



9th One Health Bangladesh Conference

Achieving Sustainable Development Goals (SDGs) through One Health
Approach

ABSTRACT BOOK

17-18 September 2017

Dhaka, Bangladesh

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Preface

One Health Bangladesh has been organizing Annual Conference since its inception in 2007. This year the organization is going to organize 9th Annual Conference and the theme of the conference is “Achieving Sustainable Development Goals through One Health Approach.” The purpose of the conference is to analyze the current situation, identify the challenges and explore the possible solutions of One Health practices to support achieving sustainable development goals (SDG).

The imprint of decade long One Health movement is clearly visible in Bangladesh. The country has made tangible progress in institutionalization of One Health platforms, improving the surveillance and response system for emerging infectious diseases (EIDs) and zoonoses across the sectors, One Health workforce development, food safety and security , etc. One Health, Bangladesh has played a role of catalyst in achieving the success.

Bangladesh has been showcased for outstanding performance in achieving the targets of Millennium Development Goals (MDGs) particularly in reducing poverty, improving health and ensuring food security. Now, the United Nations has adopted Sustainable Development Goals (SDGs) otherwise known as the Global Goals, are a universal call to action to end poverty, protect the planet and ensure that all people enjoy peace and prosperity. The SDGs work in the spirit of partnership and pragmatism to make the right choices now to improve life, in a sustainable way, for future generations.

The spirit of partnership clearly align with the core principle of One Health movement and One Health Bangladesh has been working for a thriving ecosystem for the better health of human, animal and environment. The call for ending poverty and protecting planet for ensuring peace and prosperity cannot be achieved without coherent action from the partners at animal, human, ecosystems interface. The One Health approach is essential for achieving the Sustainable Development Goals. Emphasizing on it, One Health Bangladesh has selected “Achieving Sustainable Development Goals through One Health Approach.” The conference has sessions on emerging infectious diseases and zoonosis, food safety and food Security, antimicrobial resistance, One Health governance, advocacy, communication and policy. About 45 papers and 60 posters will be presented from the selected abstracts and eminent scientist and professionals will present thematic papers in the conference.

The conference findings will help the country to devise action and take appropriate steps to prevent and control EIDs and zoonoses, ensure food safety and security , containment of anti-microbial resistance, better coordination and partnership among One Health actors and improve ecosystem which will eventually help to achieve sustainable goals for the peace and prosperity of mankind.

The abstract book contains abstracts of oral, poster and key note speeches. 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. Special thanks for the members of scientific 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 making the conference a success.

Nitish C Debnath

Senior Technical Advisor, Food and Agricultural Organization of the UN and Chair , Conference Organizing Committee

Meerjady Sabrina Flora

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

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17-18 September 2017

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Select Chair and Co-Chair, time keeper for the paper- presentation session
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- Organize and print abstracts
- Organize presentation date and time

1) Dr. IqbalAnsary Khan, IEDCR	Convener
2) Dr. Ahmad Raihan Sharif, IEDCR	Jt Convener
3) Dr. Mujadded Ahmed, IEDCR	Member
4) Dr. AHM Saiful Islam Khan , DLS	Member
5) Dr. Quazi Ahmed Zaki, IEDCR	Member
6) Dr. SamsadRabbany Khan, IEDCR	Member
7) Dr. Sajib Kumar Hazari, IEDCR	Member
8) Dr. KaziSelim Anwar, IEDCR	Member
9) Dr. Shahenur Islam, DLS	Member
10) Dr. Shariful Islam, EcoHealth Alliance	Member
11) MahbubulAlam, IT Consultant, IEDCR	Member

Responsibility:

