Mannan[1], Aarifa Munny[1], Nadia Nishat[1], M. Sawkat Anwer[3] and Md. Ahasanul Hoque[2]

Chattogram Veterinary and Animal Sciences University,

Email of corresponding author: easrat750@gmail.com

Introduction: One Health concept was first introduced in Bangladesh in 2012, but relevant student communities are mostly unaware of this concept. Therefore, International Veterinary Student Association (IVSA) and One Health Young Voice (OHYV), Bangladesh conducted a series of activities to increase awareness of One Health concept and assess the level of knowledge of One Health practices among students of different disciplines.

Methods: With the support of the OIE Twinning Bangladesh Project, a series of activities related to the One Health were organized jointly by IVSA and OHYV, Bangladesh in 2018-2019. Students of relevant disciplines were invited to participate in different seminars, workshops, One Health lectures, field campaigns, school kid programmes, surveys, One Health quiz contest and debate competition.

Results: Feedback responses on One Health concept and practices after each event were very affirmative. Most of the participating students (70-80%) found the One Health approach and practices are very interesting and useful in understanding complex One Health issues and are very keen to learn more about One Health. Students' engagement in One Health quiz competition was overwhelming. Amazingly, about 80% students got the right answer in most of the questions. A wide range of seminar presentations given by students on Zika, Dengue, Chikungunea, Lumpy Skin Disease, Rabies, West Nile virus, etc followed by open discussion were example of cooperative One Health activities among students. Attending One Health lectures (Lecture 1: "Importance of One Health Culture at Educational Environment and its Society Impact") given by Prof Nitish Chandra Debnath; Lecture 2: "Integrating One Health into university education: experiences from Hong Kong and Thailand" by Lisa Kohnle) followed by interactive sessions was effective for students to understand One Health concept and application. These activities definitely help create a One Health culture among student communities at the institutional level.

Conclusion: Students are now more interested to learn about One Health participating in One Health activities at CVASU. To make it more impactful we will continue our One Health programmes.

Key words:CVASU,IVSA, OHYV

ID 19-141: **Behavioral Risk Practices and Zoonotic Disease Emergence at High-risk Communities in Bangladesh: An Explorative Qualitative Study**

Shahanaj Shano[1,2]Ariful Islam[2,3], Emily Hagan[2], Melinda K Rostral[2], Stephanie Martinez[2],Leilani Francisco[2], Abir Hossain[1,2],Jonathan H Epstein[2], Peter Daszak[2], Meerjady Sabrina Flora[1]

[1]Institute of Epidemiology, Disease Control and Research (IEDCR),[2]EcoHealth Alliance,[3]Deakin University.E-mail of corresponding author: shahanajshano@gmail.com

Introduction: Nearly 75 percent of all new, emerging, or re-emerging diseases affecting humans at the beginning of the 21st century are zoonotic. Human behaviors and practices are key risk components for pathogen spillover, amplification, and the spread of zoonotic diseases. This exploratory qualitative study aims to understand the behaviors, practices, circumstances thatcould increase the risk of zoonotic disease spillover from animals to humans.

Methods: Participant observation (30 hours) and in-depth ethnographic interviews (130) wereconducted from October2018 to March2019 in four different districts namely, Dhaka, Madaripur, Faridpur, and Dinajpur in Bangladesh. Interview data were coded using computational data analysis software (MaxQDA), and emergent themes were identified using a grounded theory approach.

Results: The participants from Madaripur and Dhaka felt there were clear links between anthropogenic landscape change and associated activitiesand an increased potential for human-macaque interaction. As natural food and water sources were depleted, macaques became increasingly dependent on humanresources.In response, many residents reported reactingantagonistically, which led to aggressive biting and scratching events.Indigenous communities in Faridpur and Dinajpur districtsreportedpartaking in high-risk activities including, hunting wild animalsas a traditional practice and akey source of protein. Additionally,several people reported that bat meat and bones cure asthma and joint pain, which was consistent with their traditional beliefs. In Dinajpur, animal traders indicated that most of the cattle and buffalo were brought from India and the livestockthey sold would eventually reach the markets in Dhaka. We found thatthe traders had limited knowledge about zoonotic diseases and animal welfare. Participants reported that animals are not tested for diseases in the market and people handle them with bare hands.

Conclusion: This study identified important drivers of disease transmission from animals to humans, includingthe conversion of landscapes, changing agriculture and food production systems, wildlife hunting, and trans-boundary animal trading. These provide opportunities for pathogensspillover from animals to humans.Behavior change interventions should be developed to reduce zoonotic spillover by mitigating the risks associated with human-animal interactions at high risk interfaces in Bangladesh.

Keywords:zoonotic diseases, emerging diseases, pathogen, spillover, wildlife

ID 19-72**Evidence of Exposure to *Brucella* among Humans and Cowsin ShahjadpurSub-district, a High Milk-producing Area in Bangladesh**

Ireen Sultana Shanta[1], James D Heffelfinger[2,3], Mohammad Abdullah Heel Kafi[1], Firoz Ahmed[1,4], Shabiha Sultana[1], Rebekah Tiller[2], Erin D Kennedy[2], Melissa Kadzik[2], Ausraful Islam[1], Syed Sayeem Uddin Ahmed[1,5], AKM Anisur Rahman[6], Md. Giasuddin[7] and Johanna S. Salzer[2]

[1]International Centre for Diarrhoeal Disease Research,[2]Centers for Disease Control and Prevention (CDC),[3]World Health Organization,[4]Noakhali Science and Technology University,[5]Sylhet Agricultural University,[6]Bangladesh Agricultural University,[7]Bangladesh Livestock Research Institute.

E-mail of corresponding author: ireenshanta@icddrb.org

Introduction:Brucellosis is a zoonotic disease caused by *Brucella* spp. that can cause abortion, reproductive problems and reduced milk production in cattleand undulant fever, arthritis, and orchitis in humans. Transmission from cattle to humans occurs mainlyby contact with infected animals or by ingestion of contaminated dairy products.Our objective was to identify the prevalence of *Brucella* antibodies and risk factors among cattle and humans in Shahjadpur sub-district, one of the highest milk-producing areas in Bangladesh.

Methods: A cross-sectional study was conducted from September 2015 to February 2016. We identified 303 milk producing villages inthis sub-district and randomly selected25 villages. From each village, we randomly selected 5% of the total households. From each household, we randomly enrolled up to three humans (≥ 15 years old) for interview and specimen collection. If the households had cows (> two years old), we randomly enrolled up to three cows. We testedcow's milk andhuman and cow serumto detect anti-*Brucella*IgG using indirect ELISA.We conducted multiple logistic regression, adjusting for household/farm-level clustering effect to evaluate the risk factors for human and animal *Brucella*seropositivity.

Results: We enrolled 647 households, 1,313 humans and 698 cows;360 cows were lactating. Of enrolledhouseholds, 443 (69%) had livestock. IgG antibodies to *Brucella* were detected in sera from 27 (2.1%, 95%CI:1.2-2.9%) humans. Among the sera and milk specimens collected from cows, 11 (1.6 %, 95% 0.6%-2.4%)cows had at least one positive specimen;6 (0.9%, 95% CI: 0.2%-1.5%)had positive sera and 9 (2.5%,95% CI: 0.1%-4.6%)had positivemilk. No significant association was found between cattle-raising practices and the presence of IgG antibodies to *Brucella* among cattle. Also, no significant association was found between the presence of IgG antibodies to *Brucella*inhumansanddemographic variables, history of raw milk consumption andrespondents' livestock exposure history.

Conclusion: Though the prevalence of *Brucella*seropositivitywas low in this study area, the public health importance of this disease cannot be ruled out. Further in-depth studies throughout the country would help define the countrywide prevalence and risk factors associated with the disease.

Key words: Brucella, humans, cows andBangladesh

Poster Presentation Day 2

ID 19-25: **Evaluation of immune response of a heat killed *Brucella abortus* vaccine in guinea pig by ELISA**

F. Yeasmin, A. A. Maruf, M. F. Karim, S. Tasnin, A. K. M. A. Rahman, M. M. Hasan, M. M. Hossain[1], D. Fretin[2], M. S. Rahman

[1]BAU [2]Sciensano, Belgium

E-mail of corresponding author: nupurnupur.fn@gmail.com

Introduction: Brucellosis, a zoonotic disease, is endemic in many countries of the world including Bangladesh. It affects both, public health and animal production. Brucellosis is caused by a Gram-negative, facultative intracellular bacterium of the genus *Brucella* (*B.*).

To control bovine brucellosis two types of vaccines are available- vaccine S19 and vaccine SRB51 but they have some adverse effects. On the other hand the heat killed vaccine has no adverse effects. Vaccination against brucellosis in Bangladesh has not yet been initiated. But in commercial management systems the prevalence is reported to be higher and vaccination may be initiated. Before importing live vaccine locally prepared killed vaccine can be tested for its immune response. Hence this study was undertaken to evaluate the immune response of heat killed vaccine prepared from local isolate in guinea pig using ELISA.

Methods: *Brucella* abortus isolated from aborted fetal membranes was used for vaccine production. Pour plate technique was used to count cfu/ml of *Brucella abortus* for dose calculation of heat killed vaccine. Bacterial pellet was prepared by centrifugation of 200ml of the cultured broth at 10,000 rpm for 10 mins.The bacterial pellet was mixed with required amount of PBS to obtain 40×10^9 cfu organisms in 2ml dose for guinea pig inoculation. Then the organisms were heated at 80˚C for 90 minutes and the prepared vaccine was inoculated subcutaneously 2ml (4×10^{10}cfu) in each of the guinea pig in total four guinea pigs. The sera of guinea pigs were collected at 1st, 2nd, 4th, 6th and 9th week after inoculation to examine the rise of antibody level by Enzyme-Linked Immunosorbent Assay (ELISA).

Results: The antibody level started to rise significantly ($p<0.01$) from the 2nd week (OD value 0.2287) and reached a peak level at 4th week (OD value 0.2842) and then started to decline significantly ($p<0.01$) from 6th week (OD value 0.1832) to 9th week (OD value 0.1015).

Conclusion: Heat killed vaccine without adjuvant induces immune response in guinea pigs which persists for a maximum period of 6 weeks. A further study to investigate the immune response of killed vaccine with adjuvant is recommended.

Key words: Brucellosis, Heat killed vaccine, Immune response, ELISA

ID 19-47: **Pathogenic *E. coli* in Drinking Water: Are They Human or Animal in Origin?**

Jannatul Ferdous[1,2], Ridwan Bin Rashid[1], Rebeca Sultana[1,2], Sabera Saima[1], Musharrat Jahan[1], Anowara Begum[1], Peter Kjær Mackie Jensen[2]

[1]University of Dhaka, [2]University of Copenhagen.

E-mail of corresponding author: jannat.du2010@gmail.com

Introduction: The occurrence of pathogenic bacteria in drinking water is a global health concern. The aim of this study was to investigate the presence of diverse pathotypes of *E. coli* isolates in piped-to-plot 'improved' communal source water and in point-of-consumption of drinking water (point-of-drinking) and, to identify their origin of fecal contamination.

Methods: The study was conducted from September 2014 to October 2015 in a low-income urban community of Bangladesh. PCR was performed for characterization of pathogenic *E. coli* and phylogenetic grouping.

Results: A total of 229 *E. coli* isolates were randomly collected where 125 isolates were from 108 point-of-drinking and 104 were from 76 communal source water samples. Diverse pathotypes were identified where ETEC was the most prevalent pathotype found in point-of-drinking water (37%, 46/125) and communal source water (46%, 48/104). Phylogenetic grouping showed substantial presence of subgroup B1 (most prevalent in animals feces) in both of point-of-drinking (50%, 91/181) and source water (50%, 90/181) isolates followed by the presence of B2-3 (most prevalent human feces) in (65%, 13/20) point-of-drinking and (35%, 7/20) source water. Our findings suggest that both communal sources and point-of-drinking water of the study area were mostly contaminated by the feces from animals (181/229) and to a lesser extent by human feces (20/229).

Conclusion: The non-human mammals and birds played a vital role in fecal contamination of the water and require priority attention in future intervention effort of water quality improvement. Our results indicate that addressing human sanitation without consideration of fecal contamination from livestock sources may not be enough to prevent drinking water contamination and thus will persist as a greater contributor of diarrheal pathogens in low-income urban communities.

Keywords: *E. coli*, Drinking water, Communal source

ID 19-40: **Bacteriological and Hematological Profiles in Balb/C Mice Experimentally Infected with *Brucella abortus* Biovar 3**

Prodip Paul, Md. Ariful Islam, **Mst. Minara Khatun**

BAU

E-mail of corresponding author: mmkhatun@bau.edu.bd

Introduction: Brucellosis caused by *Brucella abortus* is one of the most widespread re-emerging bacterial zoonotic diseases in the world, affecting both humans and animals. The main purpose of this research is to determine the distribution of *B. abortus*biovar 3 in different visceral organs in mice and measure the hematological profile during acute and subacute brucellosis.

Methods: *B. abortus* biovar 3 Bangladeshi bovine strain obtained from laboratory repository of Department of Microbiology was revived onto brucella agar media. Seven weeks old mice (n=40) were experimentally infected intraperitoneally with 0.1 ml sterile solution containing 1×10^{10} CFU/ml of *B. abortus*biovar 3. Five mice were kept as uninfected control. Blood samples were collected at 0, 3, 7, 14, 21, 28, 35, 42, 56 and 60 days post infection (d.p.i) from infected mice for hematological studies and Blood film was prepared by Wright-Giemsa stain. Spleen, liver and kidney samples were collected at 0, 3, 7, 14, 21, 28, 35, 42, 56 and 60 d.p.i from infected mice for bacteriological studies.

Results: Hematological profiles showed gradual decreased of total leukocytes count after 21 days to 60 d.p.i. and total erythrocytes count after 3 days to 60 d.p.i. as compared to uninfected control. *B. abortus* biovar 3 was recovered from spleen of 75% mice (3 of 4) at 3 and 42 d.p.i. and 100% mice (4 of 4) at 7, 14, 21, 28, 35, 56 and 60 d.p.i. Splenomegaly was observed in experimentally infected mice from 3 d.p.i. up to 60 d.p.i. as compared to uninfected control mice. Blood film of acutely infected mice at 21 d.p.i. with *B. abortus*biovar 3 showed abnormal shapes of the RBC with the moderate infiltration of inflammatory cells such as lymphocytes, neutrophils and monocytes.

Conclusion: Data of this study indicated that experimental infection of BALB/c mice with *B. abortus* biovar 3 bovine strain induced leukopenia and anemia in acute and subacute stages of infection and spleen might be used as a best clinical specimens for isolation of *B. abortus* from experimentally infected mice. It can be concluded from the study that BALB/c could be used as a laboratory animal model for study of *B. abortus*biovar 3 infections.

Key words: Brucellosis, mice, bovine

ID 19-55: **Knowledge on Nipah Virus Infection among Medical Students of Dhaka city**

Abdullah SAHM*, Imtiaz KS, Jahan I, Sumi SN

**Principal author: Directorate General of Medical Services, Bangladesh Armed Forces*

E-mail: hassan_amc@yahoo.com

Introduction: Nipah viral encephalitis is one of the fatal re-emerging infections, especially in Southeast Asia. World Health Organizaiton mentioned NiV infection to its list of “priority diseases” earlier this year (2019), along with more well-known conditions like Ebola, Zika, and SARS. Bangladesh also experiences several outbreaks since 2001. Case fatality of Nipah infection ranges from 40-100%, and currently no vaccine is approved for human use. It is necessary to raise the awareness regarding this infection. Objective was to study the knowledge about Nipah among medical students of Dhaka city.

Methods: This cross-sectional type of descriptive study was done in the months of May-June, 2017. Non-probability purposive sampling was done to select 160 final year MBBS students from 04 medical colleges of Dhaka city. A semi-structured self-administered questionnaire was prepared to collect data. Results were presented in frequency, percentage and quartiles.

Results: The average age of the respondents was 22.18 years and female participants were more (101, 63.1%). Nearly 70% had correct knowledge on reservoir host, only 24.4% knew about case fatality rate, 83.7% correctly said that date juice is responsible, 70% recognized that antibiotic has no role, and 65% correctly opined for well-cooked foods/boiled juices can prevent the transmission. Level of knowledge of the respondents was measure by the correct answers of the questions and it is expressed in quartile. Only 34 (21.3%) scored very good knowledge, and poor 41(25.6%). Female respondents had the better or very good knowledge than their male, (P<.05). Participants passed from District School having better knowledge than those spent in Dhaka city or village school (P<.05). Mothers’ education of the respondents and low family income also appeared as significant determinants (P<.05)

Conclusion: A good number of students showed limited knowledge on important information of Nipah, although majority had correct knowledge on reservoir host, principal mode of transmission and symptoms. Male students, mothers’ poor education, poor socioeconomic status and students passed from Dhaka city school showed significant negative association with good knowledge.

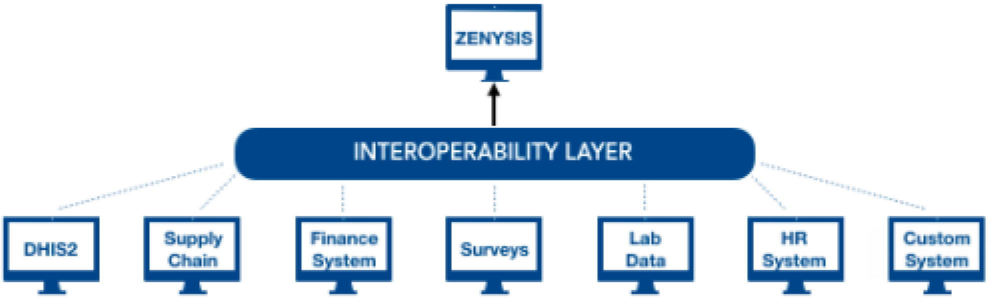
Keywords: Nipah, knowledge, medical students

ID 19-78: **One Health Application of Interoperable Technology: a feasibility of interoperability for Evidence-Based Decision-Making for Disease Surveillance and Control**

Mahbubul Alam (IT Head of Division at IEDCR), Miss. Claire Cravero (Director of Implementation at Zenysis Technologies), Mr. Anjaneya Mishra (Regional Project Director at Zenysis Technologies), Mr. Selen Appavoo (Project Launch Manager at Zenysis Technologies)

E-mail of the corresponding author: selen@zenysis.com

Introduction: The Institute of Epidemiology, Disease Control and Research (IEDCR) is responsible for epidemiological and communicable disease research as well as the functioning of disease outbreak and surveillance in Bangladesh. IEDCR will like to implement the strategic objectives of the Health Information System Revised Operational Plan 2017-2022 and move towards fully digitizing its Health Information System (HIS) by 2021 under one common platform building a robust evidence-based system. This will ensure closer collaboration between different departments (epidemiological, information technology, meteorological) and sectors to achieve better public health outcomes in line with the "One Health" approach. Zenysis is a software company that specializes in interoperability for siloed information systems.



IEDCR and Zenysis Technologies have partnered for a 5 months pilot project to strengthen the capacity of IEDCR epidemiological surveillance for priority diseases. This study aims to evaluate the impact of this new interoperability platform to extract actionable insights through advanced collaboration between different departments to achieve better public health outcomes.

Methods: There are two central aims of this feasibility study based on the "One Health" approach:

1) **Technical feasibility -** Evaluate the technical feasibility of integrating multiple siloed systems into one analytical view
2) **Acceptability -** Evaluate the acceptability of the platform by assessing it's usability and usefulness to target users.

Technical feasibility will be evaluated through quality assurance protocols and platform performance metrics. This protocol will assess whether the data that has been integrated into the interoperability layer reflects the same values as the source systems prior to integration.

Acceptability will be evaluated through quantitative usage metrics and qualitative interviews with target users and decision-makers. The research team will define a success metric and will evaluate how many users are independently able to successfully use the platform without additional assistance.

Results: This feasibility study is currently ongoing, and the results of the feasibility study will be ready for presentation by end of October.

Conclusion: The conclusion of this study will be in regards to the feasibility of the platform which allows multiple departments to share data and work together to achieve better public health outcomes through enhanced analytics and data driven decision-making.

Key words: IEDCR, One Health, interoperability, disease surveillance, epidemiology

ID 19-146: **South Asia One Health Disease Surveillance Network: Regional Approach against Emerging Infectious Diseases**

Sithar Dorjee[¥]; **Nitish Debnath[£]**; Mark Smolinski[§]; NomitaDivi[§]

[¥]KhesarGyalpo University of Medical Sciences of Bhutan, Thimphu, Bhutan; [£]Chittagong Veterinary University, Chittagong, Bangladesh; [§]Ending Pandemics, USA

E-mail of the corresponding author: NITISH.DEBNATH@CVASU.AC.BD

Background: South Asia One Health Disease Surveillance Network (SAOH-DiSNet) has been established and operationalized since December 2017. A shared vision and roadmap of the network was developed by high-level experts from government agencies, academic and research institutions, NGOs from human and animal health sectors from 8 SAARC countries. South Asia is a potential hotspot for emerging infectious diseases and close to 1.8 billion people are at risk. However, there is no One Health platform or regional cooperation specifically on disease surveillance before the establishment of this network. Knowing every country is as vulnerable as its neighbor to an emerging or re-emerging infectious disease, regional cooperation isessential for rapid action.

Therefore, the eight countries in South Asia developed as shared vision as "***We, the eight countries in South Asia, envision a future where regional cooperation allows every country to find, verify, and respond to outbreaks fast enough to prevent local emergence from becoming a public health emergency of international concern."***

The eight countries also mapped their capacities in animal health and human health disease surveillance and committed to a cross-sectoral, cross-border approach to finding, verifying, and responding to outbreaks faster, taking a One Health approach.

Methods: A second meeting of the Network was conducted recently from 19-20 September, 2019 in Bhutan to finalize a list of priority diseases for inclusion into the regional surveillance program, identify a formal Secretariat of the network, and train the key officials on the use of Portal for Readiness Exercises and Planning (PREP™) tool for conducting disease outbreak simulation and response exercises. CDC disease prioritization methodology was adapted to be able to apply it towards regional disease prioritization.

Results: The methodology used to establish a regional disease prioritization will be shared. Members from human and animal health sectors participated in the meeting. The secretariat used the PREP tool remotely to complete prework for the disease prioritization. Virtual meetings were used to align member efforts form the 8 countries. The in-person meeting was used to score the diseases based the criteria developed remotely. This presentation will share the preliminary results of the prioritization exercise, the network governance structure, and priorities activities for the coming years.

Conclusion: All countries committed to support this regional network to strengthen a cross-sectoral, cross-border approach to finding, verifying, and responding to outbreaks faster and effectively using One Health approach.

Key words: PREP, cross-border, simulation

ID 19-41: **Chemokine Receptor-5 (CCR5): a new hope in the immunoregulation of rhinovirus-induced severe refractive non-Th2 asthma exacerbation**

Hossain FMA[1], Rahman MM[1], Eo SK[2]

[1]Sylhet Agricultural University, Bangladesh [2]Chonbuk National University, Republic of Korea.