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

1) Prof Dr. Be- Nazir Ahmed, NIPSOM	Convener
2) Dr. M SalimUzzaman, IEDCR	Jt Convener
3) Dr. Md. MehediHossain, Director, DLS	Member
4) Dr. AbulKhair, Deputy Director, DLS	Member
5) Dr. ASM Alamgir, IEDCR	Member
6) Dr. ZakirHossainHabib, IEDCR	Member
7) Dr. AninditaShabnamQuarishi, IEDCR	Member
8) Dr. Huzzattullah, DLS	Member
9) Dr. GolamAzamChowdhury , DLS	Member
10) Dr. MdNurul Islam, IEDCR	Member
11) Stephanie Doan, USCDC	Member
12) Dr. Ariful Islam, Eco Health Alliance	Member

Responsibility:

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

1) Professor Dr. SanyaTahmina, Director, CDC, DGHS	Convener
2) Dr. M Mushtuq Husain, IEDCR	Jt. Convener
3) NehaKapil, Unicef	Member
4) Dr. NawsherAlom, IEDCR	Member
5) AMAM ZonaedSiddiki, CVASU	Member
6) Dr. NazneenAkter	member
7) Dr. Mohammad Mahmudul Hassan, CVASU	Member
8) Dr. Ayesha Siddika , DLS	Member
9) Dr. Sushmita, EHA/ IEDCR	Member
10) Dr. KaziMunisul Islam, IEDCR	Member
11) Dr. Mohammed Asaduzzaman, icddrb	Member
12) Md. AbulKalam, P&R	Member
13) Dr. MdNurul Islam, IEDCR	Member
14) Dr. Omar FaruqLiton, LRI	Member

Responsibility:

- Communicating with all OH Members and participants to keep them updated
- Advertisement on print and electronic media
- Co-opt member(s) as and when required



9th One Health Bangladesh Conference

17-18 September 2017



Program Schedule

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

Day 1 17 September 2017 Sunday

08:00 - 09:00 Conference Kit Distribution

Morning Session (09:00 – 12:00)

Emerging Infectious Diseases & Zoonosis-1

Co-Chairs: **M A Faiz**, Professor Medicine & Former Director General of Health Services

Md Rafiqul Islam, Professor Pathology, Bangladesh Agricultural University

Rapporteurs: Mallic Masum Billah

Anindita Quraishi

TABM Muzaffor Goni Osmani

09:00 – 09:20 **Thematic paper**

BALZAC – An Interdisciplinary Project for Developing Interventions Reducing Avian Influenza Transmission in Bangladesh’s Poultry Trade Network

Dirk U Pfeiffer, Chair Professor of One Health, City University of Hong Kong

09:20 – 09:25 Questions & Answers

09:25 – 09:32 Screening of Avian Influenza Virus in Dhaka and Chittagong Live Bird Markets, Bangladesh

Paritosh K Biswas, Mohammed Giasuddin, Younjung Kim, Md Ahasanul Hoque, Mahmudul Hasan, Rashed Mahmud, Guillaume Fournié, Nitish C Debnath, Dirk Pfeiffer

09:32 – 09:39 Association Between Biosecurity Measures and Environmental Contamination with Avian Influenza Viruses in Live Bird Markets, Bangladesh

Sukanta Chowdhury, Eduardo Azziz-Baumgartner, Susan C Trock, Ahasanul Hoque, Nord Zeidner, Ziaur Rahman, SM Nazrul Islam, Enayet Hossain, Syed Sayeem Uddin Ahmed, Katharine Sturm-Ramirez, Erin D Kennedy, and Emily S Gurley