E-mail of the corresponding author: ferdaus.dps@sau.ac.bd

Introduction: Respiratory viral infections involved nearly 80% cases for hospitalized pediatric asthma exacerbations, rhinoviruses (RVs) dominate as the most prevalent pathogen responsible for around 70% of virus-associated asthma burdesn. Nowadays, corticosteroid resistant non-Th2 asthma burdens brag huge attention due to poor prognosis and even fatalities. Of note, the mechanistic pathways involved in non-canonical (neutrophilic) asthma progressions yet been clearly elucidated. To characterize the exacerated asthmatic response and mechasistic pathways involving severe refractive asthma (SRA), we hypothesize that CC chemokine receptor-5(CCR5)is a crticalimmunoregulatory molecule of hRV induced aggravated asthma.

Methods: Usingin-vivo infectious mice model (BL/6 & CCR5 knock out mice) of excaerbated asthma, we have characterized the logical debates regarding innate and adaptive immune responses, and mechaistic pathway contributing in hRV induced non-Th2 (neutrophilic) asthma.

Results and conclusions: Here we corroborated that CCR5 is a critical player to attenuate neutrophilic asthmatic response through conserving equilibrium of $CD4^+FoxP3^+$Tregs and IL-$17A^+CD4^+$ Th17 cells in OVA challenged RV-1B induced exacerbated asthma. CCR5 KO mice showed a rapidly increased frequency and absolute number of IL-17A-producing $CD4^+$ Th17 cells in airways &lung tissues after challenge with OVA and hRV, whereas $CD4^+FoxP3^+$Treg cells were observed with decreased infiltration, compared to BL/6 mice. Likewise, we also found that CCR5(-/-) mice manifested with influx of $CD45^+CD11b^+$Siglec-F^+Gr-1^+ neutrophils, reduced $CD3^+CD4^+/CD8^+$ T cells, and induction of IL-17A, IFN-γ, IL-6, IL-1β cytokines in asthmatic airways. We also documented that CCR5 ablation resulted with increased induction of Muc5a, Muc5b, Gob5, and disruption of cytoskeleton integrities (ZO-1, claudin-4, claudin-5) in asthmatic lungs. Taken together, our findings indicate that CCR5 attenuatesneutrophilic asthmatic response through maintaining TJPs integrities along with an equilibrium of $CD4^+FoxP3^+$Tregs and IL-17Aproducing$CD4^+$ Th17 cells. in allergen challenged hRV induced exacerbated airways. Best of knowledge, we, ever first reported that CCR5 is a critical molecule to combat Th17 asthma response. So CCR5 can be a potential immunotherapeutic candidate against pediatric asthma.

Keywords: Asthma exacerbation, pediatric asthma, neutrophilia, Th17 response

ID 19-124: **Rabies the deadly disease; How much we aware?**

Ariful Basher[1]

[1]*Mymensingh Medical College Hospital.*

E-mail of the corresponding author: ariful bashir_vet@yahoo.com

Introduction: Human rabies is a hundred percent fatal but hundred percent preventable neglected tropical disease of the developing countries and is well controlled or eliminated in most of the developed countries. Rabies and animal bite cases are being routinely reported from the National & District Rabies Prevention and control centers in Bangladesh. The aim of the study is to observe the present situation and management of animal bite cases specially rabies patient

Methods: Here we describe 6 cases of rabies patient rushed to one infectious diseases hospital during the period Jun 2014 to December 2015.

Results: During this period total 2,648 patients were given post exposure vaccination (ID-ARV). Most were (80%) due to dog bite, 10% cat bite, 5% fox bite and 5% others like bobcats, mongooses , monkey etc including rabid human bite. Age range from 1 $^{1}/_{2}$ years to 85 years. Of the total bitten patients; 30% were WHO-Category III bite and 15% of them got Rabies Immunoglobulin (RIG) along with vaccine. Total 6 Patients developed Rabies. Five developed Rabies during the course of active immunization; two even after inoculation of RIG. One 85 year old man admitted to the Hospital with history of multiple deep seated bites on both thigh and leg. Patient was given ARV, tetanus and antibiotic prophylaxis. RIG was given on next day due to unavailability of the drug. On 5th day he felt discomfort, salivation followed by respiratory difficulties and died. Another baby 18 month admitted with lacerated wound around the face due to dog bite died on third day inspite of giving ARV and RIG. Three patients with WHO-Cat-III developed rabies after 3rd doses of ARV. One girl 7 year old looked frighten, excessive salivation, aggressive and hydrophobic. She had history of dog bite 18 month back with no history of ARV. The patient died on next day.

Conclusion: Here all patients died in their house. We have no facilities to keep them into hospital. So, complete evaluations and reporting of the patients were not possible. It is essential to develop a setup and standard operative procedure for human rabies management.

Key words: animal, bite, RIG, ARV

ID 19-45: **Addressing governance challenges of preparedness and response to infectious threats and antimicrobial resistance through a sustainable, coordinated international network: SoNAR-Global**

Nahitun Naher[1]**,** Syed Masud Ahmed[1], Sabina Faiz Rashid[1], SoNARGlobal Consortium[2]

[1]BRAC University [2]SoNAR Global Consortium.
E-mail of the corresponding author: nahitun.naher@bracu.ac.bd

Introduction: Experiences from Ebola epidemic and similar events have shown that governance is a key challenge in effective preparedness and response to emerging infectious diseases (EIDs) and antimicrobial resistance (AMR). There has been a long history of misunderstanding of local culture and practice while managing epidemics. National governments and global health organizations therefore have historically undertaken the global health governance of infectious threats, targeting their actions toward public health and clinical research. However, the complex social, political, economic and ecological realities show that interconnections through a One Health (OH) approach and linkages with local communities are essential.

Methods: The idea of establishing such a network to contribute to the 'prevent-detect-respond' activities for epidemic preparedness and the control of AMR motivated the researchers to establish SoNAR-Global, a Global Social Sciences Network for Infectious Threats and Antimicrobial Resistance. This network is led by social scientistsof eleven renowned institutions from nine countries (France, Netherlands, Austria, Ukraine, United Kingdom, Uganda, Senegal, Thailand and Bangladesh), and is supported by the European Commission. Central to the project is a platform for collaboration among social scientists, public health institutions and existing networks engaged in preparedness and response to epidemics and AMR throughout the world.

Results: SoNAR Global underscores three major challenges that global health governance of preparedness and response to EIDs and AMR must address: scalability, inter-sectoral and inclusivity challenges. To address these challenges, the consortium is building a sustainable international social science network to engage the active participation and promote complementarily and synergy in the governance of prevention and response to EID and AMR. It is leading activities through a program that builds governance from the ground up by vulnerability assessment and community engagement pilots. It is conducting operational research on lessons learned from governance of networks in response to infectious threats. It is adapting and testing One Health tools among populations at risk with EIDs and AMR-related threatsto promote engagement build capacity and ensure accountability.

Conclusion: SoNAR-Global, a resilient, impact-directed network can ameliorate effective governance to EIDs and AMR by applying decentralized approach with a solid grasp on complexities and local ways of confrontation.

Key words: Governance, Infectious Diseases, One Health

ID 19-66: **Epilepsy like illness in pig rearing villages in Bangladesh, 2016**

Shamim Sarkar, Stephen P. Luby

[1]icddr,b, Bangladesh [2]Stanford University, USA.

E-mail of the corresponding author: shamim.sarkar@icddrb.org

Introduction: Pig parasites, *Taenia soilium* casue human cysticercosis, which is a major cause of epilepsy in endemic countries. Cllective studies identified consumtion of infected pork with undercooked, use of human faces for feeding pigs, oepn defecation, and poor sanitation act as importnant risk factors for human cycticerisis.The aforementioned risk practices were prevailing in the pig rearing communities in the swine surveillance settings in Rajshahi. Our study objective was to investigate the occurrence of epilepsy like illness among humans of pig rearing villages.

Methods: In 2016, May, we conducted a cross sectional household survey by leveraging the swine surveillance settings in Rajshahi. We conducted face to face interview in each enrolled household using screening question among pig rearing households and asked the household members if anybody in their household members had epilepsy like illness. We used 'epilepsy like illness' case as any member of pig rearing household was reporting of any episode of seizure, at least one event, in the past one year (12 months). We calculated proportion by dividing the number of individual with history of epilepsy like illness in the past 12 months by the total number of individuals those were asked about occurrence of epilepsy like illness during the past 12 months. We calculated 95% confidence intervals (95% CI) for proportion.

Results: In the surveyed pig rearing communities, we found 1088 individuals among 240 households in two subdistricts (Tanore and Godagari). The median number of household member was 5 (range: 1-9) per household. About half of the residents were male (49%) and remaining were female. We identified eight cases of epilepsy like illness. The percentage of epilepsy like cases was 0.73% (95% CI: 0.31-1.4). The median age of epilepsy like case was 35 (IQR: 19-45). Two third of cases were male (75%, 6/8). All cases were reported they eat pork frequently and close contact with pigs in their households.

Conclusion: The study provides an evidence of occurrence of epilepsy like illness among humans in the pig rearing communities which warrant further studies to investigate the etiology and risk factors for occurrence of epilepsy like illness cases.

Key words: cysticercosis, surveillance, Rajshahi

ID 19-70: **Vermicompost production and marketing system from different organic materials using of the earthworm to ensuresoil health**

Sahjahan Ali and Md.Abul Kashem

Sylhet Agricultural University

E-mail of the corresponding author: sahjahanali37@gmail.com

Earthworms are largest animal biomass in most temperate ecosystems, where they strongly influence the physical, chemical, and biological properties of soil and ensure environmental health. The main objective of this article is to observe the production of vermicompost produced and marketing from different organic materials.The experiment was carried on the vermicompost production shed at Department of Soil Science, Sylhet Agricultural University, Sylhet during the August 2018 to January 2019. *Eudriluseugeniae*earthworms species used inthis experiment. The experiment was conducted four treatments *viz* T_1= Cowdung (100%), T_2= Cowdung + Poultry litter (60:40), T_3= Cowdung + Water hyacinth (60:40) and T_4= Cowdung + Poultry litter + Water hyacinth (40:30:30). The experiment was laid out in a complete randomized design (CRD) with three replications. The uniform quantity 10 kg per *chari* of partial decompose organic materials were used as per treatments. The fixed quantity (100 g) of earthworm was used in each *chari*on 24 September 2018. Data were taken on earthworm growth and vermicompost production with different physicochemical parameters like temperature, moisture and pH. Vermicompost were harvested on 26 November T_1 and T_3 and, 7 December T_2 andT_4.The temperature during the process of vermicomposting was declined and moisture per cent of 70 to 90 at harvest from initial. The pH in compost media was near neutral at harvest period. Vermiculture production was highest weight found in Cowdung than other treatments but in case of different treatment combinations,vermicompost production was higher in Cowdung + Poultry litter than cowdung alone which was used as substratum. The average cost of vermicompost production was \$ 649.10 t^{-1}. The material costs were high than other costs. Total cost of vermicompost production and sale was \$672.15 t^{-1}. The net return of vermicompost was \$423.70 t^{-1}. Benefit cost ratio was found in 1.63. The producer-seller sold the produce to users of different level consumers. One marketing channels were found in the study area for vermicompost marketing and highest vermicompost was used by farmers.Bangladesh is over populate agro-based country, need more production for every day diet and for that reason farmer always uses chemical fertilizers, pesticides, insecticides etc. Consequentially, chemically challenged food intake cause a significant public health concern. As vermicompost is a completely organic eco-friendly product and easier to process and use in agriculture that could be reduced chemical use and ameliorate environmental health.

Key words: earthworms, Sylhet, CRD

ID 19-24: **Wild animal's tuberculosis (TB);a hidden source of spreading zoonotic TB**

S. M. Shariful Hoque Belal[1], Tahmina Ruba[2], Sajeda Sultana[2], Mahmuda Islam[2], Md. GolamAzam Chowdhury[1], Mohammad Nizam Uddin Chowdhury[3], Nazmul Hoda[1], UmmeKulsum Rima[4], Abu Saleh Mahfuzul Bari[2], Mohammad Abu Hadi Noor Ali Khan[2]*.

[1]Department of Livestock Services, Bangladesh [2]Bangladesh Agricultural University [3]Bangladesh Forest Department [4]Hajee Mohammad Danesh Science and Technology University

**Corresponding author's E-mail: hadi.khan@bau.edu.bd*

Introduction: Bangladesh is one of the top ten tuberculosis (TB) burden countries in the world. Bangladesh has been trying to reduce TB burden through National Tuberculosis Control Program (NTP) with difficulties; this may be due to unidentified corner of TB in wildlife. This study was designed to detect specific cause of tuberculosis in wild animals by using impression smear staining, histopathology and PCR.

Methods: Wild animals died of chronic illness during the last 18months wereinvestigated. Twelve animals of nine different species investigated werespotted deer, gayal, giraffe, bhutanese cow, white lion, impala, wildebeest, kangaroo andrabbit.The dead animals were examined in situ, necropsy and gross pathological examinationwerecarried out. Impression smears onto the slides from the visceral organs were stained with Ziehl Neelsen stain. Portion of the visceral organs were used in genomic DNA extractionfor themultiplex and uniplex PCR detection of specific species of TB.The uniplex PCR targeting Rv3479HP gene of *Mycobacterium tuberculosis* (667bp) and MPB83 gene (600bp) of *Mycobacterium bovis*were also carried out. Portion of organswas preserved in 10% neutral buffered formalin, processed, sectioned and stained withH&E and Ziehl Neelsen staining.

Results: Lungs was the predominant site for tuberculous infection.Creamy to yellowish caseous cut surface andgranulomas in lungs consisting of peripheral cuff of lymphocytes, epitheloid cells, Langhan's type multinucleated giant cells with calcification were seen.Pink color bacilli under microscope were detected in six animal's tissues. PCR confirmed*Mycobacterial* infectivity (1030bp) and infectivity due to *Mycobacterium tuberculosis* complex (372bp) in seven cases. Uniplex PCR showed three animals (two spotted deer and a gayal) were infected with *M. tuberculosis* and four animals (Bhutanese cow, giraffe, white lion and impala)with *M. bovis*.

Conclusion: *M. tuberculosis*and *M. bovis* are extremely zoonotic pathogen and found to infect captive wildlife. Both the organisms can be transmitted inwildlife,caretakers, visitors, veterinarians etc. and this silent corner of TB may affectthe country's NTP and TB-related deathsto human. It requires massivesurveillance of zoo animals to detect TB at regular intervals and enabling country policy maker to curtail its burden.

Keywords: Tuberculosis, PCR, Wildlife, Zoonosis, Histopathology

ID 19-04: **Changes in the Reproductive System of the Male Mice Immunized With a Plasmid DNA Vaccine Encoding GNRH-1 And T Helper Epitopes**

Israt Jerin

LRI, Dhaka-1212

E-mail of the corresponding author: isratjerin@gmail.com

Neutralization of Gonadotrophin releasing hormone is necessary to control mammalian reproduction also prevention of prostate cancer in human.If reproductive capacity and sexual behavior need to be prevented, a contraceptive vaccine that neutralizes GnRH-1 would be preferred. Active immunization against GnRH-1using peptide based vaccine has gained wide spread acceptance and reached to field use. The GnRH-1molecule requires conjugating with a carrier protein along with an adjuvant to act as an antigen. As an alterative to peptide conjugates DNA vaccine can be used. The DNA vaccine that was used in this study containing eight repeated units of GnRH-1 peptides interspersed in eight Th-2 epitopes in a fusion protein. The vaccine was administered into male mice in conjuction with Phosphate buffer saline(Group-1), non ionized surfactant vesicle(Group-2) and bilesom (Group-3) solution. The highest suppression of the epididymalsperm count was seen in Group2(0.907±0.1554,p=0.0043)followed by Group-3 (1.790±0.3751,p=0.0009) and Group-1 (2.647±1.3972,p=0.0024),respectively. Testicular weight of the vaccinated mice showed highest suppression in Group2 (0.105±0.0043,p=0.003) followed by Group-3 (0.106±0.0049,p=0.0123) and Group-1(0.111±0.0089,p=0.0042). Result of the testicular score count revealed a highest suppression of testicular spermatogenesis (score 7-10) in Group-2 mice testes followed by Group-3 and Group-1 mice. An average, testicular score 10 were 4.00 ±1.73,5.00±3.00,13.67 ±4.16 and 14.00 ±1.73 for Group-2,3,1 and 4 control mice respectively. Epididymal weight of the treated mice showed highest suppression in group-2 (0.021 ±0.0011,p=0.0034). Prostate and seminal vesicles of the all vaccinated mice showed reduced diameter of the glandular alveoli and decreased stored secretions and highest suppression were seen in Group-2 followed by Group-3 and Group-1. Evaluation of GnRH-1 mRNA expression in testicular tissues using GnRH-1 specific primers by RT-PCR successfully detected GnRH-1 mRNA expression in vaccinated mice. This is an indication of the reversibility of the sexual function following vaccination.Success with the research would enable us to design future vaccine against HIV, PPR in Goat, Anthrax and TB in man and animal.

Keywords: DNA vaccine, plasmid, GNRH-1, Contraceptive vaccine, T-helper epitopes, Sexual function

ID 19-95: **Study of Prevalence and Associated Risk Factors of Anaplasmosis and Theileriasis in Cattle**

Md. Faruk Islam, Sandip Kispotta and Md. Shajedur Rahman

Hajee Mohammad Danesh Science & Technology University

E-mail of the corresponding author: faruk_vet@yahoo.com

Introduction: Haemoprotozoan diseases are one of the major impediments in health and productive performance of cattle in all over the world including Bangladesh. The diseases cause a serious economic impact through substantial losses resulting from death and lowered production and working efficiency of the animals. Therefore, a detailed cross-sectional study was carried out to investigate the prevalence and associated risk factors of Theileriosis and Anaplasmosis in cattle of Dinajpur District over a period of six months from January to June 2014.

Methods: A total of 200 samples were randomly collected from the cattle. A pretested questionnaire was implemented to collect data on different risk factors. Blood smears were prepared and examined under microscope (100x) with Giemsa's stain.

Results: The study revealed proportional prevalence was 10% for Theileriasis and 18.5% for Anaplasmosis. The percentages of Theileriasis and Anaplasmosis affected male and female were 6%, 12%; 14% and 25%, respectively. In both cases, female showed higher positivity in compare with male. The univariate logistic regression analysis revealed cattle with a herd size >10 (OR=4.3), temperature (≥ 103) (OR=3.27), presence of tick in the body surface (OR=3.09) and record of Ivermectin treatment (OR=4.47) were found significantly associated with Theileriasis prevalence ($p<0.05$) and irregular bathing history was found significantly associated in the case of anaplasmosis prevalence (OR=0.23). However, in multivariate analysis, temperature (≥ 103) (OR=2.89), presence of tick in the body surface (OR=2.80) and animal with a record of Ivermectin treatment (OR=4.24) showed significant association with Theileriasis and herd size >10, deep brown; white colour and bathing history were significantly associated ($P < 0.05$) with the Anaplasmosis.

Conclusion: Good husbandry practice and adoption of hygienic measures are needed among the high risk group or individuals to minimize the spread of the disease.

Keywords: Theileriasis, Anaplasmosis, Ivermectin, Prevalence

ID 19-23: **Survey of Coxiellosis related to reproductive disorders in small ruminants**

Md. Hemayatul Islam[1], Md. Jalal Uddin Sarder[1], Md. Siddiqur Rahman[2], Md. Shofinur Rahman[3] and Md. Shofiqul Islam[4]

[1]University of Rajshahi [2]Bangladesh Agricultural University, [3]Youth Training Centre, Naogaon, [4]Plannet Animal Health

Corresponding author's email: hislam.islam@gmail.com

Introduction: Q (Query or Queensland) fever is a vector borne zoonotic infection affecting a variety of animals. The present study was to evaluate the survey of Coxiellosis related to reproductive disorders in small ruminants at Northern Barind Tract (NBT) in Bangladesh.

Methods: A total 475 blood samples were collected from those animals that were positive *Brucella, common Brucella and Toxoplasma* positive and randomly selected (location wise) total 91 serum samples were send to National Reference Laboratory (NRL) in Germany to identify *Coxiella* in small ruminants from January, 2012 to June, 2015. Serological test was performed by iELISA on goat and sheep database created with Microsoft Office software Excel 2007 (Microsoft®, Redmond) and SPSS program with descriptive methods of regression and chi square test was done for statistical test.

Results: An overall seroprevalence of *Brucella, Toxoplasma* and *Coxiella* were found 12%, 56% and 11% respectively. Goats was significantly (P<0.01) lower seroprevalence than sheep, respectively 5.6% and 30.0%. Small ruminants had significantly (P<0.05) higher chance of *Coxiella* in animals reared at smaller size flock (13.1%) and city adjacent to border (Rajshahi, Naogaon & Chapai Nawabjong) than their corresponding groups. The seropositivity was higher in Local breed (7.7%), female animals (7.7%), older age (6.6%), medium & heavy body weight (5.5%), traditional biosecurity (6.6%) and rainy season (7.7%) than others groups and had insignificant effect (P>0.01). The parity and pregnancy status of SR were negative correlation but significant effect (P<0.01) with Q fever infection in experimental area. The animals from the stall feeding (4.4%) had negative but insignificant (P>0.01) association and lower seroprevalence than animals from the grazing on field (6.6%).

Conclusion: It is the first report of *Q* fever presences in goat and sheep in Bangladesh. Q fever threat was higher in female, goat and >3rd parity and rainy season than their respective other groups.

Key Words: Coxiellosis, reproductive disorders, zoonotic disease, small ruminants and Northern Barind tract

ID 19-71: **Pilot Experiments to Estimate Respirable Aerosols Produced During Poultry Slaughteringand Defeathering**

Nadia Ali Rimi[1], William G. Lindsley[2], Andrew Clark[3], David E. Swayne[4],James C. Kile[6], Md. Habibullah Fahad[1], Kamal Hossain[1], Rebeca Sultana[1], Ireen Sultana Shanta[1], Zakiul Hassan[1],Md. Giasuddin[5], Erin D. Kennedy[6]

[1]icddr,b, Bangladesh [2] National Institute for Occupational Safety and Health (NIOSH), USA [3]University of Georgia, USA [4]U.S. Department of Agriculture, Georgia, USA [5]Bangladesh Livestock Research Institute [6]Centers for Disease Control and Prevention (CDC), USA.

E-mail of the corresponding author: nadiarimi@icddrb.org

Introduction: Influenza viruses can be aerosolized during slaughter of infected chickens, which can increase the risk of zoonotic transmission. We developed interventions designed to decrease production of aerosols during these processes and conducted an experiment to monitor aerosol generation during slaughtering and defeathering to inform a protocol designed to evaluate these interventions.

Methods: Inside a booth within a temperature-controlled room, we slaughtered 10 chickens by severing the cervical blood vessels and placing them in an open barrel to exsanguinate,anddefeathered 10chickens using a defeathering machine.Six PATS+ and one Sidepakaerosol monitorswere used to measure concentrationsof airborne particles <2.5 µm at baseline and during slaughtering and defeathering; we subtracted baseline measurements from experimental measurements to calculate average particle concentrations.The instruments were placed 148 cm above the floorduring slaughtering and defeathering, corresponding to a worker's breathing level; 56 cmduring slaughter, corresponding to the height of the mouth of the barrel; and 107 cm, during defeatheringcorresponding to the mouth of the machine.

Results: During slaughter, the average particle concentrations at 148 cm were 75.8 µg/m^3 (SD 55.5) by the PATS+ instruments and 23.4 µg/m^3 (SD 10.3)by the Sidepak. At 56 cm, the average concentrations were 23.8 µg/m^3 (SD 20.7; PATS+) and 10.2 µg/m^3 (SD 9.3; Sidepak). During defeathering, the average concentrations at 148 cm were 19.9 µg/m^3(SD 8.2; PATS+) and 9 µg/m^3(SD 2.6; Sidepak). At 107 cm, the average concentrations were 16.1 µg/m^3(SD 4.7; PATS+) and 9 µg/m^3(SD 2.9; Sidepak).

Conclusion: The experimental design allowed us to measure increases in aerosol concentrations during laughtering and defeathering. This protocol can be used to test airborne particle generation during different slaughtering and defeathering techniques in order to identify procedures that can minimize workers' exposure to potentially hazardous aerosol particles.

Keywords: Avian influenza, aerosolization, air particle, slaughtering, defeathering

ID 19-133: **Live Poultry Exposure at the Human-Poultry Interface in Urban Bangladesh: Preliminary Results from a Cross-Sectional Cell-phone Based Survey**

Isha Berry[1],Punam Mangtani[2], Mahbubur Rahman[3], Amy Greer[4], Shaun K Morris[1,5], IqbalAnsary Khan[3], Sudipta Sarkar[3], Tanzila Naureen[3], Monalisa[3], David Fisman[1+], Meerjady Sabrina Flora[3+]

[1]Dalla Lana School of Public Health, Canada. [2]London School of Hygiene and Tropical Medicine.[3]Institute of Epidemiology, Disease Control and Research, Dhaka, Bangladesh.[4]University of Guelph, Canada. [5]The Hospital for Sick Children, Toronto, Canada.[+]These individuals have contributed equally

Introduction: Exposure to live poultry is an important risk factor for zoonotic transmission of avian influenza. Specific high-risk practicesinclude slaughtering/de-feathering poultry and visiting live bird markets (LBMs).Avian influenza is endemic in Bangladesh, wheregreater than 90% of poultry and poultry products are marketed through LBMs, with the majority of these sold in an unprocessed form. However, patterns of poultry exposure in the general urban population have not been systematically evaluated in this setting. Theseare of particular importancegiven that they can inform prevention measures at key human-animal interfaces.

Methods: Between September and November 2019, we are conductinga cross-sectional study nested withina cell-phone based disease surveillance platformto measurelive poultry exposure in Dhaka City Corporation (DCC). We utilize random-digit-dialing to recruitparticipants from the general urban population aged ≥18 years, stratified by sex and phone-company. Information regarding demographics, poultry purchasing, contact and prevention behaviours are collected using a structured questionnaire. Poultry exposure is defined as visiting an LBM or participation in slaughtering, de-feathering, eviscerating or cutting live poultry in the past year. The estimated population prevalence of poultry exposure is presented and descriptive statistics are used to summarize patterns separately for males and females.

Results: As of 17 October 2019, of the 1268 eligible individuals who received calls 783 (61.8%) were successfully enrolled in our survey. The overall population prevalence of poultry exposure was 74.8% (95%CI: 71.8-77.9), with 46.0% (95%CI: 42.5-49.5) reporting visiting LBMs in the past year. Amongst market goers, the majority report 1-2 visits/week (56.9%) or 1-3 visits/month (28.1%). Visiting LBMs was more common amongst males (64.2%, 95%CI: 59.2-69.1) than in females (35.8%, 95%CI: 30.9-40.8). However, exposure through food preparation was greatest in females, with 79.5% (95%CI: 73.7-82.0) reporting cutting poultry purchased from LBMs within the past year.

Conclusion: Poultry exposure is high in the general urban population of Dhaka, Bangladesh. This suggests a substantial risk of exposure to avian influenza viruses. Sources of exposure appear to differ by sex, suggesting that customized preventions strategies may be more effective. The proposed study is timely, and can support the creation of innovative evidence-based recommendations to reduce avian influenza exposure at the human-poultry interface in Bangladesh.

Key words: LBM, humain-poultry interface, DCC

ID: 19-33: **First Isolation, identification and genetic characterization of *Brucellaabortus*biovar 3 in dairy cattle from some selected areas of Bangladesh**

Md. Sadequl Islam, Mst. Minara Khatun, Sukumar Saha, **Md. Ariful Islam***

Bangladesh Agricultural University

**Corresponding and presenting author's E-mail: islamma@bau.edu.bd*

Introduction: Brucellosis is a worldwide zoonotic infection of economic and public health importance. Brucellosis in cattle is caused by *B. abortus* which results in abortion, infertility, still birth and reduced milk production. It is endemic in humans and domesticated animals in Bangladesh. This study was conducted for isolation, identification and genetic characterization of *Brucella* spp. in dairy cattle.

Methods: Twenty two dairy farms housed 1285 dairy cattle located at Mymensingh, Savar, Gazipur, Jamalpur and Dinajpurwere selected.Sera (n=496), uterine discharge (n=45), milk (n=115), vaginal swab (n=71), placenta (n=7) and aborted fetus (n=2) were collected from dairy cattle with the history of abortion, retained placenta, infertility and still birth. Sera of cattle were tested by the Rose Bengal plate test (RBPT). Samples were streaked duplicate onto *Brucella* selective agar and inocubated at 37°C for 7-14 days in an incubator supplied with 5% CO_2 for isolation of *Brucella* spp. Identification of *Brucella*was performed by routine bacteriological and classical biotyping (CO_2 requirement for growth, H_2S production and growth in presence of thionine and basic fuchsin) methods, Molecular confirmation of *Brucella*was done by PCR assays. Genetic characterization of *Brucella* spp. was performed by multi-locus variable- number tandem-repeat assay-16 (MLVA-16).

Results: Thirty nine sera (7.86%) were tested positive by RBPT. Ten *Brucella* isolates were recovered from uterine discharge (n=7), milk (n=2) and vaginal swabs (n=1), which were confirmed as *B. abortus* by enhanced AMOS-ERY PCR assay. The classical biotyping method confirmed all 10 *B. abortus* isolates belonged to the biovar 3. The MLVA-16 assay indicates that all *B. abortus* isolates were identical and shared the same genotype 40, based on panel 1 MLVA-8. Dendrogram and minimum spanning tree (MST) analysis when compared with 1633 global isolates of *B. abortus* revealed that *B. abortus* isolates of this study were genetically similar with three isolates of Brazil and one isolate of France. The MST analysis also revealed that 10 Bangladeshi *B. abortus* isolates belonged to clade C1 and sub-group 3b of biovar 3.

Conclusion: Data of the present work may be useful to formulate policy and strategies for the control of bovine brucellosis in Bangladesh.

Keywords: B. abortusbiovar 3, dairy cattle, Bangladesh, MLVA 16 assay, genetic characterization

ID 19-56: **Ebola virus disease (EVD)- A retrospective study amongst 149 confirmed cases at Ebola Treatment Unit (ETU), Bong County, Liberia**

Lt Col (Dr) Nazmul Huda Khan. Cumilla Cantonment

E-mail of the corresponding author: nazmul29@yahoo.com

Introduction*:* Ebola is a great concern of global health because of its high fatality rate. Ebola virus can spread between humans by contact with blood, body fluids and excretions and tissues. During the acute stage of the disease, filoviruses are also found in many secretions and excretions that are not visibly contaminated with blood, including saliva, tears, breast milk, semen and feces.

In human populations, the African filoviruses usually have high mortality rates. Zaire Ebola virus is the most pathogenic virus. The case fatality rate for this infection was 59% to 88% in all outbreaks to 2008. Sudan Ebola virus is less virulent, with a case fatality rate of 41-65%. We have been deployed in Liberia as UN peacekeepers during deadly outbreak of EVD in Liberia in the year 2014-15. At present Ebola is prevalent in Congo DR where a large number of Bangladeshi Peacekeepers are deployed there. It can bring epic threat to our country at any time. In this situation, the objectives of the study were to find out the mode of spread and mortality rates and ratio amongst different sex and age group of confirmed Ebola cases.

Methods: This was a descriptive retrospective study carried out to explore the mode of spread and mortality rates and ratio amongst different sex and age group of confirmed Ebola cases. The study population (149) were all confirmed Ebola cases who received treatment from Bong County Ebola treatment unit, Liberia during the period of July to December 2015. Data was collected by reviewing the information sheets of patients received from the Bong county health authority, Liberia.

Results*:* The study revealed that about one fourth 38 (26%) of the EVD cases were from the age group between 31-40 years, followed by 27 (18%), 26 (17%) and 21 (14%) from age group between 21-30, 41-50 and 51-60 years respectively. In this study population 77 (52%) were female and 72(48%) were male. Among all cases, 92(56%) survived after treatment while 57(44%) expired. Regarding the mode of spread, direct contact was the main mode of infection 74 (49.66%), followed by patient transport 24 (16%), contact with body fluid 19(13%), participants at funeral 12(8%) amongst others.

Conclusion: The deadly EVD has high incidence of fatality and places a substantial burden on the health care delivery system and leads to the great concern and public health issue globally. Careful study and analysis in this regard definitely will explore new dimension to combat this devastating health burden of the African countries, the world as a whole and Bangladesh if threats prevail.

Key words: Ebola virus disease (EVD), Ebola treatment unit (ETU), Suspected, Probable and Confirmed EVD cases

ID 19-09: **One Health perceptions of Q fever among the animal science and veterinary students, South Australia**

Md Rezanur Rahaman[1], Adriana Milazzo [1], Helen Marshall [2], Anne-LiseChaber[3], Peng Bi [1]

[1, 2, 3] *University of Adelaide, Australia*

E-mail of the corresponding author: rezammc@yahoo.com

Introduction: Animal science and veterinary studies may place students at risk of Q fever, transmissible from animals to humans, particularly when unvaccinated. A One Health approach that combines animal, human and the environmental health sectors is a suitable framework to prevent Q fever. This online survey aimed to gauge the animal science and veterinary students' perceptions about Q fever and its prevention strategies.

Methods: All animal science and veterinary students enrolled at the University of Adelaide in 2019 were invited to participate in an online survey using SurveyMonkey. Students were provided with the survey link. Descriptive analysis was performed.

Results: Of the 694 invited students, 317 completed the survey with a response rate of 45.7%. Forty-three percent of the students had no/negligible knowledge about Q fever. The majority (68%) were unsure about disease transmission through consumption of unpasteurized dairy products, laundering of clothes of an animal worker and sexual transmission. Most (91%) students reported at least some contact with dogs, sheep, horses and beef cattle during their studies. Seventy-one percent of the students rarely/never used a facemask during their contact with animals, despite 90% believing it is effective in preventing airborne transmission. Twenty percent of the students reported they were unvaccinated against Q fever. Identified challenges for vaccination included cost (84%), time (73%), and poor healthcare access (61%). Most (91%) students suggested that use of a social media, subsidized vaccination, improving healthcare access, and improving workers' and veterinary practitioners' knowledge are likely to be effective in improving vaccination uptake.

Conclusion: Knowledge on One Health approach, and Q fever among the surveyed students, particularly about disease transmission is less-than-optimal. Students' adherence to biosecurity guidelines, particularly those related to airborne transmission prevention e.g. using a facemask could potentially reduce Q fever transmission. Unvaccinated students need urgent vaccination for adequate protection.

Keywords: One Health, animal science and veterinary, Q fever, prevention, South Australia

ID 19-111: **Protective and immuno-efficacy of F-34 Stern strain Anthrax vaccine in mice model**

Provat Chandra Saha[1], GolamAzam Chowdhury[1], UmmeKulsum Rima[2],Priya Mohan Das[3], Mohammad Abu Hadi Noor Ali Khan[3]

[1]Department of Livestock Services [2]Hajee Mohammad Danesh Science and Technology University [3]Bangladesh Agricultural University (BAU)

E-mail of the corresponding author: hadi.khan@bau.edu.bd

Introduction: Anthrax is a fatal zoonotic disease that strike almost all warm-blooded animals. It is caused by a gram-positive bacterium, *Bacillus anthracis*. The disease is common in farm ruminants, causes regular mortality and can be prevented by using vaccine. The Sterne strain F-34vaccine has been using in ruminants for more than five decades in Bangladesh but little work is done in terms of protective efficacy. This study was aimed to evaluate protective efficacy of F-34 Sterne strain Anthrax vaccine in mice model in terms of protective efficacy and IgG antibody response.

Methods: Anthrax vaccine vials containing F-34 Stern strain was obtained from CDIL, Dhaka and used inimmunization trial. A virulent field isolate was isolated on PLETE agar medium and used in challenge trails. Group C (n=05) and D (n=05) female mice were immunized intramuscularly with 0.1ml of Anthrax vaccine and Group A and B mice left immunized. Following 06 months of immunization the Group B (n=05) and Group D (n=05) mice were challenged intra-peritoneally with $2x10^4$ colony forming unit (CFU) of virulent field isolate of *B. anthracis*. Polymerase chain reaction (PCR) was carried out to detect pX02 gene (1035bp) specific Cap protein gene of*B. anthracis* from the challenges mice.

Results: The Sterne vaccine strain induces higher anti anthrax IgGantibody in vaccinated mice (OD value >0.975±0.219). Slide agglutination test carried out using the vaccine sera even after six months of immunization found to agglutinate vaccine and field bacteria. In vivo infection to vaccinated mice with virulent field isolate found to confer solid protection. Non-immunized mice received challenge infection appeared dead within 18-24 hours of infection. Control mice experimentally infected with Anthrax showed wide spread haemorrhages and black berry jam spleencharacteristics of Anthrax and PCR confirmed *B. anthracis* bacteria from the infected mice.

Conclusion: The Sterne strain F-34 Anthrax vaccinefound protective in mice model and generated fairly higher level of anti AnthraxIgGAbresponse up to 06 months of immunization. It needs to study whether the vaccine response persisted longer and higher in mice and farm animalsand areprotective in challenge infection.

Keywords: Anthrax, vaccine,F-34, efficacy, mice

ID 19-140: **An Outbreak Investigation of Anthrax Disease in Gangni, MeherpurDistrict 2019**

Provat Chandra Saha[1], Golam Azam Chowdhuary[2], Faisol Talukder[3], **Md. Murshidul Ahsan[3],** Md. Shakif-Ul-Azam[3], Md. Abu Sufian[3]

[1]Livestock Research Institute (LRI) [2]Central Disease Investigation Laboratory (CDIL) [3]Department of Livestock Services

E-mail of the corresponding author: murshidvet@gmail.com

Introduction: Anthrax, caused by *Bacillus anthracis* is a zoonotic disease and annually causes animal-human outbreaks in Bangladesh. It is considered one of the potential threat diseases to global health security. The objective of the study was to describe the outbreak situation and to minimize the risk factorsfor future outbreak in the endemic area.

Methods: Each of the outbreak sites was visited and participatory epidemiology tools were used to realize the knowledge and practices of local people/cattle keepers. Meat, blood, soil and grass samples were collected from the suspected case and sites.The samples were tested in Central Investigation Laboratory (CDIL) by Polychrome Methylene Blue (PMB) staining and RT-PCR.

Results: Based on the investigation during August-September, 2019 in Gangni, Meherpur the team find out three different outbreak spots where 20 animals (3 Cattle, 17 Goats) were affected (dead/slaughtered).There were 17 human anthrax cases were confirmed in cutaneous form due to involve in slaughtering, handling and processing of infected meat from anthrax affected sick animals. The average affected rate in animal was 65%, whereas, in human 15%. The CDIL confirmed *Bacillus anthracis* organisms in the meat samples by PMB staining and RT-PCR analysis. The infected slaughtered and dead animals found to be in non-vaccinated status and uncontrolled animal movement is considered to be responsible for new outbreaks in a vaccinated zone where execution of veterinary legislation was inadequate. It was found that the area was anthrax endemic area where people are not very conscious about anthrax outbreak. Lack of consciousness about anthrax vaccination timely, feeding grass from low lands and slaughtering practice of sick animal were the factors of the anthrax outbreak.

Conclusion: We recommended to give emphasis on active disease surveillance, motivate people for vaccination, generate awareness about anthrax disease and zoonoses and work together of DLS and Health sector in One Health approach.

Keywords: Anthrax outbreak, Knowledge, Meherpur, One health

ID 19-139: **A Baseline Survey on Anthrax Disease in Sirajganj and Meherpur District, Bangladesh**

Md. Murshidul Ahsan[1], Md.Shohidul Islam Khokon[1,2], Md. Shakif-Ul-Azam[1],Md. Abu Sufian[1]

[1]Department of Livestock Services [1,2]Institute of Epidemiology, Disease Control and Research (IEDCR)

E-mail of the corresponding author: murshidvet@gmail.com

Introduction: Several outbreaks of anthrax in animals and humans have been reported in Sirajganj and Meherpur district in last few years. This study was conducted to assess knowledge, attitudes and practices regarding anthrax to provide baseline information.

Methods: A cross sectional study was conducted among heads of farmer in seven upazila of Meherpur and Sirajgonj in July and August 2019. Semi-structured questionnaires were used to collect data from household members in the community. Questions were scored and descriptively analyzed using MS Excel spreadsheet.

Results: A total of 881 community members were recruited in this study. More than three quarters of the participants (74%) were self-employed doing crop and livestock farming. In this study the overall 69% community members considered that anthrax is the fatal disease for cattle and goat. Around 45% participants heard about anthrax from their neighbors and remaining from others. A total of 450 (75%) and 484 (77%) respondents had knowledge about the symptoms of human and animal anthrax. Majority of the community members (60.5%) knew that infected meat can transmit anthrax from animal to human. Of the interviewed respondents, 90% of them said that they buried the dead animal deeply in the soil while 8% of them thrown dead animal into the water. However, about 74% participant know that the vaccination is only the preventive method for the prevention of anthrax. Moreover, only 8% respondent said that they know about the outbreak of anthrax.

Conclusion: The survey data revealed that many people heard the name of anthrax or torka but many of them did not have any clear idea and practicing risky methods forfuture anthrax outbreak. This study suggested enhanced active surveillance and response program to control and prevent anthrax disease in Bangladesh.

Keywords: Anthrax, Knowledge, Meherpur, Sirajgonj and Practices

ID 19-18: ***Leptospira* epidemiology in dairy cattle of Bangladesh**

M.R. Faruque[1*]’A. Ahad[1], M.A. Parvez[1], M. Ahaduzzaman[1], M.I. Uddin[1], M.S. Pallab[1], A. Sayeed[3], M.F. Hossain[2] and M.A. Hoque[1]

[1]Chattogram Veterinary and Animal Sciences University [2] Department of Livestock Services [3]Jhinedah Government Veterinary College

E-mail of the corresponding author: rayhan@cvasu.ac.bd

Bovine Leptospirosis causes enormous economic loss due to reproduction failure and production loss. It has been perceived as a rising global public health concern. Bovine species acts as career or vectors, whereas human are the dead end host. No scientific attempt has previously been taken to investigate epidemiological diversity of *Leptospira* in commercial dairy cattle in Bangladesh. Hence, a cross – sectional study was conducted in commercial dairy cattle in Bangladesh to describe epidemiological scenario of *Leptospira*. Nineteen upazillas from 12 districts of 7 divisions were randomly chosen for the study. A total 43 dairy cattle farm, 1 – 6 farms per upazilla was recruited based on the presence of increasing abortion history within past six months. A pretested questionnaire was used to collect epidemiological information through face to face interview and direct observation. Blood and urine samples and aborted fetuses were collected for laboratory evaluation. Sero–positivity for *Leptospira hardjo* was evaluated on the samples obtained using OIE protocol based ELISA technique. Dark Field Microscopy examination was carried on urine samples. Aborted fetus was evaluated through bacteriological culturing followed by PCR. The PCR positive samples were further sequenced for phylogenetic analysis. The overall sero – prevalence of *Leptospira* was 17.9% (95% CI: 9.4% – 31.4%) in dairy cattle in Bangladesh. The proportionate *Leptospira* prevalence was 55.6 % in cattle (n=45 urine samples) and 32% in fetuses (n=25) and 32% in specimens obtained from fetuses (n=100) were estimated from urine and fetal sample, respectively. Breed (Exotic Vs Cross: OR= 3.4) and age (≤4.5 Vs ≥4.6: OR= 5.0) were identified as potential risk factors for *Leptospira* sero – prevalence in dairy cattle. One of the sequences of *Leptospira* isolatein the present study had a close congener (78%) of the sequence of *Leptospira* isolated from cattle in Brazil. Overall results suggest *Leptospira* is commonly circulating in dairy cattle in Bangladesh.Preventive measures including breed selection, vaccination status, quarantine of new animals, and exclusion of wildlife vectors, and farm superintendence should be practiced. Field veterinarians should also be properly educated in handling abortion cases and treating animals for prophylactic measures.

Keywords: Leptospirosis, sero-prevalence, dairy cattle, Bangladesh

ID 19-77: **Antibacterial efficacy of *Allium sativum* and *Zingiber officinale* against multi drug resistant (MDR) poultry pathogens**

Zakaria Al Noman, Md. Abdus Sobur[1], Tasnia Tabassum Anika, Md. Tanvir Rahman[1], Md. Mahmudul Hasan Sikder*

[1]*Bangladesh Agricultural University*

**Corresponding E-mail address: drmsikder@bau.edu.bd*

Introduction: Spices are used as traditional therapeutic agents against various pathological alterations since ancient times. Multidrug resistant pathogens are increasing at alarming rate worldwide which aims to find sustainable alternatives for effective treatment and health care.

Methods: Antibacterial sensitivity of garlic (*Allium sativum*) and ginger (*Zingiber officinale*) crude extracts were tested against multidrug resistant *E. coli* and *Salmonella* spp. isolated from poultry. Bioactive antibacterial compounds were identified by TLC Bioautography.

Results: Inhibitory activities of garlic were ZI = 14.03 ±0.15mm and 19.70± 0.36mm, MIC: 0.625 and 0.325 mg/mland for ginger was ZI = 14.63±0.30mm and 11.56±0.51mm, MIC: 9.0 mg/ml in both against *E. coli and Salmonella* spp. respectively. Two bands of garlic (R_f value = 0.31 and 0.50) and single of ginger (R_f value = 0.71) of TLC showed inhibitory potential in bioautography technique against both MDR isolates.

Conclusion: Garlic and ginger were found effective against multidrug resistant *E. coli* and *Salmonella* spp. and might be sustainable alternative at antibiotic void.

Keywords: Spices, MDR pathogen, Antibiotic sensitivity, MIC, TLC-Bioautography

ID 19-130: **Ecology of bat drinking behavior and antimicrobial resistant patterns of *Salmonella spp., Staphylococcus spp*. and *Escherichia coli recoveredfrom*fecal droppings of fruitbats and water in Bangladesh**

Md. Helal Uddin[1], Mohammed A Samad[2], Md Kaisar Rahman[3,4] Shariful Islam[3,4], Muhammad Sazzad Hossain[2], Md. Shahjalal Sagor[2], Melinda K. Rostal[4], Md Giasuddin[2], Meerjady Sabrina Flora[3], Jonathan H. Epstein[4.] , Sharmin Chawdhury[1]and Ariful Islam[*4]

[1]Chattogram Veterinary and Animal Sciences University [2]Bangladesh Livestock Research Institute (BLRI) [3]Institute of Epidemiology Disease Control and Research (IEDCR) [4]EcoHealth Alliance, USA

E-mail of the corresponding author: helal.cvasu43@gmail.com

Introduction: Bat species that often lives in close proximity to people and livestock may contribute to their exposure to antimicrobial-resistant(AMR) enteric pathogens. A cross-sectional study was conducted to determine the epidemiology of AMRpatterns in *Salmonella* spp., *Staphylococcus spp.* and *Escherichia coli* isolated from fruits bats, and observe their drinking behaviors to track the possible source of their infection with AMR bacteria.