- 09:39 – 09:46 Recent H9N2 Avian Influenza Viruses Revealed Genetic Evolution of the Virus in Bangladesh
Rokshana Parvin, JA Begum, TW Vahlenkamp, EH Chowdhury and MR Islam
- 09:46 – 09:53 Initial Results of the Cross-sectional Survey of Live Bird Market Hygiene and Respiratory Contamination among Live Bird Market Workers in Bangladesh
Mahbubur Rahman, Punam Mangtani, Jacqueline M Cardwell, Mahmudur Rahman, Md Ahasanul Hoque, ASM Alamgir, M Salimuzzaman, A K M Muraduzzaman, **Sudipta Sarkar**, Md Abdus Samad, Md Giasuddin, Guillaume Fournie, Nitish Chandra Debnath, Dirk U Pfeiffer, Meerjady Sabrina Flora
- 09:53 – 10:00 Outbreak Investigation of Avian Influenza in a Turkey Farm at Northern Dhaka and Trace of Possible Human Contacts
Kazi Munisul Islam, Mohammad Nurul Islam, Md Golam Azam Chowdhury Tulu, Ariful Islam, ASM Alamgir, Meerjady Sabrina Flora
- 10:00 – 10:07 One Health Investigation of a Crow Mortality Event Linked to Potential Circulation of Highly Pathogenic Avian Influenza Virus at Live Bird Markets in Bangladesh
Ariful Islam, Shariful Islam, Md Kaiser Rahman, Md Ziaur Rahman, Mohammad A Samad, Mallick Masum Billah, Mohammed Enayet Hossain, Mahbubur Rahman, Md Rezaul Karim, Md Golam Azam Chawdhury, Mehedi Hossain, NC Debnath, ASM Alamgir, Emily Hagan, Melinda K Rostal, Md Giasuddin, Jonathan H Epstein and Meerjady Sabrina Flora
- 10:07 – 10:30 Questions & Answers
- 10:30 – 10:45 Tea Break

Day 1: Noon Session (10:45 – 12:00)

Emerging Infectious Diseases & Zoonosis-2

Co-Chairs:	Firdausi Qadri , Emeritus Scientist and Acting Senior Director (IDD), icddr,b Micheal S Friedman , Country Director Bangladesh, US CDC
Rapporteurs:	Shusmita Dutta Choudhury Manjur Hossain Khan Mohammad Nizam Uddin Chowdhury
10:45 – 11:05	Thematic Paper Making the Case for Integrating Risk Communication and Community Engagement into Routine Public Health Programs: Lessons Learned from Ebola, Zika and Measles Outbreaks Mario Mosquera-Vasquez , UNICEF
11:05 – 11:10	Questions & Answers
11:10 – 11:17	Epidemiological Investigation and Molecular Characterization of <i>Bacillus anthracis</i> from Soils in Selected Districts of Bangladesh Maidul Islam, Md Shahjahan Ali Sarker, Md Shahab Uddin, Jafrul Hasan Ripon, ShuryaKhanam, TaslimaAkterShapna, Md Muket Mahmud and KHM Nazmul Hussain Nazir
11:17 – 11:24	Isolation and Molecular Detection of Brucella spp. in Bovine Milk from Some Selected Areas of Bangladesh Md Samiul Bashir , Minara Khatun, Md Ariful Islam
11:24 – 11:31	Evaluation of Hospital Based Surveillance for Japanese Encephalitis in Bangladesh, 2007 to 2015 Nusrat Sharmin Popy , S Sharmin, Hossain MS Sazzad, Kishor K Paul, S Chai, AR Sharif, M Rahman, Meerjady Sabrina Flora, Erin D Kennedy, ES Gurley
11:31 – 11:38	Sero-prevalence and Determinants of Q Fever in Dairy Cattle Moumita Das , Sharmin Akhter, Suman Paul
11:38 – 11:45	Anthrax Outbreak Investigation in Pabna and Sirajganj, 2017 Mallick Masum Billah , M Salimuzzaman, Faisol Talukder, Meerjady Sabrina Flora
11:45 – 12:00	Questions & Answers
12:00 – 12:55	Lunch Break, prayer & poster session