Methods: We collected fresh feces samples (N=369) non-invasively from free-ranging fruit bats. We observed water bodies during day, and evening, and collected 21 water samples from different water bodies in Dhaka city between December 2016 and June 2017. To recover the isolates selective media; biochemical test was performed followed by PCR.The susceptibility of isolates to antibiotics was performed using the disc diffusion techniquefor 12 commonly used antimicrobials.

Results: We found bat visits to lagoons and other water bodies that are also utilized by humans, animals and birds. Of 369 bat samples, 7.3% (27/369;95%CI:5-11), 26.3% (97/369;95%CI:22-31) and 28.1% (104/369;95%CI:24-33) were positive for *Salmonella* spp., *Staphylococcus* spp. and *E. coli,* respectively; while 4% (n=7/21,95%CI:18-62) and 76.1% (16/21;95%CI:52.9-91.8) of water samples were positive for *Salmonella* spp and *E.coli*, respectively. *Salmonella* spp. were resistant to Tetracycline (93%), Sulphamethoxazoal-Trimethoprime (80%), Amoxicillin-Clavulanic acid (42%), Azithromycin (76%) & Chloramphenicol (62%). *Staphylococcus sp.* showed resistance to Ampicillin (55%), Methicillin, Oxacillin, Streptomycin and Tigecycline by 12%.*E. coli* showed resistance against Cefepime (16%) and Ampicillin (13%). Water samples showed resistance to Tetracycline (86%), Amoxicillin-Clavulanic acid (75%), Ceftriaxone (72%), Ciprofloxacin (71%) followed by Chloramphenicol (57%) & Sulphamethoxazoal-Trimethoprime (58%).

Conclusion: The study indicates presence of AMR *Salmonella* spp., *Staphylococcus spp.* and *E.coli* in bats; and *Salmonella* spp and *E.coli*from water bodies. It is unclear how bats were infected with AMR bacteria, however presence of AMR *Salmonella* spp. in might be water contaminated by people and/or livestock may be a source of AMR in bats. Screening people and livestock for similar resistant bacterial species will improve understanding of pathogen transmission among wildlife, livestock and human interface.

Keywords: Antibiotics Resistance, Bat, Prevalence, *Bangladesh*

ID 19-58: **Epididymal spermatozoa ex-vivo: A potential source for preservation of male gametes for wildlife conservation**

Ziban Chandra Das*, Md. KhokanHossain, Anup Kumar Talukder, Md. NazmulHoqueand Abu Nasar Md. AminoorRahman

Bangabandhu Sheikh Mujibur Rahman Agricultural University

E-mail: zibangor@bsmrau.edu.bd

Introduction: Epididymal spermatozoa (ESp) is an important source of germplasm for animal genetic resource conservation. When semen collection through standard procedures is challenging particularly in wildlife, the postmortem recovery of ESpprovides opportunity to preserve the male gametes from animals of high value or endangered species. Here, we used a model in Black Bengal goat to evaluate the ESp recovery, quality and fertility rate following artificial insemination (AI) using epididymal spermatozoa retrieved at different post-mortem storage time (PMT) at 4ºC.

Methods: Testes were collected from local slaughterhouses in a plastic bag and brought to the laboratory within 2-3 hafter slaughtered. Spermatozoa from one epididymis, of each buck were recovered and analyzed for motility, mass activity, viability and morphology. The contra-lateral epididymis–testicular complexes were stored at 4°C for PMT 24, 36, 48 and 72 h to observe the PMT effects on sperm quality and fertility rate. The fertility rate of buck Eps retrieved at PMT 0, 24, 36 and 48 h were evaluated following AI in estrus-synchronized does. The effect ofPMT on motility, mass activity and viability (mean ± SEM) of Eps in each treatment group (0, 24, 36, 48 and 72 h) were evaluated. Frozen-thawed (FT) spermatozoa collected from BRAC served as control.

Results: It was found that the quality of ESpwas better than FT spermatozoa ($p<0.05$). The quality of ESp progressively decreased ($p<0.05$) from PMT 0 to 72 h. Fertility rate of ESpretrieved at different PMT following AI was higher than FT spermatozoa (33.3%). In case of epididymal spermatozoa PMT at 0 and 24 h, fertility rate (66.6%) was significantly higher than PMT 36 and 48 h (50%).

Conclusion: The study concluded that the quality and fertility rate of ESpcollected from slaughterhouses and stored in a refrigerator at least 48 h were better than FT spermatozoa and it could be used for AI in goat at the field level.Our study using goat model suggests that the ESpcould be a potential source for preservation of male germplasm and thus restoration of rare and endangered wildlife, which requires further investigation.

Key words: Epididymal spermatozoa, post-mortem storage time, conservation, Wildlife

ID 19-106: **The viral etiology of acute febrile illness of in Dhaka, Bangladesh in the year of 2017**

Arifa Akram, A K M Muraduzzaman, Ahmed Nawsher Alam, Sharmin Sultana, Manjur Hossain Khan, Meerjady Sabrina Flora, Tahmina Shirin

Institute of Epidemiology, Disease Control and Research (IEDCR)

Presenting Author Arifa Akram E-mail: drbarna43@gmail.com/ dr.arifa@iedcr.gov.bd

Introduction: This is sometimes a challenge to identify the etiologies of acute febrile illnesses (AFI) due to non-specific clinical presentation as well as limited availability of diagnostic facilities. Bangladesh is very much suitable for vector borne viral infections like Dengue, Chikungunya and Zika due to hot and humid climate. In 2017 during the period of April to November there was an outbreak of febrile illness in Dhaka city, the capital of Bangladesh. With the aim to explore the situation Institute of Epidemiology, Disease Control and Research (IEDCR) took an initiative to investigate the etiology of febrile illness.

Methods: Serum samples were collected from sixteen hundred and thirty two patients with history of acute onset of fever with or without arthalgia and rash, who attended to IEDCR during the period of April to November 2017 and tested for febrile illness of viral etiology (Dengue, Chikungunya and Zika) by multiplex PCR.

Results: Among the 1632 cases about 74% was positive of febrile illness of viral etiology. About 66%, 7% and 0.4% were positive for Chikungunya, Dengue and co-infected with both pathogens respectively. Dengue virus positive serum samples were further analyzed for serotyping and found re-emergence of DEN-3 in the circulation along with existing serotypes DEN-1 and DEN-2. None of the cases was positive for Zika.

Conclusion: Considering the climatic condition and existence of domestic and peri-domestic setup in Bangladesh correlate with persistent mosquito breeding and survival as well as transmissibility of vector borne viral diseases. Thus continuous surveillance is required from public health point of view for prevention and control of arboviral diseases in Bangladesh.

Keywords: Acute febrile illness, Arboviruses, Aedes mosquitoes

ID 19-90: **Management of an Outbreak of Babesiosis in a Herd of Sheep**

Begum Fatema Zohara[1]*, Md. Golam Shahi Alam[2] and Farida Yeasmin Bari[2]

[1]Hajee Mohammad Danesh Science and Technology University [2]Bangladesh Agricultural University, Mymensingh, Bangladesh

**Corresponding author's E-mail: begumfatemafatema@ymail.com*

Introduction: Babesiosis is a tick-borne disease caused by hematotropic parasite of genus Babesia affects both livestock and human with life threatening implications, particularly in the immune compromised individuals. Babesia infection is also associated with huge worldwide economic losses. An Outbreak of babesiosis in a sheep herd and its successful management is described.

Methods: A total of 30 indigenous ewes, 2–3 years old and weighing 15–19 kg, with body condition score 2–3.5, were infected. The ewes were managed semi intensively.

Results: The ewes were presented with clinical signs of pyrexia, anorexia, weakness, pale mucous membrane, layed with their head and *neck extended,* increased respiratory rate, coffee colored urine and presence of ticks on their ear and other hairless parts of the body. Two ewes died out within twenty four hours. Diagnosis of ovine babesiosis was carried out on the basis of clinical signs and microscopic examination of Giemsa-stained blood smears. On microscopic examination, small piroplasms in erythrocytes were evaluated. The ewes were treated with a single dose of Diminazene aceturate (Berenil®) IM, at 3.5mg/kg BW, with supportive therapy using NSAIDs, B complex vitamins (Hematopen B_{12}®) , stomachic and fluid therapy was given I/V. Ivermectin pour on was applied topically against the blood parasites and for both endo and ecto parasites. The ewes were clinically recovered after two weeks.

Conclusion: It can be controlled by vector control and chemoprophylaxis.

Keywords: Babesiosis, diagnosis, management, tick-borne, sheep

ID: 19-118: **Immunogenicity of the local anthrax vaccine strain in animal models**

Farzana Islam Rume[1,2]*, Md Robiul Karim[3], Paritosh Kumar Biswas[4], Mahmuda Yasmin[1] and Chowdhury Rafiqul Ahsan[1]

[1] University of Dhaka [2]Patuakhali Science and Technology University, Barisal, Bangladesh [3]Bangabandhu Sheikh Mujibur Rahman Agricultural University [4]Chittagong Veterinary and Animal Sciences University

**Presenting author; Email: rumerp@yahoo.com*

Introduction: In Bangladesh, anthrax is considered an endemic disease mostly affecting ruminants. There have been numerous episodes of anthrax outbreaks in this country since 2009 and the most common source of infection for ruminants is ingestion of spores during grazing in contaminated pastures or through water contaminated with anthrax bacilli spores. There are many factors, including the immunogenicity of the present vaccine strain, are thought to be associated with the recent outbreaks. Therefore, the present study was undertaken to evaluate the immunogenicity of the present anthrax vaccine in animal models.

Methods: The master-seed of the anthrax vaccine, which is living spores of the non-capsulated attenuated Sterne F-24 strain of *Bacillus anthracis*, was obtained from the Livestock Research Institute, Mohakhali, Dhaka. A total of four cattle were immunized with the anthrax vaccine following standard protocol and six mice were immunized intraperitoneally with the sonicated extract of the vaccine (85 µg protein/mouse) following the same protocol. Sera were collected four weeks after the last dose of immunization and Western blot technique was applied to check the immunogenicity of the vaccine and the sonicated extract. Sera collected from similar number of cattle or mice, without any immunization, were used as control sera.

Results: A 36 kDa prominent antigenic band was obtained from immunized cattle sera, whereas, at least three antigenic bands, 30, 36 and 83 kDa, were obtained from the sonicate extract immunized mice sera. However, control sera from both cattle or mice showed no such bands.

Conclusion: The present anthrax vaccine showed immunogenicity in the cattle model. However, the sonicated extract immunized mice sera showed some more bands, including an 83 kDa, the molecular weight similar to the protective antigen (PA). Recently our group reported the presence of four different genotypes with remarkable genetic variations of *B. anthracis*in the soil of numerous outbreaks. The absence of the 83 kDa band in the sera of the vaccine immunized cattle or the presence of new genetic variants of *B. anthracis* in the environment, could be related to the recent outbreaks of this organism. However, this genetic mismatching between the vaccine strain and the strains circulating in the environment is contributing to vaccine failure needs to be studied further.

Keywords: Anthrax vaccine, immunogenicity, animal models, Western blot

Poster Presentation Day 3

ID 19-136: **Prevalence of *E coli* and *Salmonella* spp. in Fresh Tomatoes at Different Markets**

Nure Alam Siddiky[1], RuhenaBegum[1], Mohammad Asheak Mahmud[1], Rabeya Akter[1],Mohammad Taifur Rahman[1], ASM Ashab Uddin[1],Tazinur Rahman[1], Rahima Akter[4],Md. Giasuddin[1,2], Sinh Dang-Xuan[4], Corey Watts[4], Johanna Lindahl[4], Hung Nguyen[4], Mohammed A. Samad*[1,2]

[1,2] Bangladesh Livestock Research Institute (BLRI) [3] International Livestock Research Institute, Vietnam [4]Jahangirnagar University

Presenting Author: Nure Alam Siddiky

**Corresponding author email: samad_blri@yahoo.co.nz*

Tomato is the world's popular vegetable crop and famousfor delicious salads and mashes in the community of Bangladesh. A cross-sectional study was done to assess the prevalence of *E. coli*and *Salmonella* spp.infresh tomatoesatdifferent markets, i.e. rural, peri-urban and urban. A total of 366 samples were collected from Dhaka city (urban), Savar&Dhamraisub-districts, (peri-urban) and Netrokona district (rural)duringNovember2018 to June 2019. Isolation and identification of *E. coli* and *Salmonella* spp. were carried outthrough conventional culture method.Thereafter, 5% of the isolates were reconfirmed with the application of Vitek-2 (bioMérieux, France). The average prevalence of *E. coli*was found 13.93% (n=51;95%CI: 10.76-17.86) wherehighest prevalence observedinperi-urban (30%, n=29; 95%CI: 21.93-40.01) followed by rural (10.41%, n=10; 95%CI: 5.76-18.12) and urban (6.89%,n=12;95%CI: 3.99-11.67) market respectively.Likewise, the average prevalence of *Salmonella* spp. was 7.38% (n=27; 95%CI: 5.12-10.52) withhighest prevalence observed in rural (15.63%,n=15;95%CI: 9.70-24.19) followed by urban (5.75%,n=10; 95%CI: 3.15-10.25) and peri-urban (2.1%, n=2; 95%CI: 0.57-7.28) market.Antibiotic susceptibility test was performed against 11 antibiotics belongs to nine different groups including beta-lactam, penicillin, tetracycline, phenicols, cephems, aminoglycosides, folate pathway inhibitors, quinolones and macrolides. The prevalence of multi-drug resistant (MDR) *E. coli* and *Salmonella* were 94.11% (n=48; 95%CI:84.08-97.98) and 59.25% (n=16; 95%CI: 40.73-75.49) respectively. In behavioral and practice survey, 100% vendors ensured they never use chemicals & preservatives but 88% worried more about chemicals rather than microbes. However, it was found that 36% vendors used water to keep the products fresh, and flies were observed on tomatoes in 87% of the shops. About 94.17% vendors believedthat nobody would be sick by eating tomato. Consumersreported that they used same knife (96%) and cutting board (80%) for vegetables, fish and meat processing. In addition, 19% customers didn't wash cutting board between uses. Variations inthe prevalence of *E. coli* and *Salmonella* spp. may be due to soil& environmental contamination during harvesting and poor quality water used during marketing. Hygienic practices and awareness may reduce the microbial contamination of tomato.

Keywords: *E. coli*, *Salmonella* spp.vitek-2, multi-drug resistance, antimicrobial susceptibility testing

ID 19-137: **Prevalence of *Vibrio cholerae* in Pangasius fish with public practice and perception: A food safety concern**

Ruhena Begum[1], Rabeya Akter[1], Mohammad Taifur Rahman[1], A.S.M. Ashab Uddin[1], NureAlam Siddiky[1],Rahima Akter[4], Mohammad Asheak Mahmud[1], Md.Giasuddin[1,2],Sinh Dang-Xuan[3], Corey Watts[3], Johanna Lindahl[3], Hung Nguyen[3],Mohammed A. Samad*[1,2]

[1, 2] Bangladesh Livestock Research Institute (BLRI) [3]International Livestock Research Institute, Vietnam [4]Jahangirnagar University, Savar, Dhaka-1342

Presenting Author: Ruhena Begum

**Corresponding author email: samad_blri@yahoo.co.nz*

Vibrio cholerae is considered as one of the major pathogenic bacteria having public health concern worldwide. Pangasius fish is one of the most available and cheap protein sources in Bangladesh. A cross-sectional study was conducted to determine the prevalence of antimicrobial resistant*V.cholerae* in and to know the peoples' perceptions regarding food safety.Isolation and identification were done using ISO: 21872-1:2007. Antibiotic susceptibility was done by disk diffusion test according to CLSI 2014.A total of 123 Pangasius fish (49 fromtraditional markets,74 from supermarkets) were sampled and 265 people (86 Pangasius fish vendors and 179 consumers) were interviewed at Dhakacity fromJanuary to June 2019. Out of 123 samples, 62 isolates (50.41%, 95% CI: 41.69-59.10) were found positive of *V.cholerae* (55.10%, n=27 in traditional markets and 47.29%, n=35 in supermarkets).Antibiotic susceptibility was tested against 11 antibiotics of penicillin, β-lactam, cephems, phenicols, tetracycline, aminoglycosides, folate pathway, quinolones and macrolides classes. In susceptibility test, highest resistance was found against penicillin G (100%) followed bytetracycline (45.16%), erythromycin (24.19%) and nalidixic acid (14.52%). Over 80% isolates were sensitive against chloramphenicol, cefixime, ceftriaxone, gentamicin, amoxicillin-clavulanate, streptomycin and sulfamethoxazole-trimethoprim.In addition,31% isolates (n=19, 95% CI: 20.58-42.97) revealed multi-drug resistance (MDR). No vendors said that they use any chemical or preservative to extend shelf-life of the fishes.In 66.67% (n=82, CI: 57.94-74.38) cases fly were observed on the fishes. Most of thevendors (80%,n=99, 95% CI: 72.40-86.64) weremore worried about chemicals thanmicrobesin the food. Similarly, only 2.8% (n=5, 95% CI: 01.20-06.37) consumers reported being worried about germs in food. About 47% (95% CI: 39.76-54.23) of the consumers reported about using same knives and chopping board for processing fish/meat and vegetables. Moreover, 11% consumers (n=20, 95% CI: 07.35-16.63) do not wash knives and chopping board between uses. High prevalence of MDR *V. cholerae* in marketed pangasius fish and risk behaviors are greatpublic health concerns. Interventions on the basis of root cause analysis and awareness campaign may contribute to decrease the cross contamination.

Keywords: *Vibrio cholerae*, food safety, antimicrobial resistance, risk behaviors, Pangasius

ID 19-43: **Isolation, Identification and Anitibiogram Assay of *Salmonella* from Chicken Eggs**

Md. Shajahan Ali, Wahidur Rahman, Md. Saroat Hossain, **Tania Sultana**, and K. M. Mozaffor Hossain*

University of Rajshahi

**Corresponding author's email: mozaffor@ru.ac.bd*

Introduction: Poultry eggs can effectively fulfill the shortage of protein requirement, since it can be produced at the least cost, lowest time and efforts than the other protein producing animals. However, the advancement of poultry industry is seriously hampered due to the outbreak of various infectious and non-infectious diseases. Among the bacterial diseases, salmonellosis caused by the genus *Salmonella* is of major problems in the poultry industry in Bangladesh. Therefore, an investigation was carried out to isolate and identify *Salmonella* from chicken eggs with antibiogram assay.

Methods: A total of 120 chicken eggs comprising 60 commercial layer chicken eggs and 60 indigenous chicken eggs were collected from farm, whole seller and retailer, and screened to determine the prevalence of *Salmonella.* After enrichment on nutrient broth, broth culture was streaked onto SS agar for the isolation of *Salmonella*. The isolated *Salmonella* were identified based on their morphology, staining, cultural and biochemical properties. Antimicrobial sensitivity test was done by using disc diffusion method.

Results: Overall prevalence of *Salmonella* was 23.33% in chicken eggs, where 36.67% was in indigenous chicken eggs and 10% was in commercial layer chicken eggs. Prevalence of *Salmonella* was 20.83% in egg shells, where 33.33% was on indigenous chicken egg shells and 8.33% was on commercial layer chicken egg shells. In egg content the prevalence was 2.5%, where 3.33% was in indigenous chicken egg content and 1.67% was in commercial layer chicken egg content. For commercial layer chicken eggs, the prevalence of *Salmonella* was 5%, 15% 10% in farm eggs, whole seller eggs, and retailers eggs, respectively. For indigenous chicken eggs, prevalence was 50% in whole seller eggs and 23.33% was in retailer eggs. The isolated *Salmonella* showed 100%, 100%, 55%, 40% and 25% resistant to penicillin, nalidixic acid, sulfamethoxasole-trimethoprim, ampicillin and amoxicillin, respectively. Furthermore, the sensitivity pattern of the isolates showed 90%, 80%, 75% and 70% sensitive to ciprofloxacin, gentamicin, amoxicillin and streptomycin, respectively.

Conclusion: The prevalence of *Salmonella* in commercial layer chicken eggs is lower than that of indigenous. The higher incidence of *Salmonella* was found in egg shells as compared to eggs content.

Keywords: Chicken eggs, *Salmonella*, Prevalence, Antibiotic resistance

ID 19-14: **Appraising meat quality of market broiler and ensuring consumer safety**

J. C. Dey1, *M. A. Hossain[1] and I. Jahan[2]

[1]*Chittagong Veterinary and Animal Sciences University* [2]*University of Chittagong*

**Corresponding author: mhossainmu@yahoo.com*

Introduction: Broiler meat has a great demand in the world's food industry to provide premiere quality of protein to the consumers. It is inevitable to maintain meat quality and food safety to meet the protein need of the consumer world. The huge protein gap of the country can be met by raising quality broiler meat. Consumers are always crazy for having quality food item at the expense of high price, because poor quality meat can adversely affect the consumer health. So special focus should be given toward quality poultry meat production, which can help to grow safe, sound, and healthy nation. It goes without saying that, consumer world can grow well both physically and mentally, if quality food item could be supplied them all the time safely. Considering the above, the study was conducted to assess the quality of broiler meat procured from four different markets of Chittagong, i.e Baddar Hat (BH), Pahartoli (PHT), Jhaowtola (JT) and Riazuddin bazar (RB).

Methods: A total of 20 shops was selected randomly and two live broilers of similar age were collected from each shop located in the different places of metropolitan city of Chittagong to conduct the experiment. Meat samples were taken from the live broilers to appraise the quality based on the H2O level, pH, water holding capacity (WHC), extract release value (ERV), tyrosine value (TV) and thiobarbituric acid reactive substance value (TBARS) through the laboratory analyses. All data were subjected to analyses by Minitab software (Minitab 16, 2000).

Results: The data revealed that the TV and TBA values differed significantly ($P<0.01$) between markets except for the other parameters (H2O, pH, WHC, ERV). The highest TV value (0.66) was found in the meat of PHT market while lowest TV value (0.54) being in BH and JT markets. The TBA value was improved ($P<0.01$) in the meat of BH and JT markets compared to that of other markets. The road distance (RD) and the transporting time (TT) for carrying birds were affected ($P<0.01$) by markets.

Conclusion: It can be concluded that the quality of broiler meat of different markets appears to be good based on the chemical evaluation, even though TT and RD might influence meat quality. Periodic research study focusing on the meat quality of market broiler could help people to ensure their food safety and healthy life style.