Inauguration Ceremony

13:00 – 15:00

Master of the Ceremony: Tanzila Naureen and Zahirul Islam

12:55	Guest taking seats
13:00 – 13:05	Welcome address by Prof Dr Meerjady Sabrina Flora , Director, Institute of Epidemiology, Disease Control & Research (IEDCR) & Chairperson, One Health Secretariat of Bangladesh
13:05 – 13:15	Key Note Presentation: <i>Achieving Sustainable Development Goals through One Health Approach</i> by Prof Nitish C Debnath , Senior Technical Adviser, FAO Bangladesh & Coordinator, One Health Bangladesh
13:15 – 13:20	Address by Mr Joel Reifman , Charge d' Affairs & Deputy Chief of Mission, Embassy of United States of America in Bangladesh
13:20 – 13:25	Address by Guest of Honour Dr N Paranietharan , WHO Representative in Bangladesh
13:25 – 13:30	Address by Guest of Honour Mr Edouard Beigbeder , UNICEF Representative in Bangladesh
13:30 – 13:35	Address by Guest of Honour Ms Sue Lautze , FAO Representative in Bangladesh
13:35 – 13:40	Address by Guest of Honour, Mr Mohammed Shafiul Alam Chowdhury , Chief Conservator of Forest
13:40 – 13:45	Address by Guest of Honour Mr Sayed Arif Azad , Director General, Department of Fisheries
13:45 – 13:50	Address by Guest of Honour Dr Md Ainul Haque , Director General, Department of Livestock Services
13:50 – 13:55	Address by Guest of Honour Kbd Md Golam Maruf , Director General, Department of Agricultural Extension
13:55 – 14:00	Address by Guest of Honour Mr Md Nazmul Islam , Additional Secretary PPC Wing, Ministry of Agriculture
14:00 – 14:10	Address by Special Guest Mr Abdullah Al Islam Jakob MP , Hon'ble Deputy Minister, Ministry of Environment and Forest
14:10-14:20	Address by Special Guest Mr Narayon Chandra Chanda MP , Hon'ble State Minister, Ministry of Fisheries and Livestock
14:20-14:35	Address by Chief Guest Mr Mohammed Nasim MP , Hon'ble Minister, Ministry of Health & Family Welfare
14:35 – 14:45	Address by Chairperson, Prof Dr Abul Kalam Azad , Director General of Health Services, Ministry of Health & Family Welfare

Day 1: Afternoon Session (15:00 - 16:30)

Antimicrobial Resistance and Its containment -1

Co-Chairs:	<p>Md Mustafizur Rahman, Director General Drug Administration</p> <p>Eric Brum, Team Lead, ECTAD FAO Bangladesh</p> <p>Mehedi Hossain, Director (Extension) DLS</p>
Rapporteurs:	<p>Ahmed Nawsher Alam</p> <p>Md Abdus Samad</p> <p>Nazmun Nahar</p>
15:00 – 15:20	<p>Thematic Paper:</p> <p>Containment of Antimicrobial Resistance: Potential Crossroads of One Health in Bangladesh</p> <p>Md Sayedur Rahman, Professor Pharmacology, Bangabandhu Sheikh Mujib Medical University, Bangladesh</p>
15:20 – 15:25	<p>Questions & Answers</p>
15:25 – 15:32	<p>Prevalence of Multi-drug Resistant ESBL- Producing <i>Escherichia coli</i> Isolated from Broiler Chicken at Sylhet Division of Bangladesh</p> <p>Md Masudur Rahman, Md Sadikul Islam, Nazmin Sultana Runa, Sabina Yesmin, Asmaul Husna, Nurjahan Yesmin Runa , Mahfuz Rahman Adnan, Md Mahabub E-Elahi</p>
15:32 – 15:39	<p>Epidemiology of Antimicrobial Resistance of Salmonella and Staphylococcus Isolated from Free-ranging Rhesus macaque (<i>Macaca mulatta</i>) in Bangladesh</p> <p>Md Kaiser Rahman, Ariful Islam, Mohammed A Samad, Shariful Islam, Md Helal Uddin, Aftabuddin Rumi, Md Shahjalal Sagor, Muhammad Sazzad Hossain, Md. Rezaul Karim, Melinda K Rostal, Emily Hagan, Mohammad Mahmudul Hassan, Meerjady Sabrina Flora and Jonathan H Epstein</p>
15:39 – 15:46	<p>Occurrence and Anti-biogram of <i>shiga</i> Toxin-producing <i>Escherichia coli</i> in Domestic Buffaloes of Bangladesh</p> <p>Mukta Das Gupta, Arup Sen and Ashutosh Das</p>
15:46 – 15:53	<p>An Investigation of Plasmid-mediated Colistin Resistance Gene, MCR in <i>Escherichia coli</i> of Human, Veterinary and Environmental Origin</p> <p>Avijit Dutta, Avijit Das, Sabuj Manohar Sarma, Himel Barua, Mohammad Shah Jalal, Sanjoy Kanti Biswas, Paritosh Kumar Biswas</p>

- 15:53 – 16:00 Epidemiological Assessment of Anti-microbial Residues in Poultry and Fish in Chittagong, Bangladesh
Jinnat Ferdous, Shafayat Zamil, SKM Azizul Islam, Alyson Bradshaw, Rubyath Binte Hasan, Ariful Islam and Md Ahasanul Hoque
- 16:00 – 16:07 Prevalence of Multi-drug Resistant Genes and Virulence Factors in *Enterococcus faecalis* Isolated from Poultry in Bangladesh
Mohammed A Samad, **Md S Sagor**, Md R Karim, Muhammad S Hossain, Md Giasuddin, Fahrin A Khan
- 16:07 – 16:20 Questions & Answers
- 16:20 – 17:30 Evening Tea Break & Cultural Program

---End of 1st Day Sessions ---

Day 2	18 September 2017 Monday
08:00 - 08:30	Conference Kit Distribution (Rest)
Morning Session (08:30 – 10:30)	
One Health Governance, Advocacy, Communication & Policy	
Co-Chairs:	Mahmudur Rahman , Former Director IEDCR and Joint Coordinator One Health Bangladesh Neha Kapil , Chief (C4D), UNICEF
Rapporteurs:	AKM Muraduzzaman ASMA Hannan Mohammad Sohel Samad
08:30 – 08:50	Thematic Paper One Health Journey in Bangladesh: from Advocacy to Action Meerjady Sabrina Flora , Director IEDCR
08:50 – 09:10	Thematic Paper A community Owned One Health Surveillance System Preventing Pandemics with Animal Origins Letrak Srikitjakarn , Faculty of Veterinary Medicine, Chiang Mai University, Thailand
09:10 – 09:20	Questions & Answers
09:20 – 09:27	Embracing the One Health Paradigm to Increasing Awareness, Prevention & Control of Zoonoses in Bangladesh K B M Saiful Islam , Raju Ahmed, Md Anwarul Hoque Beg, Md Mufazzal Hossain, Nazrul Islam
09:27 – 09:34	One Health Institute at CVASU: Creating Opportunities for Interdisciplinary Education, Research and Policy Dialogue to Resolve One Health Issues A M A M Zonaed Siddiki , MA Hoque, and NC Debnath
09:34 – 09:41	Improving Competencies of the Veterinary Workforce to Strengthen Public Health and Food Security in Bangladesh Nitish C Debnath , Mehedi Hossain, Kamrun Nahar, Sawkat Anwar, Eric Brum
09:41 – 09:48	Prioritizing Zoonotic Diseases: Going Forward with One-Health Approach in Bangladesh 2017 Rabeya Sultana , M Salim uzzaman, Md Abul Kalam, ASMA Hannan, Meerjady Sabrina Flora
09:48 – 10:00	Questions and Answers
10:00 – 10:30	Tea Break

Day 2: Noon Session (10:30 – 11:44)