Key words: Meat quality, market, pH, TBARS value, broiler chicken

ID 19-42: **Isolation, Identification and Antibiogram Study of *Escherichia Coli* from Chicken Eggs**

Md. Saroat Hossain, Wahidur Rahman, Md. Shajahan Ali, Tania Sultana, and **K. M. Mozaffor Hossain***

University of Rajshahi

**Corresponding author's email: mozaffor@ru.ac.bd*

Introduction: Chicken eggs are one of the most important foods which have a role in human diet because they are easy to obtain and nutrient rich. It contains high quality dietary proteins that provide all of the essential amino acids, fat, minerals and vitamins needed to support life and growth. In spite of chicken eggs are rich in dietary nutrients, it makes itself suitable for growth of many bacterial pathogens like *E. coli*. The contamination of the eggs with *E. coli* may lead to transmission to consumers. Antimicrobial resistance is an increasingly global problem and emerging antimicrobial resistance has become a public health issue worldwide. Therefore, the present study was undertaken determine the prevalence *E. coli* in chicken eggs with their antibiogram assay.

Methods: A total of 180 chicken eggs including 60 brown shell eggs, 60 white shell eggs and 60 indigenous chicken eggs were collected from layer farms, whole sellers and retailers, and analyzed for isolation and identification of *E. coli*. After enrichment on nutrient broth, broth culture was streaked onto EMB agar for the isolation of *E. coli*. The isolated *E. coli* were identified based on their morphology, staining, cultural and biochemical properties. Antimicrobial sensitivity test was done by using disc diffusion method.

Results: The overall prevalence of *E. coli* was 38.89% in chicken eggs, where 27.78% was on egg shells and 11.11% was in egg contents. The prevalence of *E. coli* was 58.33%, 41.66% and 16.67% in farms, whole sellers and retailers, respectively. However, the prevalence of *E. coli* was 41.47%, 25.00% and 50.00% in indigenous chicken eggs, brown shell eggs and white shell eggs, respectively. Isolated *E. coli* showed 71.42%, 71.42%, 64.28%, 57.14%, 50%, 35.71%, and 21.42% resistant to erythromycin, ampicillin, amoxicillin, tetracycline, ciprofloxacin, doxycycline and chloramphenicol, respectively. However, sensitivity was found as 100%, 92.85%, 78.57%, 64.28%, 35.71%, 21.42%, 14.29%, 14.29%, and 14.29% to meropenem, ceftriaxone, gentamycin, chloramphenicol, ciprofloxacin, amoxicillin, doxycycline, ampicillin and tetracycline, respectively.

Conclusion: The prevalence of *E. coli* was found higher on egg shells and in farm level. The prevalence of *E. coli* in chicken eggs and their drug resistance is obviously significant.

Keywords: Chicken eggs, *E. coli*, Prevalence, Antibiotic resistance

ID 19-91: **Cockroaches: A source of multidrug resistant pathogenic strains of *Escherichia coli***

Ripon Sarker, Swarup Kumar Kundu[1], Md. Saidul Islam, Md. Muket Mahmud, KHM Nazmul Hussain Nazir and **Muhammad Tofazzal Hossain***

Bangladesh Agricultural University

**Corresponding author: tofazzalmh@yahoo.com*

Introduction: Cockroaches consume garbage, rotting food, and even fecal waste of other roaches. They can easily contaminate food by leaving droppings containing pathogenic bacteria like *Escherichia coli*, *Klebsiella pneumonia*, *Salmonella* spp., *Shigella* spp. etc on food, eating utensils, kitchen surfaces, and other areas around home which can cause food borne diseases. This present study was aimed to isolate and characterize the pathogenic strains of *E. coli* from the external and internal parts of cockroaches.

Methods: A total 68 cockroaches were collected from household premises (25), dining (23) and toilet (20). The collected cockroaches were processed and inoculated in nutrient broth followed by streaked on EMB agar media. Suspected colonies were purified, chromosomal DNA was extracted followed by PCR using specific primers to detect and differentiate *E. coli*. Pathogenicity test and antibiotic susceptibility test was performed for each pathogenic isolate.

Results: A total of 47 cockroaches were found to contain *E. coli* confirmed by PCR using 16S rRNA primers of which 3 isolates were found to be positive for both *stx*1 and *stx*2 genes and 5 isolates were positive for *rfbO157* gene. The pathogenic strains of E. *coli* were able to kill all the inoculated white albino mice. All the pathogenic strains showed 100% resistancy to Cefuroxime, amoxicillin and moxifloxacin; 83% resistancy to tetracycline, doxycycline, amikacin and ceftriaxone; and 33% resistancy to ciprofloxacin, azithromycin and levofloxacin.

Conclusion: It can be concluded that cockroaches are potential source of multidrug resistant pathogenic strains of *E. coli* and hence effective preventive and control measures are required to minimize cockroach related infections.

Keywords: Cockroaches, multidrug resistant, O:157, *stx,* pathogenicity test

ID 19-51: **Prevalence and Risk Factors of *Campylobacter* Infection in Broiler and Cockerel Flocks in Mymensingh and Gazipur Districts of Bangladesh**

Md. Mehedi Hasan[1], Sudipta Talukder[1], Amit Kumar Mandal[1], SyedaTanjina Tasmim[1], Mst. Sonia Parvin[1], Md. Yamin Ali[1], Mahmudul Hasan Sikder[2] and Md. Taohidul Islam[1*]

[1]Bangladesh Agricultural University

[*]Corresponding author: Prof. Dr. Md. Taohidul Islam; Email address:taohid@bau.edu.bd

Introduction: *Campylobacter* spp. is one of the most frequent causes of foodborne gastroenteritis having zoonotic importance. This study was conducted to estimate the prevalence, and to identify the risk factors of farm-level *Campylobacter* infection in meat-type chicken flocks.

Methods: A cross-sectional study was conducted in two selected districts named Mymensingh and Gazipur in Bangladesh over the period of January to June 2019. A total of 840 cloacal swab samples were collected from 84 broiler (n=75) and cockerel (n=9) farms. Of these, 58 and 26 farms were investigated from Mymensingh and Gazipur, respectively. Ten collected samples were pooled from each flock and considered as one sample and only one flock was sampled on each farm. During sampling, data on farm management, biosecurity, and hygiene practices were collected through a face-to-face interview using a structured questionnaire in KoboCollect android mobile application.Then, *Campylobacter* spp. were isolated through bacteriological culture and identified by Gram's staining as well as biochemical tests such as catalase and oxidase test. Furthermore, the isolates were confirmed using PCR by targeting the 16SrRNA gene. Risk factors were analyzed at the farm level using multivariable logistic regression in SPSS with the significant levels of P-value≤0.05.

Results: The overallfarm-level prevalence of *Campylobacter*infectionwas estimated at40.5% (95% CI: 30.1-51.8%). Besides, the prevalence of *Campylobacter*infection in broiler and cockerel farms was 35.3% and 42.9%, respectively, in Mymensingh, and 50% for both in Gazipur. In risk factor analysis, the following factors were found significantly (P≤0.05) associated with *Campylobacter* infection in chickens: shed older than 5 years (OR: 300.29, [6.01-15015.39]),birds older than 30 days (OR: 44.89, [1.5-1345.4]), flock size with more than 1500 birds (OR: 16.6, [1.42-193.6]), downtime less than seven days (OR: 66.46, [1.95-2270.68], no disinfection of shed surroundings during rearing (OR: 37.11, [3.38-407.54]), rice husk vs. sawdust as litter materials (OR: 19.9, [1.76-255.26]), and farming experiences less than 10 years(OR=31.9, [1.03-987.64]).

Conclusion: This study identified the factors which could contribute to set the effective interventions in controlling *Campylobacter* in chickens to reduce campylobacteriosis through meat consumption.

Keywords: *Campylobacter* spp., Prevalence, Risk factors, Chickens, Cloacal swab, PCR

ID 19-76: **Investigation of anti-microbial activity of ash filtrates**

Khairun Nahar Shithi, Mohammed Nooruzzaman, Jahan Ara Begum and Emdadul Haque Chowdhury

Bangladesh Agricultural University

E-mail of the corresponding author: khokondvm@yahoo.com

Introduction: Infectious diseases are major constraints for the poultry industry in Bangladesh. Farmers use different chemical disinfectants to control infectious diseases in their biosecurity program including sanitation of eggs. Microorganisms very often get resistance to commonly used disinfectants. Organic and naturally available antimicrobials can be an alternative source. Historically household derived ashes have been used inhand sanitation, cloth and dish washing and in agricultural field to control pests. Here, we tested antimicrobial activity of ash filtrates derived from different ashes.

Methods: At first, we collected household ashes derived from 18 different fuel sources such as straw (rice, maize, mustard, and potato), rice husk, wood (plum, mango and mull berry), bamboo, banana stem, dried cow dung, charcoal, etc. We obtained ash filtrates in water using a handmade filtration system and measured the pH. For antimicrobial activity testing, we diluted ash filtrate in distilled water to obtain a range of pH from 11.0 to 8.5 and tested their antimicrobial activity against a *Salmonella* strain. 10 µl (2.58x10^6cfu) *Salmonella* was mixed with 5 ml of diluted ash filtrate, washing soda (pH 10.5), caustic soda (pH 10.5) and nutrient broth (pH 7.4) and incubated for 5 minutes at room temperature. Later, we spread 1 µl of above mixture on BG agar and incubated overnight at 37 ^{o}C.The cfu was calculated.

Results: Using our handmade filtration system, we obtained a clear ash filtrate. The pH of ash filtrates varied from 8.5 (potato straw) to 11.7 (rice straw). Interestingly, we found pH of more than 10.5 in 9 ash filtrates derived from rice straw, woods, bamboo, banana stem, mahogany leaf and tobacco root. At pH 10.5 and above, no growth of Salmonella was observed. From pH 10.5 and below, a gradual decrease in cfu count was observed indicating a dose dependent antibacterial activity of ash filtrates. Washing soda and caustic soda were used as controls and produced partial inhibition of bacterial growth. Whereas, untreated nutrient broth cultureshowed a high bacterial count (2.3x10^6cfu).

Conclusion: Majority of the ash filtrate showed very high pH (≥10) and potent antibacterial activity against *Salmonella* comparable to washing and caustic soda.

Key words: Salmonella, pH, soda

ID 19-16: **Microbial evaluation of fresh vegetables collected from different markets of Jamalpur, Netrokona and Kishoregonj districts**

Ohiduzzaman, S.M. Akramul Islam, Mohammad Arif, Md. Jahidul Islam Saddam,Muhammad TofazzalHossain and **S. M. LutfulKabir**

Bangladesh Agricultural University

E-mail of the corresponding author: lkabir79@gmail.com

Introduction: The study was conducted to evaluate bacterial flora of salad vegetables and their isolation, identification and characterization using various techniques.

Methods: In this study, a total of 90 fresh vegetable samples (tomato, carrot, cucumber, coriander leaf, green chili) were collected from different markets of Netrokona, Kishoregonj and Jamalpur districts and these samples were subjected to the determination of total viable count, total *E. coli* count, total *Staphylococcus aureus* count, total *Salmonella* count and total C*ampylobacter* count by using Plate count agar, MacConkey agar, Mannitol salt agar, Xylose lysine deoxycholate agar and Blood base agar no 2. The results of the total bacterial count were expressed as the number of colony forming units per gram (CFU/g) of meat sample. In addition, a total of 36 composite samples from mixed vegetables were prepared and these samples were used for determining the load of bacteria during before and after washing of these composite samples with tap water.

Results: The total viable count of fresh vegetables ranged from 8.19 log CFU/g to 10.51 log CFU/g. For mixed fresh vegetable samples the load of bacteria was higher in before washed sample 10.59 log CFU/g than after washed sample 8.28 log CFU/g. *Salmonella* count ranging from 2.48 log CFU/g to 8.34 log CFU/g while *E. coli* ranged from 6.30 log CFU/g to 9.59 log CFU/g, the *S. aureus*count ranged from 4.34 log CFU/g to 9.40 log CFU/g, the *Campylobacter* count ranged from 3.23 log CFU/g to 6.04 log CFU/g. For total 18 tomato samples the number(%) of *Salmonella*, *E. coli*, *S. aureus* and *Campylobacter* of Netrokona, Kishoregonj and Jamalpur districts were found 18(100), 18(100), 18(100) and 18(100) respectively. For total 18 carrot samples the number(%) of *Salmonella*, *E. coli*, *S. aureus* and *Campylobacter* of Netrokona, Kishoregonj and Jamalpur districts were found 16(88.88%), 18(100%), 18 (100%) and 18 (100%) respectively. For total 18 cucumber samples the number(%) of *Salmonella*, *E. coli*, *S. aureus* and *Campylobacter* of Netrokona, Kishoregonj and Jamalpur districts were found 18(100%), 18 (100%), 18(100%) and 18(100%) respectively. For total 18 coriander leaf samples the number(%) of *salmonella*, *E. coli*, *S. aureus* and *Campylobacter* of Netrokona, Kishoregonj and Jamalpur districts were found 14(77.77%), 18(100%), 17(94.44%) and 18(100%) respectively. For total 18 green chili samples the number(%) of *Salmonella*, *E. coli*, *S. aureus* and *Campylobacter* of Netrokona, Kishoregonj and Jamalpur districts were found 18(100%), 18(100%), 18(100%) and 18(100%) respectively.

Conclusion: The results of this study suggested that food-borne bacteria were present on fresh vegetables of different markets and their presence in fresh vegetables are alarming for public health.

Keywords: Marketed fresh vegetables, microbiological quality, hygienic condition

ID 19-48: **Detection and quantification of heavy metals and minerals in poultry feeds collected from local market of Sherpur**

Md. Khairul Islam, Quazi Forhad Quadir[1], Md. Rafiqul Islam[2], **Kazi Rafiq**

[1]Bangladesh Agricultural University, Mymensingh-2202, Bangladesh. [2]BARC

Corresponding author: KaziRafiq, E-mail: krafiq73@yahoo.com; kazirafiq@bau.edu.bd

Introduction: The present work assessed the stakeholders' knowledge, attitude and practices regarding the heavy metal contamination in poultry feed; detection and quantification of heavy metals and minerals in poultry feed samplescollected from local market.

Methods: Samples were collected from two upazila (Nalitabari, Jhenaigati) of Sherpur district of Bangladesh. A total of 22 poultry feed samples were analyzed for the concentration of heavy metals (Pb, Cr, Cd and Ni) and minerals (Na, K, Ca). Heavy metals and Calcium were analyzed by using Atomic Absorption Spectrophotometry, and Sodium and Potassium were analyzed with the help of flame emission spectrophotometer. The feed samples include 10 brand feeds and 12 non-brand feeds. In addition, a survey was conducted in the respective areas and twenty people were commented regarding heavy metals residues in poultry feed using questionnaire.

Results: Among them, 15% were illiterate and remaining 85% were literate. Almost 10% had knowledge about heavy metal contamination in poultry feeds but remaining 90% had no knowledge about heavy metal contamination in poultry feeds. The concentration of Pb and Ni were below the detectable level in all the collected samples. The average concentration of Cr in poultry feed samples collected from Nalitabari and Jhenaigati were 5.45 mg/Kg and 21.806 mg/kg, respectively. The average concentration of Cr in brand and non-brand poultry feed samples were 9.868 mg/Kg and 16.764 mg/Kg,respectively. The average concentration of Cd in poultry feed samples collected from Nalitabari and Jhenaigati were 1.362 mg/Kg and 1.296mg/kg, respectively. The average concentration of Cd in brand and non-brand poultry feed samples were 1.329 mg/Kg and 1.328 mg/Kg, respectively. The overall Cr concentration was below the maximum permissible limit (MRL) fixed by NRC (500 mg/kg) but overall Cd concentration was above the MRL fixed by EU (0.5 mg/kg). Among the minerals, the overall average concentration of Na, K, and Ca in collected samples were below the expected recommended level.

Conclusion: In the nutritional point of view, the results indicate that the poultry feed collected from local market have low mineral contents as well as contaminated by toxic heavy metals.

Key words: Bangladesh, MRL, NRC

ID 19-96: **Assessing the food safety condition of the broiler shops and broiler meats at the live bird markets in Chattogram city**

Md. Ridoan Pasha, Mohammad Mahmudul Hassan and Mohammad Rashedul Alam

Chattogram Veterinary and Animal Sciences University

Corresponding email: pasha.ctg@gmail.com

Introduction: Broiler meat is quenching the major portion of animal protein demand at Bangladesh in recent decades. With the increase of urbanization and more influx of people, broiler sale centers are increasing rapidly in the cities. But, the hygienic standards regarding rearing of birds, their slaughter and processing are not always maintained in these shops. These may cause the broiler meat to be prone to contamination and create health hazard after human consumption. This study was performed to investigate the food safety condition in the broiler shops in Chattogram city along with the comparative bacterial analysis of the meat from the traditional broiler market and super markets.

Methods: Fifty shops were taken from 5 markets to assess the hygienic condition in the shops. For bacterial analysis, 75 meat samples were collected from 25 traditional broiler shops. Further, 25 samples were collected from 5 different super shops as control. The meat samples were aseptically mashed, homogenized and inoculated in agar for colony counting of *E coli* to enumerate the bacterial load.

Results: This study showed that the hygienic condition of the studied shops were below standard. The rearing cages and feeders were not cleaned ever in 14% and 12% shops, respectively. Most of the vendors used only water to clean the feeder, drinker, and even cages (84%, 82% and 55%, respectively). Drums were used as bleeding pots for the slaughtered birds in 90% shops where cleaning of those were performed only once a day in 36% shops. The post-slaughter processing tables were found to be in very dirty condition in 66% shops. No cleaning agents were used by 28% vendors after using in-market toilets. The bacterial study showed that there were presences of higher number of bacteria in broiler shop samples (6.49 CFU/g) than the superstore (5.4 CFU/g) [p=0.001] with the significant variations among the samples from different markets (p=0.02).

Conclusion: This study revealed that the hygienic condition of the broiler shops in Chattogram city were poor and bacterial contamination of the meats were huge which may cause hazard to the health and food safety after human consumption.

Keywords: Broiler, shop, meat, hygiene, *E. coli*

ID 19-94: **Isolation and characterization of human pathogenic *Vibrio cholerae* from chicken**

Mst. Soudiya Akter Banu, Farah Zerin, Md. Tanvir Rahman and Muhammad Tofazzal Hossain*

Bangladesh Agricultural University

**Corresponding author: tofazzalmh@yahoo.com*

Introduction: Cholera caused by *Vibrio cholerae* is a potentially epidemic and life-threatening secretary diarrhea characterized by numerous, voluminous watery stools, often accompanied by vomiting, and resulting in hypovolemic shock and acidosis. The present research work was conducted for the isolation and characterization of *V. cholera* from intestine and cloacae of chicken sold in the local markets of Bangladesh Agricultural University, Mymensingh, Bangladesh.

Methods: A total of 27 samples comprising of intestinal fluid (n=20) and cloacal swabs (n=7) were collected and analyzed. *Vibrio* spp., was identified following standard cultural, staining, biochemical and PCR assay.

Results: Among the tested 27 samples, only 4 (14.81%) *Vibrio* spp. was recovered from intestinal fluid, while all the cloacal swabs were negative for *Vibrio* spp. Among the positive samples, 2 isolates were confirmed as *V. cholerae* by PCR assay with species specific primers designed from *groEL* gene. All the positive isolates were detected as pathogenic when PCR was done using *ctx* gene. In antibiogram study, both isolates were found highly sensitive to erythromycin, azithromycin, chloramphenicol, ciprofloxacin, gentamicin and norfloxacin and resistant to streptomycin.

Conclusion: It can be concluded that chicken might act as a source of *V. cholerae* for the handlers and consumers if their meat become contaminated during processing.

Keywords: *V. cholerae*, chicken, pathogenic strain, *groEL* gene

ID 19-142: **Detection of pathogens distribution, antibacterial susceptibility along with usage of antibiotics in mastitis in Chattogram: A food safety issue**

D Hossain[1], S Singha[2], G Koop[3], M Derks[4], Y Persson[5], MM Rahman[2], MA Hoque[2]

[1]*Sher-e-Bangla Agricultural University* [2]*Chattogram Veterinary and Animal Sciences University* [3]*Utrecht University,* [4]*Wageningen University and Research, The Netherlands;* [5]*National Veterinary Institute, Sweden.*

E-mail of the corresponding author: delowervet@sau.edu.bd

Introduction: Milk is an ideal source of high quality protein and micronutrients for human. Mastitis is the most costly disease of cows and has impact on milk yield and food safety. Presence of high bulk milk somatic cell count (BMSCC) and pathogens in milk are indications of milk quality. Irrational usages of antibiotics are responsible in developing antimicrobial resistance and also affect the milk value chain due to residual effect. The present work was conducted to know BMSCC, pathogens distribution, antimicrobial sensitivity and types of antibiotics use to treat mastitis.

Methods: A cross-sectional study on subclinical mastitis (SCM) and cohort study on clinical mastitis (CM) were conducted respectively on 102 and 24 randomly selected dairy farms in Chattogram. BMSCC was determined using DeLaval cell counter. Organisms were isolated using classical bacterial culture followed by MALDI-TOF for species confirmation. Beta-lactamase production and minimum inhibitory concentration (MIC) against *Staphylococcus* spp. was performed by clover leaf and micro-dilution method considering 12 antibiotics, respectively. Antibiotics usages were recorded following farmers' interview, checking drugs' vials and prescription slips.

Results: The average BMSCC estimate was 601,100 (41,000 to 2,029,000) cells/mL of milk where as in 50% the BMSCC was 414,000. Non aureus staphylococci (NAS) (38.1%) and streptococci (29.5%) were the most commonly identified pathogens in SCM where in CM, NAS was (24.0%), followed by *Streptococcus* spp. (18.6%) and *Bacillus* spp. (19.8%). The most prevalent species from SCM within genus *Staphylococcus* were *S. haemolyticus* (34.1%), *S. epidermidis* (27.5%) and *S. aureus* (14.3%) and in CM the isolated organisms were *S. sciuri* (35.7%)**,** *S. haemolyticus* (28.6%) and *S. aureus* (14.3%). Among resultant staphylococci isolates, 66.2% exhibited beta-lactamase production in SCM study. The resistance of NAS was identified for oxacillin (90.1%), penicillin (29.0%), erythromycin (29.0%). In case of resistance pattern of *S. aureus* were identified for oxacillin (100%) and erythromycin (50%). Ranges of antibiotics were used for mastitis treatment include ceftrioxone (61%), followed by gentamycin (54%) and combination of amoxicillin and colaxacillin (38%).

Conclusion: Average BMSCC was higher than threshold level in milk of Chattogram. Staphylococci were the most dominating pathogen in mastitic milk and farmers randomly used watch group of antibiotics such as ceftriaxone and ciprofloxacin.

Key words*:* Mastitis, Bulk milk somatic cell count, Non-aureus *Staphylococcus*, Antibiotics, Beta-lactamase production, Minimum inhibitory concentration.

ID 19-79: **Estrus synchronization in anestrus cows by using different protocols for the improved reproductive performance**

Md. Jalal Uddin Sarder, Md. Hemayatul Islam, Md. Niyamat Ullah, Soniya Akter Nishi and Md. Reazul Islam

University of Rajshahi

Corresponding author's email: jalalnusa@yahoo.com

Introduction: Development of estrus synchronization protocols helps in Food Safety and Food Security in our country. The aim of present study was to improve the fertility status of cows using Prostaglandins F2α analogue, GnRh and hCG at Rajshahi region of Bangladesh.

Methods: The study was carried out in private dairy farm under Rajshahi district and in the Department of Veterinary and Animal Sciences, University of Rajshahi during the period from 01-07-2017 to 30-6-2018. A total 160 ansestrus cows were selected from 980 data by using questionnaires and gynecological examination of cows were made on the basis of history, clinical examination and observation, housing, feeding and their management. Out of 160 anoestrus cows, 140 cows were selected for clinical managements. The cows were divided into eight protocols each protocol at least 20 anestrus cows. The cows were divided into eight protocols each protocol at least 20 anestrus cows. The protocols were numbered from Protocol-I to Protocol -VII were PGF2α, PGF2α -PGF2α, PGF2α -PGF2α -PGF2α (Fixed time AI), GnRH-PGF2α-GnRH (Fixed time AI), PGF2α-GnRH-PGF2α (Fixed time AI), GnRH-PGF2α, hCG, respectively and Protocol -VIII was control group (No treatment). Treatment with each groups of protocol was observed the heat and inseminated then finally diagnosed pregnancy with three methods.

Results: The overall prevalence of anestrus cows was 54.42%. The lower prevalence of anestrus was observed in indigenous cattle (50.00%). The highest occurrence of estrus was observed in cross-bred (55.00%), <4 years age (60.00%), <200kg body weight (59.64%), medium body condition (54.76%) and heifer (62.33%) cattle. The overall 77.14% anestrus cows came into estrus after 7 types of treatment where as only 20% anestrus cows came into estrus from control group. The rhythmic percentages of estrus induction with 8 protocosl by injecting PGF2α, PGF2α -PGF2α, PGF2α -PGF2α -PGF2α, GnRH–$PGF_{2\alpha}$-GnRH, $PGF_{2\alpha}$-GnRH-$PGF_{2\alpha}$, GnRH-$PGF_{2\alpha}$, hCG technique and Control group were 60%, 85%, 85%, 80%, 90%, 80%, 60%, and 20%, respectively. The 90% of anestrus cows were estrus/heat by using PG-GnRh-PG treatment protocol. The second position was PG-PG and PG-PG-PG fixed time AI (85.0%).

Conclusion: The average 77.14% anestrus cows came into estrus with 7 types of treatment. The PG-GnRh-PG treatment protocol group observed the best treatment protocol among the other groups.

Key words: Anestrus, estrus synchronization, treatment protocol, dairy cows

ID 19-112: **Assessment of Dairy Farmer's Hygienic Milking Practices and Awareness on Cattle Milk-Borne Zoonoses in Milk Shed Areas of Bangladesh**

Solama Akter Shanta, RukaiyaAkter Lima, Md. MahaumudunNabi and M. Ariful Islam*

Bangladesh Agricultural University

**Corresponding author e-mail: maislam77@bau.edu.bd*

Introduction: Many milk-borne epidemics of human diseases have been spread by contamination of milk by spoiled hands of dairy workers, unsanitary utensils, flies and polluted water supplies.Information on milking hygiene practices and farmers' awareness on cattle milk-borne zoonosesremains scare in Bangladesh. The aims of the present survey study were toassess hygiene milking practices and the general handling of milk, and to evaluate the farmers awareness on cattle milk-borne zoonoses.

Methods: A cross-sectional study was carried outin 270 randomly selected farmers of small holder dairy farmsfrom October 2018 to March 2019 in Bhaghabarighat Milk Shed Areas of Bangladesh. Three sets of questionnaire were used to perform the present survey research. Data were collected by direct observation of milking practices, handling of milk and face to face questionnaireinterview was carried out with farmers.

Results: The results of the study showed that all respondents practiced manual milking, with frequency of twice per day.Above half of the respondents (59.52%) did not wash their hands before milking and 41.52% respondents wash their hands only with water.About 67.04% respondents didn't wash udder before milking.100.0% respondents used oil as lubricant. 66.67% and 33.33 dairy farmers had access to pipe water and tube well water supply to their barn, respectively. No farmers practiced post milking teat dipping and used towel for wiping udder after washing.Most of the farmers(97%) provided feed to animal before during and after milking.100% farmers did not store milk in cool room and 78.15% farmers delivered milk within 1-2 hours to Milk Vita.In all the farmers interviewed,most of respondents (88.52%) delivered milk of drug treated cows to Milk Vita. In all the farmers interviewed, respondents' awareness levels of milk-borne zoonoses were 1.8%,5.6%, 17.4% and84.7% for brucellosis, anthrax,tuberculosis and mastitis, respectively. None had knowledge on salmonellosis.

Conclusion: Based on this study, some farmers are adhered to some dairy hygienic practices and there was little awareness about milk borne diseases. Awareness and training programs on milking hygiene and handling for small holder dairy farmers can improve disease control in animals and reduce the public health risk of milk-borne zoonoses.

Key words: Zoonoses, Dairy farmers, Milking hygiene, Awareness, Bangladesh

ID: 19-22: **Pathology of colibacillosis in chickens and molecular characterization of it's pathogen**

Md. Golam Haider*[1] and Turnalisha Chakma[1]

[1]*Bangabandhu Sheikh Mujibur Rahman Agricultural University*

Corresponding author: ghaider@bsmaru.edu.bd

Introduction: Poultry is one of the fastest growing and most promising industries with the brightest of futures for Bangladesh. Poultry sector is playing a vital role in the reduction of poverty, malnutrition and unemployment problems in Bangladesh. Colibacillosis is one of the main causes of morbidity, mortality and high of economic losses in chickens. It is caused by avian pathogenic *Escherichia coli* (*E. coli*) or APEC with worldwide distribution that causes of economic losses in the poultry industry. Due to high economic losses and its zoonotic importance. This study was conducted.

Methods: A total of 50 samples, including swabs from different organs such as liver, intestine, spleen, cloaca, heart etc, were collected from different poultry farms. The histopathological samples were collected in 10% buffered formalin and the swabs samples were collected in nutrient broth. About 20 samples (cloacal swabs) were collected from a local poultry farm from apparently healthy chickens. The used methods were isolation and identification, gross and histopathology, PCR and phylogenetic analysis. PCR was done by targeting 16S rRNA for molecular characterization of *E. coli* and gene sequencing was performed by using 3130 Genetic analyzer. Sequences were analyzed with the program developed by Sequentix Sequence Assembly Software using NCBI Gene bank databases. Randomly two Phylogenetic tree was based on extracted 16S rRNA sequences a comparison of different Enterobacteriaceae with Genebank.

Results: The prevalence rate of *E. coli* was 80% in apparently healthy and dead chickens. The highest prevalence rate of *E. coli* in dead chickens was 86.67% in the intestine and the lowest was 55% in the cloaca. *E. coli* was shown metallic sheen colonies on EMB agar. Grossly, there were seen air sacculitis, coli granuloma and egg peritonitis syndrome. Microscopic lesions of the heart are showed pericarditis which was characterized by thickening of pericardium due to infiltration of RE cells *E. coli* were identified using 27F and 1492R primer and showed 1466 bp products from each field samples after 1% agarose gel electrophoresis. A phylogenetic tree was shown based on the 16S ribosomal RNA sequences extracted from a representative set of *Enterobacteriacea* genomes and developed phylogenetic tree.

Conclusion: Colibacillosis is one of the main causes of morbidity, mortality and high economic losses in poultry industry in Bangladesh. The total prevalence rate was 80% of total 50 samples that were collected both from dead and 20 healthy chickens. The findings of the present study will help veterinarian and public health practitioner as well as researcher for controlling colibacillosis and further higher study.

Key words: Pathology, colibacillosis, characterization, phylogenetic analysis

ID 19-37: **Beneficial effects of probiotic and phytobiotic as growth promoter alternative to antibiotic for safe broiler production**

Md. Faisal Ferdous[1], Md. Shafiul Arefin[1], Md. Moshiur Rahman[1], Md. Mustafijur Rahman Ripon[1], Md. Harunur Rashid[1], Mst. Rokeya Sultana[2], Muhammad Tofazzal Hossain[3], Muslah Uddin Ahammad[4], Kazi Rafiq[1]

[1, 3, 4] Bangladesh Agriculture University [2]University of Rajshahi

Corresponding author: KaziRafiq E-mail: krafiq73@yahoo.com; kazirafiq@bau.edu.bd

Introduction: Drug residues in poultry products could lead to development of antibiotic resistant bacteria as in any living animal and human alike. Extensive use of antibiotics in animals to promote growth rate, increase feed efficiency, and prevent intestinal infections has led to the development of resistant bacteria in the gastrointestinal tract. The present study was conducted to evaluate the effects of biological supplementation of probiotic, phytobiotic, their combination over antibiotic on growth performance, microbial load and hematological parameters in Broiler.

Methods: Sixty-five broiler chicken were divided into 5 groups (12 birds in each group) namely group A (basal diet), group B (antibiotic, Renamycin 100®), group C (phytobiotic, Galibiotic®), group D (probiotic, Bio-Top®), group E (combination, Galibiotic®+Galibiotic®) and five were sacrificed for baseline data on day 0.

Results: Average final live weight gain was highest in group D (probiotic) than other groups. The feed conversion ratio was highest in group A and lowest in probiotic group (group C). Blood samples were collected on 14th and 28th day for hematological studies. The mean hematology values regarding the total erythrocyte count, haemoglobin concentration, packed cell volume, and erythrocyte sedimentation rate differed significantly ($P<0.05$) among groups. The pH of all the treatment groups was significantly decreased compared to control group ($P<0.05$) where group C was significantly ($P<0.05$) lower than all other groups. Highest total viable cell count was observed in control (group A) and total coliform count in phytobiotic (group C) was significantly lower than in other treatment groups ($P<0.05$).

Conclusion: it may conclude that biological supplements have significant positive impact on growth performance, haematological parameters, and gut microbial load in broiler chicken of which the probiotic showing the best effects. Supplementation of probiotic in feed could be one of the best candidates as an alternative to antibiotic as growth promoter for safe broiler production.

Keywords: Probiotic, phytobiotic, alternative to antibiotic, broiler chicken

ID 19-44: **Effect of meteorological factors on the density and distribution of tick vectors in Bangladesh**

Thahsin Farjana and Md. Abdul Alim

Bangladesh Agricultural University

Corresponding author: thahsin.farjana@bau.edu.bd

Introduction: Tick-borne pathogens of zoonotic and veterinary importance namely babesiosis, theileriasis,anaplasmosis and Q-fever are the increasing health burdens in Bangladesh.There is speculation that this is due to climate change affecting tick biology and disease transmission.Due to rising temperature and changing rainfall pattern, climate change is expected to have substantial effects on vector borne infectious diseases in developing countries like Bangladesh. However, this study was designed to determine the effect ofmeteorological factors on the density and distribution of tick vectors and to determine theirseasonal dynamics in Bangladesh.

Methods: Ticks were collected from seven topographic zones ofBangladesh and identified under stereo microscope.Molecular confirmation of tick species was done by polymerase chain reaction (PCR) using published primers.Their density and distribution were calculated using published formula. To study the effects of the seasons, the year was divided into summer, monsoon and winter. Relation of density and distribution of ticks with climatic factors were analyzed with linear regression model.

Results: A total of 4789 ticks were collected, among them five genera of ticks were identified.The identified ticks were *Boophilus*(*Rhipicephalus) microplus, Haemaphysalis sp.,Rhipicephalus sp., Amblyomma sp.* and *Hyalomma sp*. Among them, *B. microplus*was thepredominant species (D=68.9%), followed by other dominant species *Haemaphysalis*(D=29.4%)while *Rhipicephalus*sp. (D=1.4%) was the subdominant, and *Hyalomma*sp. (D=0.3%) and *Amblyomma*sp. (D=0.2%) were the satellite species. Considering the distribution of ticks throughout the country, *Boophilusmicroplus*(C=100%) and *Haemaphysalissp*(C=100%) were the constant species found in every places examined. *Rhipicephaloussp*(C=57.1%) was moderate species; *Amblyomma sp.* (14.2%) &*Hyalomma sp.* (C=14.2%) were sporadic species which were restricted in Hill tract and Barind tract, respectively. During the one year study, the prevalence of ticks was the highest in summer (53.2%) followed by monsoon (27.9%)and were the lowest in winter (18.9%). Ticks had positive relation with temperature, and rainfall, while they had negative relation with humidity.

Conclusion: Resultsof this study will help to predict the future pattern of tick borne disease occurrences in Bangladesh.This information is required to mitigate the effects of climate change, including its potential impact on the burden of tick-borne diseases in Bangladesh and to develop sustainable control measures.

Key words: Temperature, Rainfall, Humidity, Tick, Bangladesh

ID 19-123: **A Serological Survey of Rift Valley Fever and Q fever in sheep of Bangladesh**

Farhana Jummy[1], Shariful Islam[2,3],Tahura Khanam Munmun[1], Josefina Abedin[2,3], Md. Ashiqur Rahman[2,3], Md. Ziaur Rahman[4], Abdul Ahad[5] and Ariful Islam*[3,6]

[1, 5] Chattogram Veterinary and Animal Sciences University, Bangladesh; [2]Institute of Epidemiology, Disease Control and Research (IEDCR); [3]EcoHealth Alliance, New York, USA; [4]icddr,b, Bangladesh; [6]Deakin University, Australia.

Corresponding author: arif@ecohealthallaince.org

Introduction: Rift valley fever (RVF) and Q fever are vector bornezoonotic diseaseaffecting both humans and many animal species, and responsible for high rate of abortion in infected small ruminant. Although globally sheep are often implicated in human for RVF and Q fever outbreaks, the disease remains underestimated in sheep of Bangladesh. In order to fulfil this gap, we conducted a cross sectional study to determine the sero-prevalence of RVF, and Q fever and to identify the potential risk factors associated with their infection in indigenous sheep.

Methods: We collected 199 blood samples from indigenous sheep in Dhaka, Chattogram districts of Bangladesh between 2017 and 2018. Weadministered a pre-tested questionnaire during sample collection. We tested serum samples using competitive enzyme linked immunosorbentassay (c-ELISA) to detect RVF and G fever specific immunoglobulin (IgG).

Results: We found 3.52% (n=7; 95% CI: 01.43-07.11) of sheep had detectable immunoglobulin G for *C. burnetii*. Among studied sheep, only male sheep reared without any vector control measurement were seropositive for *C. brunetii* (n=7; 05.00%; 95% CI: 02.03-10.03).The seroprevalence was higher in adult (n=6; 03.82%; 95% CI: 01.41-08.13), poor body conditioned (n= 5; 03.62%; 95% CI: 01.19-08.25), zero grazing system feed sheep (n=6; 4.00% 95% CI: 01.48-08.50). Anbodies against RVF were not detected in any of the 199 sera tested.

Conclusion: This studyrevealed the evidence of Q fever antibodies in non-descriptive sheep of Bangladesh. Although, data findings do not provide any RFV serological evidence in studied sheep population, the probability of introduction of exotic arbovirus in Bangladesh cannot be ignored and further studies should be continued in livestock and vector population for the risk of emergence newvector borne virus in non-endemic countries.

Key words: Bangladesh, *Coxiella burnetii*, Sero-prevalence, Sheep

ID 19-100: **Entomological survey for identification of Aedes larval breeding sites and their distribution in Chattogram, Bangladesh**

M.S. Rahman, S. Chowdhury, O. Faruk, S. Tanzila, N.M. Sabbir, I.K. Emu, T.S. Ape

E-mail of the corresponding author: sahid.dvm@gmail.com

Introduction: Aedes mosquito is the vector of several viral diseases of public health importance like dengue chikungunya and zika across the tropical region. Mosquito control is the only effective tool for the prevention and control of dengue as there is no antiviral treatment or a well approved vaccine. To control the Aedes mosquito population, studying the characteristics of their habitats is essential as their juveniles (larvae and pupae) have a preference for certain types of containers. A cross-sectional entomological survey was conducted to identify different containers as Aedes larval breeding site in different locations and measure the productivity of each container type during the monsoon season (August and September 2019) in Chattogram city of Bangladesh.

Methods: Total 216 different types of private and government properties from 12 different Thana's under the Chattogram City Corporation (CCC) area (18 properties from each Thana) were randomly visited through this survey. Properties were categorized as independent house, multistoried house, slum, construction site, educational institution, hospital, police station, open place/park and bus stand/garage. The field data is recorded in pre-designed and pre-tested survey forms and then analyzed by using SPSS v25 to calculate the different indices like House index (% of houses infested with immature Aedes), container index (% of containers infested with larvae and or pupae), Pupae index (Number of pupae per 100 households) and breteau index (the number of positive containers per 100 houses) to document the primary breeding source and density of Ae. aegypti as well as predict the threat of dengue transmission.

Results: During this study around 704 wet containers of 37 different types were examined where 52 (7.39%) containers were found positive for Aedes larvae or pupae. Among the wide range of varieties plastic buckets, tires and plastic drums were found as the three most productive container types. About 9.3% of households in the study area were found positive for immature Aedes mosquitoes.

Conclusion: Removal or treatment of the most productive containers and key breeding sites could potentially reduce the mosquito density as well as prevent the dengue outbreak. The result of this study would assist the authorities for the cost effective spatial targeting mosquito control interventions.

Key words: Aedes larvae, dengue, survey, containers, breeding sites

ID: 19-99: **Antimicrobial Resistance in acute Diarrhoeal cases at Bangladesh Institute of Tropical & Infectious Diseases (BITID) from April 2017 to April 2019**

Dr. Md. Mamunur Rashid*, Prof. Dr. M.A. Hassan Chowdhury, Dr. Md. Shakeel Ahmed, Dr. Hasina Nasreen , Dr. Zakir Hossain Habib, Dr. M. Salimuzzaman, Prof. Dr. Meerjady Sabrina Flora.

BITID; Institute of Epidemiology, Disease Control & Research (IEDCR),

**Correspondance e-mail- mamunurdr30@gmail.com*

Introduction: Antimicrobial resistance (AMR) is a growing global public health threat that is imposing serious effects on management of the infectious diseases. There are few studies with data available regarding AMR in Bangladesh. The IEDCR with technical support from US CDC is doing multicenter AMR surveillance. Bangladesh Institute of Tropical & Infectious diseases (BITID) Chattogramis one of the surveillance sites. BITID is a National Institute dealing with infectious diseases, situated in the southern part of Bangladesh. Objective is to find out the status of antimicrobial resistance (AMR) among common bacterial pathogens causing acute diarrhoea.

Methods: Inclusion criteria: Patients attending OPD or hospitalized with acute onset of three or more liquid or loose stool preferably rice watery or less than three liquid or loose stool causing dehydration OR Patients attending OPD or hospitalized with three or more stools with blood and tenesmus with or without dehydration.

Stool samples were taken from diarrhoea patients. All samples were collected from out-patient & in-patient department of BITID. Stool culture was done on SS or XLD, TCBS media. Organisms were finally identified after appropriate biochemical tests & serology by specific antisera. Finally antibiotic susceptibility test was done in Muller Hinton agar media following kirbyBaver disc diffusion Method as per CLS1 M100-S25 guideline.

Results: Among 504 stool samples total 109 (22%) samples were culture positive where male were 64% & female were 45% & predominant age group was (21-30) years. In stool samples *Vibrio Cholerae* was the predominant isolate (50%) followed by *Shigella* species (26%), *Salmonella* (15%) & *E.coli* 9%. In *Vibrio cholerae* isolates higher resistance was observed in *SXT* (96%), Erythromycin (95%), Tetracycline (78%) and higher sensitivity was observed in Azithromycine (85%) Ciprofloxacine (85%). In *Shigella* isolates higher resistance was observed in Ampicillin (57%), Ciprofloxacin (50%) & higher sensitivity was observed in Ceftriaxone (93%) and Azithromycine (68%). In *Salmonella* isolates higher resistance was observed in Ciprofloxacin (81%), Ampicillin (69%), Azithromycin (63%) and higher sensitivity was observed in Cefixime (81%) and Ceftriaxone (75%).

Conclusion: In our study in acute diarrhoeal cases caused by common bacteria resistant drugs were Erythromycin, Tetracycline, SXT, Ampicillin & Ciprofloxacin and sensitive drugs wereAzithromycin, Cefixime, Ciprofloxacin (for cholera cases) & Ceftriaxone. Our results finding were similar to the study published at Regional health forum-Volume 15, number 1, 2011 where resistance to Ampicillin, SXT, & Nalidixic acid was more than 95%. Drugs like Erythromycine, Tetracycline, SXT, Ampicillin & Ciprofloxacin were found as higher resistant drugs in acute diarrhoeal cases (bacterial) in BITID. So sensitive drugs like Azithromycin, Cefixime, Ciprofloxacin (for cholera cases) & Ceftriaxone can beconsidered as appropriate antimicrobials for empirical treatment for acute diarrhoea patients with the absence of culture & sensitivity setting.

Key words: culture, sensitivity, serology, OPD

ID 19-38: **Surveillance and detection of antibiotic residues in poultry meat samples from Trishal upazila of mymensingh**

Sayekul Hasan Khan, Most. Rifat AraFerdous, MufsanaAkterMukta, TasniaTabassum Anika, Md. Rafiqul Islam[1], Kazi Rafiq

Bangladesh Agricultural University [1]BARC, Dhaka.

Corresponding author: KaziRafiq, E-mail: krafiq73@yahoo.com; kazirafiq@bau.edu.bd

Introduction: Poultry plays an important role in bridging the protein gap of animal origin in most countries of the world. Antimicrobials are being widely used in poultry farms for different purposes such as treatment, prevention and control of diseases in Bangladesh. Due to indiscriminate use and unawareness of the withdrawal periods of drugs, the treated birds are known to possess antimicrobial residues in meat. The present study attempts to evaluate the farmer’s perspectives and to examine the antibiotic residues in poultry meats from different farms.

Methods: surveillance was conducted regarding the use of antibiotics at poultry farms located in Trishalupazila of Mymensingh district by using pretested questionnaire among the farmers. Poultry were collected from 45 farms in Trishalupazila and a total of 225 samples (liver, breast muscle, thigh muscle, kidney and spleen; n=45 each) were collected from 45 poultry birds (broiler, sonali and quail; n=45 each). From every farm, one bird sample was collected and owner of the farms were randomly selected for interviewed. TLC method was used for screening of antibiotic residues in poultry tissues.

Results: According to this interview majority of the farmers completed primary education (33.33%) followed by junior secondary (26.67%), secondary (15.56%), higher secondary (8.89%) and graduate level (4.44%). However, 11.11% of them were illiterate. About 66.67% and 11.11% had knowledge about antibiotics residue and withdrawal period, respectively. The Thin Layer Chromatography revealed that out of 225 samples 48.84% samples were found positive for antibiotics residue. In organ, the highest percentage of positive samples was detected in the liver tissue (77.78 %) and the least was in the spleen (0%). In species, the highest percentage of positive samples was detected in the broiler sample (56%) and the least was in the quail sample (41.33%). Among five selected standards, the highest prevalence recorded in doxycycline (23.11%) followed by enrofloxacin (13.78%), ciprofloxacin (11.56%) and others (oxytetracycline and amoxicillin) 0%.

Conclusion: Our result shows that veterinary drugs are misused in poultry sector and farmers do not properly follow indications, instructions as well as the withdrawal periods when broiler are marketed. Therefore, poultry farmer’s knowledge, attitude and practice should be changed regarding the use of antibiotics and care should be taken to minimize the antibiotic residues in poultry products.