Food Safety and Security

Co-Chairs:	Shah Monir Hossain , Former DG Health Edwin Salvador , Deputy WHO Representative to Bangladesh
Rapporteurs:	Josefina Abedin Ahmad Raihan Sharif Samsad Rabbani Khan
10:30 – 10:50	Thematic Paper Nutrition and Food Security: What does the future hold for us? Tahmeed Ahmed , Senior Director, Nutrition & Clinical Services, icddr,b
10:50 – 10:55	Questions and Answers
10:55 – 11:02	Arsenic Mitigation in Rice (BRRI-28) through Association of an Aquatic Fern <i>Marsilea minuta</i> L. Ummehani Hassi , Md Tawhid Hossain, Monira Begum and Dr SM Imamul Huq
11:02 – 11:09	Use of Untreated Poultry Waste in Agricultural Farms Causes Microbial Contamination of Vegetables Manasi Modak, Mohammed Nooruzzaman, Sukesh Chandra Badhy, Md Saidur Rahman, Mohammad Rafiqul Islam, Emdadul Haque Chowdhury
11:09 – 11:16	Effects of Food Borne <i>Mycotoxins</i> on Toll Like Receptor Mohammad Rafiqul Islam , Bumseok Kim
11:16 – 11:23	Characterization of <i>Staphylococcus aureus</i> From Milk and Dairy Products Sold in Some Local Markets of Mymensingh District of Bangladesh Zobayda Farzana , Sukumar Saha
11:23 – 11:30	Use of Detoxified Sulphur as a Feed Supplement for Methane Mitigation of Ruminant Ashraf A Biswas , Sung Suk Lee
11:30 – 11:37	Devil in the Milk: Relevant Genetic Makeup of Cattle in Bangladesh Jahangir Alam , Nusrat Jahan, Mridha Md Kamal Hossain, Sayeeda Monira Rahman, Shohel Mahmud, Md Ariful Islam, Md Abdul Alim, Md Humayun Kabir, Salma Akter, Md Salimullah
11:37 – 11:45	Questions and Answers

Day 2: Second noon Session (11:45– 12:50)

Ecosystem Health & Conservation-1

- Co-Chairs:** **Sanya Tahmina**, Director Disease Control, Line Director CDC
Md Shahidul Islam, Ex-Director Dept Agriculture Extension
- Rapporteurs:** Rabeya Sultana
 Kazi Munisul Islam
 Md Taufiqul Islam
- 11:45 – 12:05 **Thematic Paper**
City Slickers: the reality of an urban ecosystem
Paul Reiter, Professor of Medical Entomology at the Pasteur Institute in Paris, France
- 12:05 – 12:10 Questions & Answers
- 12:10 – 12:17 Infection Dynamics and Viral Diversity in Bats Influence Nipah virus Encephalitis Outbreaks in Bangladesh
 Jonathan H Epstein, **Ariful Islam**, Simon J Anthony, A Marm Kilpatrick, Shahneaz Ali Khan, Noam Ross, Ina Smith, Carlos Zambrana-Torrel, Ausraful Islam, Kevin J Olival, Emily S Gurley, M Jahangir Hossein, Thomas Briese, Mahmudur Rahman, Gary Cramer, Lin-Fa Wang, Stephen P Luby, W Ian Lipkin, and Peter Daszak
- 12:17 –12:24 Antimicrobial Resistance Pattern of *Salmonella Spp.* Isolated from Resident Wild Birds and Environment of Bangladesh
Mohammad Mahmudul Hassan, Mahabub Alam, Abdullah Al Faruq, Md. Ahaduzzaman, Ariful Islam
- 12:24 – 12:31 Poultry Farm Biosecurity and Bioexclusion: Poultry Delivery Practices between Farmers and Traders in Chittagong, Bangladesh
Md Harun Rashid, ErlingHøg, Guillaume Fournié, Rashed Mahmud, Md Yeasin Haider Chowdhury, Md Ashiqur Rahman, Md Sadeque Abdullah Dirk U Pfeiffer and Md Ahasanul Hoque
- 12:31 – 12:38 Save Life from Slow Death Trap: Case of Environmental Health of Bangladesh
M Aminul Islam
- 12:38 – 12:45 Emergence of Multidrug Resistant *Enterococcus* in Free Range Wildlife in Bangladesh
Mohammed A Samad, Ariful Islam, Md Shahjalal Sagor, Muhammad Sazzad Hossain, Md Rezaul Karim, Md Helal Uddin, Md Kaisar Rahman, Fahria A Khan, Md Jahidul Kabir, Melinda K Rostal, Emily Hagan, Meerjady Sabrina Flora, Md Giasuddin, Jonathan H Epstein