Keywords: antibiotic residues, edible tissues, broiler, TLC

ID 19-101: AMR and AMU perspective among physicians and veterinarians: opportunities of implementing ONE Health approach

M.S. Rahman, S. Chowdhury, A. Akbar, M. F. Rinvee

E-mail of the corresponding author: sahid.dvm@gmail.com

Introduction: Antimicrobial Resistance (AMR) is one of the most alarming and emerging threat to human and animal health of this age led majorly by the misuse of antimicrobials (AMs), which creates the necessity of understanding the practitioner's depth of knowledge, meeting essential standards, adherence of guidelines and prescribing fundament of it. AMR is particularly problematic as the discovery and development of novel antibiotics has slowed while the using of antibiotic to treat bacterial infection has increased. Besides, their use in food producing animals is under scrutiny due to the perceived risk from the zoonotic transfer of resistant pathogens. A quantitative research was conducted with a self-administrated constructive questionnaire filled out by both human and vet practitioners working under government and private sectors during the period of July to September 2019 at Chattogram, Bangladesh. The aim of the survey was to assess and compare the practitioners' antimicrobial prescribing behaviours, their attitude towards antimicrobial resistance and indiscriminate use and their concept regarding possible effective solutions.

Methods: Around 200 human practitioners and 100 vet practitioners (as the numbers of vet practitioners are limited) were selected for this study on a basis of common consent. Proportions were calculated for categorical variables and their significance assessed by the Chi square or Fisher's exact test when applicable.

Results: There were common findings like scarcity of the source of information on antibiotic, avoid of any training on antibiotic prescribing in the last year and face difficulties to choose the correct antibiotic in both prescriber groups. Prescriber groups generally regarded too many antibiotic prescriptions, paying too much attention to pharmaceuticals and not talking the full course. Doctors were more likely than veterinarians to seek help from local guideline during prescription. All prescriber groups perceived that education/training in prescribing, local guideline, the availability of resistant data would be 'helpful' or 'very helpful' for effective prescribing Besides Veterinarians also thought that regular auditing and restriction of certain antibiotics would be helpful.

Conclusion: The results have provided the foundation for implementing One Health approach that emphasizes the significant roles of physicians and veterinarians for tackling the crisis through developing interventions to improve antimicrobial use and prevent resistance.

Keywords: Antimicrobial resistance, Antimicrobial use, practitioner's survey, One Health approach

ID 19-17: **Isolation, identification and antimicrobial resistance of *Campylobacter* spp. from the preputial swab samples of bulls**

Md. Jahidul Islam Saddam[1], Nazmul Hoque[1], Md. Rafikuzzaman[1], Md. Mahmudul Hasan Sikder[2], Shinji Yamasaki[3]and **S. M. Lutful Kabir[1]**

[1, 2] Bangladesh Agricultural University [3]Osaka Prefecture University

E-mail of the corresponding author: lkabir79@gmail.com

Introduction: The study was conducted for isolation, identification and characterization of *Campylobacter* species from different bull farms in Mymensingh district during the period of September 2018 to May 2019.

Methods: A total of 150 samples (preputial swab) collected from different bull farms were subjected to *Campylobacter* isolation and identification by using cultural, biochemical and molecular techniques. Furthermore, the isolated bacteria were characterized by antimicrobial susceptibility test by disk diffusion method.

Results: *Campylobacter* like organisms were presumptively identified in 43 samples. Out of 43 positive *Campylobacter* isolates,28 (65.11%) were *C. jejuni* and the rest 15 (34.88%) were predicted as other *Campylobacter* spp. Isolates were biochemically positive to catalase and oxidase tests and in hippurate hydrolysis test, some of the isolates (n=28) develop purple color that indicated the isolates were C. *jejuni* and some of the test isolates (n=15) did not developed purple color. A total of 43 *Campylobacter* isolates gave specific amplification (1530 bp) to 16S rRNA gene based PCR. Out of 43 *Campylobacter* isolates, 28 isolates gave specific amplification (735 bp) to hipO gene based PCR which confirmed these isolates were *C. jejuni*. Antimicrobial susceptibility test was performed to know the susceptibility and resistance patterns of the isolates to different antimicrobial agents. C. *jejuni* were susceptible to gentamicin, streptomycin, ciprofloxacin, and ceftriaxone and resistant to amoxicillin, erythromycin, azithromycin. Furthermore, other *Campylobacter* spp. were susceptible to gentamycin, ciproflaxacin and resistant to amoxicillin and erythromycin. Out of 43 *Campylobacter* isolates, 64.28% *Campylobacter jejuni*and 73.33% other *Campylobacter spp.*were detected as multidrug resistant.

Conclusion: To the best of our knowledge, this study has brought the first report on the occurrence of *Campylobacter species* with their antibiogram profiles in any bull farm of Bangladesh.

Keywords: Bulls, *Campylobacter*, prevalence, characterization, antimicrobial resistance

ID 19-57: **Occurrence of antimicrobial resistance genes amongshiga toxin-producing *Escherichia coli*isolated from sheep in Chittagong, Bangladesh**

Mukta Das Gupta[1], ***Arup Sen***[1], *Avijit Dutta*[1], *Mishuk Saha*[2]*and Ashutosh Das*[2*]

[1, 2] *Chattogram Veterinary and Animal Sciences University*

[*]*Corresponding author: ashutosh.das@cvasu.ac.bd*

Introduction: The principal control method for most of the bacterial diseases in sheep of Bangladesh is the treatment with commonly used antimicrobials. This practice can pose the risk for the development of the resistance against antimicrobials in bacteria as a part of their survival in the host. Sharing the same homesteads for living and rearing of sheep in close human contact might have a higher chance of transmission of zoonotic diseasesfrom sheepto human if sheep is harboring zoonotic pathogens such as shiga toxin-producing *Escherichia coli* (STEC).STEC can cause severe diseases including life-threatening hemolytic uremic syndrome (HUS). Therefore, this study aimed to examine the sheep in rural Bangladesh for the presence of antimicrobial resistant STEC.

Methods: In total, 200 sheep from three upazilasfrom Chittagong district in Bangladesh were sampled from July 2015 to June 2016. Fecal materials originated from the recto-anal junction (RAJ) were screened using both phenotypic methods (cultural methods) and genotypic method (polymerase chain reaction-PCR). Phenotypically positive *E. coli* isolates on culture medium were examined for the presence of any of the two shiga toxin-producing genes – *stx1* and *stx2*. PCR positive STEC isolates were investigated for the presence of antimicrobial resistance genes-, *blaTEM*, *sul,* and *sul2*.

Results: In total, 123of the 200 tested samples were confirmed positive *E. coli* by phenotypic growth in cultured based methods as producers of pink colored colonies in MacConkey agar and metallic sheen colonies Methylene Blue (EMB) agar. PCR for shiga toxin-producing genes revealed 17(13.8%) of the 123 *E. coli* isolates harbored ≥ 1 virulent gene (stx1 and stx2) of STEC.In this study, six of the tested STEC isolates exhibited *blaTEM* gene, eight STEC isolates harbored *sul1*gene and the presence of a *sul2* gene in ten STEC isolates was revealed.

Conclusion: In our knowledge, this study is the first to reveal a significant proportion of STEC isolated from sheep in rural Bangladesh harboring antimicrobial resistance genes. This finding would be useful in advocating any future approach targeting source-mitigation of zoonotic pathogens to protect the public health in rural Bangladesh.

Keywords: antimicrobial resistance*, E. coli*, sheep

ID 19-62: **Virulence determinants and antimicrobial resistance of *E. coli* in house flies (*Muscadomestica*) captured from various environmental settings in Mymensingh, Bangladesh**

Md. AbdusSobur, **Md. Saiful Islam** and Md. Tanvir Rahman*****

Bangladesh Agricultural University

**Corresponding author E-mail: tanvirahman@bau.edu.bd*

Introduction: Antibiotic resistance is one of the greatest threats to the global health.House flies (*Muscadomestica*) have been recognized as a mechanical vector for spreading pathogenic multidrug resistant bacteria. Considering the fact, the present study was carried out to investigate the occurrence of pathogenic *Escherichia coli* associated with house flies, determining their antibiotic resistance pattern and identification of the resistance genes using molecular based approach.

Methods: A total of 300 house flies were collected from areas close to hospitals, food centers around the hospital-adjacent areas, dustbins and dairy farms located in Mymensingh city.Isolation and identification of *E. coli* was performed based on culture and PCR test. Antimicrobial susceptibility testing was conducted using disk diffusion test. Identification of virulence and resistance genes were detected by PCR with published primers.

Results: About 61% flies were found positive for *E. coli* by culture and PCR. The highest prevalence of *E. coli* was recorded in dairy farm (70.67%) followed by food center (65.33%), dustbin (64%) and areas close to hospital (44%). The isolated *E. coli* were also found positive for toxin producing genes *stx1, stx2* and *rfbO157* with a highest recovery from dairy farm (37.73%) environment. Phenotypically, highest resistant was observed against tetracycline (92.35%) followed by erythromycin (91.8%), streptomycin (87.4%), meropenem (78.7%) and ampicillin (61.75%), while lower resistance against gentamycin, ciprofloxacin, imipenem, colistin and chloramphenicol by disk diffusion test. By PCR the prevalence of *tetA, tetB*, *ereA, CITM, SHV, mcr3* and *catA1* were found in 88.75%, 48.52%, 41.67%, 37.17%, 27.77%, 18.37% and 14.81% isolates respectively. None of the isolates were found positive for *aac(6')-Ib-cr, aac (3)-IV* and *aadA1*.

Conclusion: To the best of our knowledge, this is the first study in Bangladesh describing molecular based evidence for the detection of pathogenic multidrug resistant *E. coli* in dairy farm and hospital-adjacent areas that are potential threat for human and animal health which requires a one-health approach to delineate their control.

Keywords: House flies, pathogenic *E. coli,* multidrug resistance, antibiotic resistance genes, environments

ID 19-28: **Assessment of Antibiotic Residues and Bacterial Load in Eggs Collected from Local Markets of Selected Areas of Mymensingh District**

Mufsana Akter Mukta, Most. Rifat Ara Ferdous, Sayekul Hasan Khan, **Tasnia Tabassum Anika,** Md. Rafiqul Islam[1], Kazi Rafiq

Bangladesh Agricultural University [1]BARC

Corresponding author: Kazi Rafiq, E-mail: krafiq73@yahoo.com; kazirafiq@bau.edu.bd

Introduction: Inappropriate use of antibiotics can lead to production of eggs with antibiotic residues. The presence of antibiotic residues in egg causes health hazards to human. This study was designed to detect antibiotic residues in eggs with bacterial load both inner and outer surfaces.

Methods: A questionnaire survey was conducted to understand the farmers' knowledge, attitude and perspective regarding antibiotics residue.A total of 100 egg samples (layer, n=32; deshi, n=32; and duck, n=36) were collected from four different unions of Trishalupzila of Mymensingh district for the detection of selected four antibiotics residue (oxytetracycline, ciprofloxacin, enrofloxacin and amoxicillin) using Thin Layer Chromatography (TLC) as well as exterior & interior bacterial load by Total Viable Count (TVC).

Results: According to the survey, most of the farmers completed secondary level of education (33.33%). About 60% farmers had knowledge about antibiotic residues and only 13.33% farmers were familiar with withdrawal period. Only 26.67% of farmers follow the prescription according to the suggestion of veterinary doctors and remaining 73.33% follow prescription according to feed and medicine seller. The TLC revealed that out of 100 egg samples 29% samples were found positive for antibiotics residue. No enrofloxacin and amoxicillin residues were detected by TLC. Oxytetracycline was the most prominent antibiotic detected (17%) among the four antibiotics followed by ciprofloxacin (12%). Among the four union in Trishalupzila, Balipara union had the highest percentage of antibiotic residues detected (44%) followed by Bailar union (36%). The lowest percentage was detected in Trishal union (16%) followed by Dhanikhola union (20%). The mean of TVC in the egg surface was $82\times10^4\pm60\times10^4$ CFU/g in layer, $62\times10^9\pm56\times10^9$ CFU/g in deshi, and $62\times10^9\pm44\times10^9$ CFU/g in duck egg samples. There was no viable growth in the internal content of egg samples.

Conclusion: These results suggested that antibiotics residue is present in eggs. Measures are needed to ensure public health safety regarding antibiotics use in poultry sector for safe egg production. In addition, bacterial load is present on the egg surface. Therefore, proper hygienic management should be taken before processing of eggs for human consumption.

Keywords: antibiotic residues, TVC, egg, TLC

ID 19-52: **Socio-demographic determinants of use and misuse of antibiotics in commercial poultry farms in Bangladesh**

Syeda Tanjina Tasmim[1], Md. Mehedi Hasan[1], Sudipta Talukder[1], Amit Kumar Mandal[1], Mst. Sonia Parvin[1], Md. Yamin Ali[1], Md. Amimul Ehsan[1]and Md. Taohidul Islam[1*]

[1]*Bangladesh Agricultural University, Mymensingh-2202, Bangladesh.*

[*]*Corresponding author: Prof. Dr. Md. Taohidul Islam; Email address: taohid@bau.edu.bd*

Introduction: Antimicrobial resistance (AMR) has been identified as one of the major threats to global health, food security and development today. While there has been considerable attention about the use and misuse of antibiotics amongst human populations in both research and policy environments, there is no definitive estimate of the extent of misuse of antibiotics in the veterinary sector and its contribution to AMR in humans.This survey was conducted to point out some of the socio-demographic factors, practices, gaps in understanding and misconceptions about use of antibiotics among the commercial broiler and layer farmers with to assess poultry farmer’s knowledge and practices regarding antibiotics, antibiotic use and antimicrobial resistance and to identify the factors that influence the misuse of antibiotics in commercial poultry.

Methods: A qualitative survey of 70 farmers was conducted in Gazipur, Mymensingh and Kishoreganj districts during March to May 2019. Data were collected using structured questionnaire through face to face interview. Bi-variate and multivariable logistic regression model were used to identify factors associated with inappropriate use of antibiotic.

Results: Demographic analysis revealed that 47.1% farmers were unable to explain about antibiotic, 54.3% used antibiotic from the first day of a batch, 14.3% went to veterinarian to take primary treatment, 42.9% used antibiotic for preventive purpose, 4.3% used antibiotic as growth promoter, 25.7% used antibiotic suggested by veterinarian, 42.9% farmers used left-over antibiotics, 51.4% didn’t complete the antibiotic course, 35.7% didn’t maintain withdrawal period, 99% farmers had no knowledge about AMR, 80% had no contact with veterinary surgeon. In bi-variate regression analysis, two variables were significantly associated with the inappropriate use of antibiotics while only one ‘no contact with veterinary surgeon’ was identified as the potential risk factor in multi-variable regression analysis.

Conclusion: The findings of this survey point to the urgent need to improve understanding about antibiotics and antibiotic resistance among the poultry farmers, particularly marginal commercial poultry farmers.

Keywords: AMR, Antibiotic misuse, Poultry, Qualitative research, Socio-demographic determinants

ID 19-61: **Prescribing antibioticdrugs for Bangladeshi patients: evidence from a scoping review**

Samiun Nazrin Bente Kamal Tune[1*], Nahitun Naher[1], Syed Masud Ahmed[1]

[1]*BRAC University*

[*]*Correspondence: samiun.tune@gmail.com*

Introduction: Irrational and excess use of antibiotics is common in many low and middle income countries, Bangladesh is no exception. Prescribing behaviour is important as the variation in service providers practice explains the difference in expenditure in the health sector and patient experiences also differs with practice variations.

Methods: A scoping review was conducted to identify antibiotics prescribing patterns of healthcare providers in Bangladesh, its usage by patients and morbidity profile for which antibiotics are prescribed. Usingkey searchterms 'prescription survey', 'prescribing antibiotics', 'pharmaceutical promotion', 'antibiotic resistance', 'use of antibiotics', 'Bangladesh' documents were searched in Google Scholar and PubMed. ThirteenPeer-reviewed English journal articles published between Jan. 2009 and Aug. 2019 were selected and reviewed using template developed for data extraction and analysis.

Results: Data were collected from the patients who visited drug shops (5),out-patient and in-patient departmentsofpublic (7) and private hospitals (2) and doctor's chamber (1). Prescriptions were provided either by formal (physicians) or informal (unqualified/semi-qualified) providers. Antibiotics were most frequently prescribed for common cold, fever, diarrhea, gonorrhea, cesarean-section complications, typhoid and infections of respiratory, urinarytract, ear, nose, throat, commonly prescribed antibiotic groups were cephalosporins,quinolones and penicillins in drug shops and ceftriaxone,cefixime and azithromycin in public hospitals.Two or more antibiotics were prescribed frequentlyby both formal and informal providers. Majority of the antibiotics were prescribed without any laboratory tests before starting of therapy. Studies done in privatehospitals or drug shops have no findings on cost of antibiotics.One study in public hospital reported patients who received antibiotics paid on average BDT 105.90 more than the group not received an antibiotic.24.5% of patientin one study complained of not getting free antibiotics from hospital. A nationwide survey revealed that the cost varied from 7% to 20% of weekly income of the extreme poor for treating different diseases with antibiotics.

Conclusion: Prescribers' irrationalprescribing behavior on antibiotics is evident in both formal and informal settings which indicates the need of adherence to awareness and regulation.

Key Words: Prescription survey, prescribing antibiotic, rational drug use, antibiotic use, Bangladesh

ID 19-82: **Prevalence of ESBL-producing multi-drug resistant *E. coli*, *Salmonella* and *P. multocida* in buffalo calves at Sylhet and Barisal division of Bangladesh**

PranthoMalakar Dipta[1], Juned Ahmed[1], Shampa DebNath[1], TaslimaAkter[1], IffatAra[1], MahfuzRahman Adnan[1], Asmaul Husna[1], Mohammad Al Mamun[1], NahidArjuman Banu[1], Bashu Deb Paul[2], Abu Hena Mustafa Kamal[1], Mohammad Rafiqul Islam[3]and Md. Masudur Rahman[1*]

[1, 2] Sylhet Agricultural University [3]Bangladesh Agricultural Research Council

**Corresponding author: rahmanmm.dpp@sau.ac.bd, mmrahman.sau@gmail.com*

Introduction: Antimicrobial resistance has become a matter of concern for both human and animals. Moreover, food-producing animals have become a growing reservoir of antibiotic resistantzoonotic bacteria. Therefore, the study was conducted to determine the antibiotic resistance profiles of*E. coli, Salmonella* and *P. multocida*isolated from buffalo calves at Sylhet and Barishal divisions of Bangladesh.

Methods: A total of 300 fecal (for *E. coli* and *Salmonella*) and 300 nasal swab (for *P. multocida*) samples were collected randomly from buffalo calvesduring the period from March 2018 to February 2019. Isolation and identification of *E. coli, Salmonella,* and *P. multocida* were performed by using cultural, morphological and biochemical tests. Antimicrobial resistance properties and ESBL positivity of those bacteria were determined by disk diffusion method according to CLSI and CDC guidelines respectively.

Results: Among 300 fecal and 300 nasal swab samples, prevalence of *E. coli*, *Salmonella* and *P. multocida* were found as 52.66%, 17.33% and 7.66%, respectively. *E. coli* isolates showed the highest resistance to amoxicillin (92.40%) followed by ampicillin (78.47%) and erythromycin (71.52%). On the other hand, 100% of *E. coli* isolates were sensitive to colistin. Similarly, in case of *Salmonella,* the highest resistance was observed to amoxicillin (88.46%) and all of the isolates (100%) were found sensitive to gentamycin, levofloxacin and colistin. Furthermore, *P. multocida*were found 100% resistant to amoxicillin and ampicillin and 100% sensitive to colistin. The overall prevalence of multi-drug resistant *E. coli, Salmonella* and *P. multocida*were 53.79%, 34.62% and 52.17%, respectively. Among the isolates, ESBL producing *E. coli, Salmonella* and *P. multocida* were 13.92%, 5.77% and 13.04% respectively.

Conclusion: The results of the current study demonstrated a broad scenario of the presence of antibiotic resistant zoonotic bacteria like *E. coli, Salmonella* and *P. multocida*in buffalo calves which might act as a possible source of transferring resistance genes to other pathogens.

Key words: Bacteria, Antibiotic resistance, Buffalo calves, Bangladesh

ID 19-135: **Isolation and characterization of bacteria causing pneumonia and establishment of treatment protocol in pneumonic goats brought to S A Quaderi Teaching Veterinary Hospital (SAQTVH), CVASU**

Shanta Barua and Mohammed Y.E Chowdhury Chattogram Veterinary and Animal Sciences University, Chattogram 4225. E-mail of the corresponding author: shantabarua007@gmail.com

Introduction: Goats are fairly susceptible to the bacterial pneumonia due to exposure of physical stress in unfavorable environmental conditions. Bacteria including Pasteurella multocida, Escherichia coli, Staphylococcus aureus, Streptococcus pneumoniae, Klebsiella pneumoniae etc are the main causes of pneumonia and antimicrobial agents like penicillin, oxytetracyclin, amoxicillin, ampicillin, cephalosporin, ciprofloxacin and sulphonamides are commonly using to combat them. However, due to indiscriminate use, these agents are losing their ability to stop growing or killing of bacteria. Moreover, resistance of antibiotic consequences the prolongation of treatment and delayed the responses against diseases. As a result, farmer suffers a lot, subsequently; resistant organisms are becoming more resistant and human get resistance to the antibiotics due to transmission of resistant organism in human body from environment and food animal. Furthermore, no comprehensive research has been done yet regarding organisms and their antibiotic resistance pattern from pneumonic goats in Bangladesh. Therefore, present study is undertaken to isolate and identify pneumonia causing organisms and to determine their resistance profile against antibiotics for establishment of treatment protocol in pneumonic goats.

Methods: Nasal swab samples (20 among 150 samples) were collected from the pneumonic goats brought to SAQTVH, CVASU. Samples were transferred into buffered peptone pre-enriched broth medium and culture were inoculated in blood agar, mannitol salt agar, Mac conkey agar, Eosin methylene blue (EMB) agar for the isolation of different bacteria. Bacteria were confirmed by Gram's staining, cultural properties, biochemical tests and by multiplex PCR techniques. Antibiotic resistance of bacterial isolates will be performed using CS test against 10 commonly used antimicrobial agents in SAQTVH.

Results and Conclusion: Among samples (n=150), 20 were tested till now and 4 were confirmed as Staphylococcus aureus and 2 were as Escheria coli. Remaining samples are under investigation to detect organisms and their antimicrobial resistance pattern. This study will give the baseline information of organisms and their resistance profile against antibiotics using to treat bacterial pneumonia which might be necessary to take proper measures and set treatment protocol against pneumonia in goats.

Keywords: Pneumonia, goats, bacteria, antimicrobial agents, SAQTVH

ID 19-50: **Antimicrobial resistance pattern of foodborne bacteria in wholesale chicken markets in Bangladesh**

Mst. Sonia Parvin[1], Amit Kumar Mandal[1], Md. Yamin Ali[1], Md. Tanvir Rahman[2], Md. Taohidul Islam[1*]

[1, 2] *Bangladesh Agricultural University*

**Corresponding author: Prof. Dr. Md. Taohidul Islam; E-mail: taohid@bau.edu.bd*

Introduction: Antimicrobial resistance among foodborne bacteria is a well-known public health problem. A cross-sectional sink survey was conducted to determine the prevalence, and antimicrobial resistance pattern (AMR) of foodborne bacteria (*E. coli*, *Salmonella* spp. and *Staphylococcus aureus*) in cloacal swab and sewage samples from wholesale chicken markets in Bangladesh.