12:45 - 13:00	Questions and Answers
13:00 – 13:30	Poster Session
13:30 – 14:15	Lunch and Prayer

Day 2: Afternoon Session (14:15-15:15)

Ecosystem Health and Conservation-2

Co-Chairs:	Jahidul Kabir , CF, Wildlife & Nature Conservation Circle Paritosh K Biswas , CVASU
Rapporteurs:	Zakir Hossain Habib Quazi Ahmed Zaki Anupam Sarker
14:15 – 14:35	Thematic paper The Global Virome Diversity: The <i>Beginning of the End of the Pandemic Era</i> Leticia Gutiérrez Jiménez , Field Veterinarian – Disease Ecologist, EcoHealth Alliance
14:35 – 14:45	Questions & Answers
14:45 – 14:52	Diversity of Gastrointestinal Parasite in Rhesus Macaque (<i>Macaca mulatta</i>) in Human-wild Life Ecosystem in Bangladesh Shariful Islam , Md Kaiser Rahman, Md Helal Uddin, Md Mustafizur Rahman, Mohammad Nizam Uddin Chowdhury, Mohammad Mahmudul Hassan, Meerjady Sabrina Flora and Ariful Islam
14:52 – 14:59	Determining Hotspots of Human Exposure to Rodents, Bats and Monkeys in Bangladesh Ireen Sultana Shanta , Stephen P Luby, Kamal Hossain, Syed Sayeem Uddin Ahmed, Taifur Rahman, Erin Kennedy, Yushuf Sharker, A Marm Kilpatrick, JRC Pulliam, Emily S Gurley
14:59 – 15:06	Assessing Viral Diversity in Peridomestic Small Mammals, Bangladesh Ariful Islam, Mohammed Ziaur Rahman , Mohammad Enayet Hossain, Melinda K Rostal, Simon J Anthony Emily Hagan, Ausraful Islam, NajmulHaider, Peter Daszak, and Jonathan H Epstein
15:06 – 15:13	Nesting Ecology and Biomorphometry of Yellow-wattled Lapwing (<i>Vanellus malabaricus</i>) Nearby a Protected area at Gazipur District in Bangladesh Abu Nasar Md Aminoor Rahman and Ziban Chandra Das
15:13 – 15:20	Questions and Answers
15:20	Wrap-up
15:20 – 15:30	Afternoon Tea

Annual General Meeting (15:30 – 17:00)

Participants: All life and General Member of One Health Bangladesh

Conference Key Note Speech

Achieving Sustainable Development Goals through One Health Approach

Nitish C Debnath

Senior Technical Advisor, FAO Bangladesh and National Coordinator, One Health Bangladesh.