Methods: A total of 55 samples, comprising cloacal swabs (n = 50) of broiler chickens and sewage (n = 5), were collected from 5 wholesale chicken markets of Dhaka district in Bangladesh. Isolation and identification of bacteria were done based on cultural, staining, biochemical properties and PCR assay. Isolates were subjected to AST, and resistance genes were determined by mPCR. ESBL-producing bacteria and MRSA were screened by double-disk synergy test and cefoxitin disk diffusion test, respectively.

Results: The prevalence of ESBL-*E. coli* was higher (97.7% vs 100%) in cloacal swab and sewage samples, respectively than ESBL-*Salmonella* (76.3% vs 33.3%). In addition, the prevalence of MRSA was 47.2% in cloacal swab, however, none of the isolates from sewage samples were positive for MRSA. For *E. coli*, highest resistance was observed against pefloxacin (88.6% vs 100%), ampicillin (86.4% vs 80%) and trimethoprim-sulfamethoxazole (81.8% vs 100%) in cloacal swab and sewage samples, respectively. Moreover, 90% of *E. coli* exhibited multidrug resistance (MDR), of which 93.2% isolates were from cloacal swab and 60.0% from sewage. All the isolates of *Salmonella* were MDR, and highest resistance (84-100%) was observed against doxycycline, polymyxin B, colistin, nalidixic acid, and pefloxacin with no significant difference in resistance pattern between cloacal swab and sewage samples. In case of *S. aureus*, highest resistance was found in nalidixic acid (94.4% vs 75%), oxacillin (88.9% vs 50%), gatifloxacin (83.3% vs 50%), and cefoxitin (80.6% vs 50%), and 97.4% and 100% isolates showed MDR in cloacal swab and sewage, respectively. Screening of ESBL-encoding genes revealed that all isolates of *E. coli* and *Salmonella* spp. were positive for *bla*TEM gene. However, no isolates were positive for *bla*SHV, *bla*CTX-M-1 and *bla*CTX-M-2 genes. In case of fluoroquinolones encoding genes in *E. coli* isolates, 10.2% were positive for *qnr*A and 67.3% were *qnr*S among both samples. For *Salmonella* spp., only one isolate was positive for *qnr*S. In both *E. coli* and *Salmonella* spp., *qnr*B was not found in any type of samples. For *S. aureus*, the prevalence of *MecA* gene was 17 (47.2%) and 1 (20.0%), respectively in cloacal swab and sewage samples.

Conclusion: The results of our study highlight the need for rapid implementation of an integrated program for surveillance of antimicrobial resistance in order to monitor trends, raise awareness, and help promote practices to safeguard later generation antimicrobial agents.

Keywords: Foodborne bacteria, antimicrobial resistance, resistance genes, wholesale chicken markets, Bangladesh

ID 19-53: **Multi-drug resistant and extended spectrum β-lactamasesproducing *Salmonella* spp. in red meat of cattle**

Md. Yamin Ali[1], Mst. Sonia Parvin[1], Sudipta Talukder[1], Md. Mehedi Hasan[1],Md. Tanvir Rahman[2] and Md. Taohidul Islam[1*]

[1, 2] Bangladesh Agricultural University, Mymensingh-2202.

**Corresponding author e-mail:taohid@bau.edu.bd*

Introduction: Globally, MDR and extended spectrum β-lactamases producing (ESBL)*Salmonella*is highly risk resulting foodborne illness associated with meat products reported widely in human and animals. We estimated the prevalence, resistance pattern and ESBL producing *Salmonella* spp.in beefcollected from butcher shopfromten districts of five divisions in Bangladesh.

Methods: During July, 2018 to September, 2019, a total of 240 samples aseptically collected and tested using standard bacteriological methods like colony characteristics, staining, biochemical reaction and sugar tests. Antimicrobial susceptibility test was performed using Kirby-Bauer disc diffusion test using 20 antibiotics of 9 classes and ESBL producing *Salmonella* were screening by double disc synergistic test.

Results: Theoverall prevalence of *Salmonella* spp. was 40% (96/240)of which 40.9% were ESBL producing. Moreover, 37(38.5%) of the isolates were MDR and exhibited resistant to oxytetracyclin (85.5%), polymyxin B(80.2%), colistinsulphate(79.2%) and imipenem (56.3%). The highest classes of antibiotic resistant weredetected 77.1%in polymyxin,74% in tetracyclineand 36.5 %in sulfonamides. All isolates exhibited resistant to seven or more potential antimicrobial like colistinsulphate(79.2%), polymyxinB (80.2%), imipenem (56.3%),oxytetracyclin (85.5%) nalidixic acid (32.3%) and gentamicin(16.7%).

Conclusion: The emergence of MDR and ESBL producing *Salmonella*in beef of butcher shop may constitute a public health concern, adequate cooking and reinforce good hygiene practice of butcher shop to avoid cross-contamination. Further,serotyping and resistance gene identification is strongly recommended.

Keywords: Drug resistant, ESBL producing*Salmonella*spp, antibiotics, resistance gene

ID 19-05: **Irrational use of antibiotics and risk of bacterial resistance among Bangladeshi population: A Scoping Review**

Samiun Nazrin Bente Kamal Tune[1], Shabnam Mostari[2]

[1]BRAC University [2]Access to Information (a2i)

Introduction: Antibiotic resistance (ABR) is a pivotal public health concern worldwide. It became a life-threatening problem in several developing countries including Bangladesh due to poor healthcare services, and irrational use of antibiotics. This scoping review aimed to identify the current picture of using antibiotic, its resistance pattern among the Bangladeshi population and intersectoral engagement in mitigating the ABR.

Methods: Google Scholar and PubMed, these two search engines were used to identify the relevant articles conducted in Bangladesh regarding the use of antibiotics and ABR. Only peer-reviewed articles were included in this scoping review. We selected 32 articles published between July 2009 to July 2019 in English language. Search strategy focused on following key terms: antibiotic/antimicrobial resistance, use/misuse/overuse/irrational use of antibiotic, intersectoral engagement/involvement, Bangladesh.

Results: Most of the studies were conducted in Dhaka city, however, very few studies took place in other parts of Bangladesh. Antibiotics were mostly prescribed due to acute respiratory tract infections, gastrointestinal disorders, acute watery diarrhea, and severe trauma. Amoxycillin, Ceftriaxone, Cefiximeand were identified as the topmost prescribed antibiotics. Most of the articles did not mention the source of bacterial infection (facility/community). Disk diffusion method was executed for antimicrobial susceptibility test and data interpretation was performed using the Clinical and Laboratory Standards Institute (CLSI) guidelines in the majority of the studies. High prevalence of antibiotic resistance was notified in most of the tested pathogens, and various commonly used first-line drugs were mostly ineffective. Several studies showed that E. coli was resistant to the commonly used antibiotics such as amoxicillin, ampicillin, azithromycin, ceftriaxone, ciprofloxacin, and levofloxacin. This scoping review did not find any article comprised the role of intersectoral involvement for mitigating the ABR.

Conclusion: Our scoping review revealed that the use of antibiotics and the risk of ABR is increasing over time. Both Bangladesh government, development partners including non-governmental organizations (NGOs) should take initiative to reduce the irrational use of antibiotics through designing policy, implementing intervention and counseling program for community people to make them cognizant about the risk of ABR to reduce the overall burden. Hence, intersectoral engagement is important.

Key Words: Antibiotic resistance, antibiotic use, antibiotic overuse, intersectoral engagement, Bangladesh

ID 19-29: **Screening of Antibiotics Residue in Broiler and Layer Meat in Mymensingh of Bangladesh**

Tania Sultana, Md. Tarikul Islam, Md. Rafiqul Islam[1], KaziRafiq

Bangladesh Agricultural University [1]BARC

**Corresponding author: KaziRafiq, E-mail: krafiq73@yahoo.com; kazirafiq@bau.edu.bd*

Introduction: The present study was designed to evaluate the farmer's perspectives and to detect the antibiotic residues in poultry meats from different farms of mymensinghUpazilla.

Methods: Surveillance study was conducted regarding the use of antibiotic and it residues in poultry meatto poultry farmersofMymensinghSadarby using pretested questionnaire. Poultry were collected from fifteen farms in MymensinghSadar and a total of 180 samples were collected from 45 poultry. From every farm, nine poultry samples were collected from three different species (broiler, layer, deshi) and owners of the farms were randomly selected for interviewed. TLC method was used for screening of doxycycline, colistin, tylosin, ciprofloxacin, and enrofloxacin residues in poultry tissues.

Results: According to this survey, 27% farmers cross primary education level, 33% farmers had secondary educationlevel and 40% reached level of higher education. About 60%, 67% and 67% had knowledge about biosecurity, withdrawal period and residue of antibiotic, respectively. Only 27% of farmers follow prescription according to the suggestion of veterinary doctors and 73% follow prescription according to feed and medicine seller. In this study, out of 180 samples 41.11%samples were found positive for antibiotics residue. In organ, the highest percentage of positive samples was detected in the liver tissue (75.55 %) and the least was in the spleen (0%). In species, the highest percentage of positive samples was detected in the broiler sample (53.33%) and the least was in the deshi sample (25%). Among five selected standards, the highest prevalence recorded in doxycycline (17.22%), then enrofloxacin (3.88%) and others (tylosin, ciprofloxacin, colistin) 0%.

Conclusions: Veterinary drugs are misused in poultry sector of Bangladesh, and farmers do not follow indications and instructions as well as the withdrawal periods when poultry are marketed. Therefore, poultry farmer's knowledge, attitude and practice should be changed regarding the use of antibiotics and care should be taken to minimize the antibiotic residues in poultry products.

Keywords: antibiotic residues, broiler, layer, deshi, thin layer chromatography

ID 19-60: **Isolation and molecular characterization of multi-drug resistant *Salmonella typhimurium* DT104 from selected dairy farm environments at Mymensingh**

*ShaykaTasnim Pritha, **Sadia Afrin Punom,** SaifurRahman, Dr. K.H.M. Nazmul Hossain Nazir, Dr. Md.Shafiqul Islam**

E-mail of the corresponding author: dvm39867@bau.edu.bd

Introduction: *The Salmonella typhimurium* DT104 is an emerging cause of human illness has received an increasing attention due to its multidrug properties. Since it has been isolated from humans and other sources including food-producing animals around the world; it has become a worldwide public health concern. It was first demonstrated a typical pattern of penta-resistance to ampicillin, chloramphenicol, streptomycin, sulfonamide, and tetracycline (ACSSuT). The present study was designed to isolate, identify and study the antibiogram profile of multidrug resistant *Salmonella typhimurium*DT104 from different dairy farms in Mymensingh district, Bangladesh.

Methods: A total of 135 samples from dairy farms were collected aseptically among which 39(28.88%) samples showed positive results for *Salmonella* spp. in cultural, staining and PCR with*invA*genus specific primer and 6 (15.38%) out of 39 isolates were detected as *Salmonella typhimurium* DT104 in species specific *Salmonella typhimurium DT104* primer. Isolated *Salmonella* were subjected to antibiotic sensitivity test by disc diffusion assay using 10 commercially available antibiotics.

Results and Conclusion: The antibiotic resistance patterns of the dairy farm isolates were 100% to Erythromycin followed by Tetracycline (73.68%), Colistin (89.47%), Ampicillin (47.36%), Gentamycin (21.05%), Ciprofloxacine (31.57%), Streptomycin (42.10%), Enrofloxacine (10.52%) and Chlormphenicol (31.57%). About 23.07% isolates were resistant to more than 5 antibiotics. All the isolates were 100% sensitive to Amikacin. It can be concluded that the presence of *Salmonella typhimurium*DT104 to animal is very alarming. It can impose great threat to public health. Public awareness about proper hygiene, sanitation and multidrug resistance should be improved at farm level as well as national level to combat such threat.

Keywords: *Salmonella typhimurium*DT104, Cattle, PCR, Antibiogram

ID 19-114: **Assessment of pet bird husbandry practices and antimicrobial resistant patterns of Escherichia *coli* and *Staphylococcus* spp. isolated from Budgerigar (*Melopsittacus undulatus*) bird of Chattogram, Bangladesh**

Md. Saddam Hossain[1*], Ariful Islam[2,3], Kohei Makita[4], Shariful Islam[2,3], Kaisar Rahman[2,3], Aftabuddin Rumi[5], Md Helal Uddin[5], Abu Sayeed[5], Chandan Nath[5],Jonathan H. Epstein[2] and Mohammad Mahmudul Hassan[5]

*[1, 5] Chittagong Veterinary and Animal Sciences University [2]EcoHealth Alliance, NY; [3]Institute of Epidemiology Disease Control and Research (IEDCR); [4]Rakuno Gakuen University, Japan. *Corresponding author E-mail: drsaddamcvasu@gmail.com*

Introduction: In Bangladesh, at least 20 species of pet birds are reared, and the Budgerigar bird is the most common among them. Antimicrobial resistance (AMR) is a significant public health issue for pet bird owners, but little is known about the risks for infection. Thus, this study aimed to characterize the pet bird rearing practices and to determine the epidemiology of antibiotic resistance patterns of *E. coli* and *Staphylococcus* spp. isolated from Budgerigar bird in Chattogram, Bangladesh.

Methods: From December 2016 to June 2017, we collected cloacal swabs from 220 budgerigars and interviewed 49 pet bird owners using a pretested questionnaire regarding pet bird husbandry practices and disease ecology at the farm level. We tested swab samples using standard bacteriological tests for isolation and identification andperformed antibiogramwithdisc diffusion method for nine commercially available antibiotics.

Results: The prevalence of *E. coli* and *Staphylococcus* spp. were recorded as 22.3% (n=49) and 18.2% (n=40), respectively. All E. *coli* isolates were 100% resistant against amoxicillin, sulfomethoxazol, trimethoprim, and cefixime, however only 6.1% isolates were resistant to ciprofloxacin. Moreover, enrofloxacin and gentamycin were 100% *Staphylococcus* spp. isolates, and 5% of isolates were resistant to ciprofloxacin and azithromycin.Poor body condition score ($p \leq 0.04$) and use of tap water ($p \leq 0.03$) were associated with higher AMR level of *E. coli* in budgerigar. In case of AMR patterns of *Staphylococcus* spp. young bird ($p \leq 0.003$) and diseased bird ($p \leq 0.001$) were found as significant variables.

Conclusion: This study demonstratesmultidrug resistantin E. *coli* and *Staphylococcus* spp. isolated from the Budgerigar bird thatmay acquire at some point their rearing practices and indiscriminate use of antibiotics.Further research is recommended to determine the role of education of pet owners in altering higher risk pet practices and indiscriminate use of antibiotics on pet birds.

Key words: Pet birds Antimicrobial, Epidemiology, Resistant, and Bacteria

ID 19-07: **Carriage of coagulase positive methicillin-resistant *Staphylococcus aureus* and *Staphylococcus pseudintermedius* among dogs at teaching veterinary hospital in Bangladesh**

Eaftekhar Ahmed Rana, Md. Zohorul Islam, AvijitDutta,Tridip Das, Abdul Ahad, Paritosh Kumar Biswas, HimelBarua

Chattogram veterinary and Animal Sciences University

E-mail of the corresponding author: eaftekhar787@gmail.com

Introduction: The emergence of methicillin-resistant *Staphylococcus aureus*(MRSA) and *Staphylococcus pseudintermedius* (MRSP) have a significant health impact on occupational peoples and pet owners. As there is a lack of knowledge on the carriage frequency of these two organisms in dogs in Bangladesh, we conducted a cross-sectional study to determine the prevalence and risk factor (s) of *S. aureus, S. pseudintermedius,* MRSA*,* and MRSP in clinically healthy and sick dogs.

Methods: A total of 358 swab samples were collected from different body sites of 150 dogs admitted to a university teaching hospital through January to July 2018. Standard bacteriological methods were followed for the isolation and identification of *S. aureus*and *S. pseudintermedius*and, which was further confirmedby the presence of the *nuc* and *pse*genes, respectively. The isolates were tested for the susceptibility to a panel of 14 antimicrobials. Isolates displayed resistance to cefoxitin and oxacillin were screened further for the presence of the *mecA* gene to identify MRSA and MRSP. The risk factors were investigated using multivariable logistic regression model.

Results: The prevalence of *S. aureus* and *S. psudintermedius* in dogs were 16% (95% confidence interval (CI), 11-23%) and 49% (95% CI, 41-57%), respectively. Notably, all staphylococcal isolates showed resistance to ≥3 classes of antimicrobials (multi-drug resistant; MDR). The prevalence of MRSA and MRSP was 8.67% (95% CI, 5.02 to 14.38) and 6% (95% CI, 3.04 to 11.16), respectively. Dogs with dermatitis (odds ratio [OR], 12.24; 95% CI, 3.12 to 57.33; P <0.001) and with the history of antibiotic use (OR 8.73; 95% CI, 2.23 to 43.10; P <0.001) more frequently carried MRSA while the presence of otitis (OR 14.22; 95% CI, 1.64 to 103.58; P <0.008) and oral lesions (OR 9.48; 95% CI, 1.14 to 64.82; P<0.002) were identified as the significant risk factors for the carriage of MRSP in dogs.

Conclusion: The detection of chromosome mediated *mec-A* gene within the *S. aureus*and *S. pseudintermedius*isolates from dogs is an emerging finding in veterinary hospital as well as significant concern for human medicine.

Key words: MRSA, MRSP, Carriage, Dogs, Bangladesh

ID 19-109: **Antimicrobial usage and resistance on commercial chicken farms in Chattogram, Bangladesh**

M Foysal[1*], *SB Das*[1], *T Imam*[1], *J Gibson*[2], *G Fournie*[3], *J Henning*[2]and *MA Hoque*[1]

[1]*Chattogram Veterinary and Animal Sciences University, Bangladesh,* [2]*University of Queensland, Australia and* [3]*The Royal Veterinary College, UK.*

E-mail: faisalcvasu108@gmail.com (corresponding and presenting author)*[1]

Introduction: Increased antimicrobial resistance is a global threat for animal and human health.Thisstudy aimed to assessthe usage of antimicrobials in commercial chicken farms, and the prevalence of resistance to commonly used antimicrobials in*Escherichia coli* and *Salmonella*spp.

Methods: A total of 140 poultry farms were selected from eight upazilas (sub-districts) of Chattogram. One pool of cloacal swabs (from 5 birds) and one pool of environmental swabs (5 sites) per farm were collected. Epidemiological dataonfarm characteristics, husbandry practices andantimicrobial usagewere obtained through a structured questionnaire containing closed and open ended questions and physical inspection.*Escherichia coli* and *Salmonella* spp. were isolatedand antimicrobial susceptibility testing was performed by disc diffusion for 12 antimicrobials of veterinary and/or human health importance.

Results: The farm level prevalence of *Escherichia coli* and *Salmonella*spp.were 60.7% (95%CI: 52.5-68.9%) and 42.9% (95%CI: 34.6-51.2%) according to cloacal swab evaluation and58.6% (95%CI: 50.3-66.8%)and 47.9% (95%CI: 39.5-56.2%) according to environmental swab evaluation,respectively.Theprevalence of both bacteria was comparablein layerandbroiler farms:86% and 77.1% (p=0.192)for *E.coli*, 63.2% and 63.9% (p=0.933) for *Salmonella*spp., respectively.A wide range of antimicrobials were used in surveyed farms, for therapeutic (16.4%), prophylactic (22.2%) or both (61.4%) purposes. While 90.7% of farms used "**Access**" groupantimicrobials (amoxicillin, ampicillin, cephalexin, oxytetracyclineetc.), antimicrobials from the "**Watch**" group (azithromycin, ciprofloxacin, enrofloxacin, erythromycin etc.) and the "**Reserve**" group(colistin and fosfomycin)were used by 62.9% and 60.7% of farms, respectively. The proportion of farms for which isolated *E. coli*strains wereresistant to amoxicillin, ampicillin, erythromycin and cephalexin reached 100%. This proportion was 98.4% forpefloxacin; 95.1% for trimethoprim and sulfamethoxazole; 92.6% fordoxycycline; 71.3% forazithromycin; 54.9% forneomycin; 41.8% forgentamicin and 4.1% forcolistin. Resistance profile of *Salmonella*spp.was 100% to amoxicillin, ampicillin, doxycycline, cephalexin, pefloxacinanderythromycin, 87.5% to azithromycin,75% to trimethoprim and sulfamethoxazole and 50% to neomycin, 37.5% to gentamicin and 12.5% to colistin.

Conclusion: Ourresults suggest that the prevalence of *E. coli* and *Salmonella*spp.is high in chicken farms in Chattogram. "Watch" and "Reserve" group of antimicrobialsare used extensively andthe level of antimicrobialresistance in *E.coli* and *Salmonella*spp.is extremely high for commonly used antimicrobials, reaching 100% for several of them.

Keywords: Poultry pathogens, Antimicrobials, Poultry farms, Chattogram, Bangladesh

List of Reviewers

(in alphabetical order)

Name of the Reviewer	Institution
A.S.M. Lutful Kabir	BAU
Abul Kalam Azad	USAID
Ahsanul haque Rukan	CVASU
Aminur Rahman	BSMRAU
Ashraful Islam Khan	icddrb
Emdadul Haque Chowdhury	BAU
Iqbal Ansary Khan	IEDCR
Kazi Munisul Islam	icddrb
KBM Saiful Islam	SAU
M Salimuzzaman	IEDCR
Masudur Rahman	SAU
Md Ziaur Rahman	icddrb
Md. Nure Alam Siddiky	BLRI
Minara Khatun	BAU
Mohammad Atikuzzaman	SAU
Mohammed A Samad	BLRI
Mukter Hossain	SAU
Nadia Ali Rimi	icddrb
Nazmul H. Nazir	BAU
Paritosh Kumar Biswas	CVASU
Shadiuzzaman	BAU
Shahneaz Ali Khan	CVASU
Sharmin Sultana	IEDCR
Syed Abul Hasan Md Abdullah	DGMS
T A B M Muzaffar GoniOsmani	DLS
Tanvir Rahman	BAU
Zakir Hossain Habib	IEDCR
Zobaidul Hoque Khan	EPHF

Name of the Reviewer	Instituition
Abu Hannan	DLS
Ahmed Nawsher Alam	IEDCR
AMAM Zonaed Siddiki	CVASU
Ariful Islam	EcoHealth Alliance
ASM Alamgir	IEDCR
Himel Barua	CVASU
Jahidul Kabir	BFD
Kazi Rafiqul Islam	BAU
Khorshed Alam Bhuiyan	BSMRAU
Mahmudur Rahman	icddrb
Md Bashir Uddin	SAU
Md. Giasuddin	BLRI
Meerjady Sabrina Flora	IEDCR
Mizanur Rahman	CVASU
Mohammad Mahmudul Hasan Milad	CVASU
Mostafa Anwar	PSTU
Mushtuq Hossain	Consultant
Nasrin Sultana Juyena	BAU
Nitish Debnath	CVASU
Rafiqul Islam	BARC
Shahana Begum	SAU
Sharmin Chowdhury	CVASU
Suman Paul	SAU
Syed Sayeem Uddin Ahmed	SAU
Tahmina Shirin	IEDCR
Taohidul Islam	BAU
Ziaur Rahim	icddrb