In order to transform our world, the 2030 agenda for sustainable development agreed by almost all nations of the world, was adopted by the UN General Assembly in September 2015. A set of 17 goals is backed by 169 targets and all are interconnected and to be achieved by 2030 which will result in transformation. The relationship between health and wellbeing and sustainable development is that health can be a contributor, a beneficiary and vehicle to measure success in achieving sustainable development. In recent years, global public health security has been threatened by the emergence of new diseases those mostly originated in animals living in the barn or house or in the wild. Concurrently, endemic zoonoses continue as a health and economic burden particularly for the socially and economically disadvantaged populations. Continued emergence of resistant pathogens to antimicrobials has made the world population more vulnerable to infections and science based prediction of 10 million deaths per annum by 2050 is extremely disturbing. The unprecedented growth of food production, processing and supply with inadequate control systems in place has put consumer's health at an insurmountable risk. Accelerating climatic disruption, land degradation, growing water scarcity, fisheries degradation, pollution, and biodiversity loss have already begun to negatively impact health of all species. These health concerns underpin the need for further cohesive actions and partnership among sectors and disciplines. The post-2015 development agenda provides a unique opportunity to advance One Health concept by making integrated approach to improving human health, animal health and environmental health. The world community while embodying the SDGs dreams for a world without hunger and poverty that will ensure health, wellbeing and quality education. The world will also strive for reducing the existing gender and other inequalities and develop a thriving ecosystem caring the life on the land and below water and provide the global population safe water, good sanitation and clean energy by building strong institutions for securing peace and justice. The SDG also targets for decent work, promote innovations, responsible consumption and production. Building partnership is the central to the SDGs which clearly aligns with the core principle of One Health.

Thematic Paper: Emerging Infectious Diseases & Zoonosis-1

BALZAC – An Interdisciplinary Project for Developing Interventions Reducing Avian Influenza Transmission in Bangladesh's Poultry Trade Network

Dirk U Pfeiffer^{1,2}, Guillaume Fournié¹, Ahasanul Hoque³, Erling Hoeg⁴, Tony Barnett⁴, Paritosh Biswas³, Mohammad Giasuddin⁵, Natalie Moyaen¹, Chris Desmond⁶, Kaushik Chattopadhyay⁷, Suman Gupta⁸, David Harper⁷, David Heymann⁷, Mahmudul Hasan⁵, Mehedi Hossain⁹, Rashed Mahmud³, Mahbubur Rahman¹, Marianne Carson¹, Sudipta Sarkar¹⁰, Joerg Henning⁸, Punam Mangtani⁴, MeerjadyFlora¹⁰, Mahmudur Rahman¹⁰, Nitish C Debnath¹¹

¹Royal Veterinary College, London, UK; ²City University, Hong Kong; ³Chittagong Veterinary and Animal Science University, Chittagong, Bangladesh; ⁴London School of Hygiene and Tropical Medicine, London, UK; ⁵Bangladesh Livestock Research Institute, Savar, Bangladesh; ⁶Human Sciences Research Council, Pretoria, South Africa; ⁷Chatham House, London, UK; ⁸University of Queensland, Australia; ⁹Department of Livestock Services, Bangladesh; ¹⁰Institute of Epidemiology, Disease Control and Research, Dhaka, Bangladesh; ¹¹FAO, Dhaka, Bangladesh

Several strains of avian influenza viruses (AIVs), including H5N1 and H9N2, are endemic in Bangladesh, with poultry trade being a major transmission route. The BALZAC project aims to develop interventions for reducing the risk of AIV spread and persistence within the poultry trade network. An interdisciplinary approach has been adopted, combining epidemiological and ethnographic surveys, virology and mathematical modelling. Interviews of 2500 poultry production stakeholders allowed the mapping of poultry trade networks supplying Dhaka and Chittagong, the two main urban centres of the country, and the identification of socio-economic, cultural and epidemiological factors shaping them. Demand and availability of poultry greatly varies according to poultry breeds and species, resulting in different trading patterns. Poultry origin and market destination patterns change daily and there is a high level of mixing between birds of different geographical origins along their respective value chains. Through live bird markets, these transaction chains together result in a highly connected poultry trade network, within which poultry of all breeds, species and geographical origins are mixed. During an outbreak, economic risks faced by farmers mean that local reconfiguration of these networks is likely to further promote AIV spread. Moreover, decreasing levels of biosecurity along the value chains promote viral contamination of markets. This was confirmed by virological surveys conducted in markets in Dhaka and Chittagong. AIV bird-level prevalence in marketed poultry were more than 10-times as high as in farms supplying those markets. Conditions have thus been created for epidemiological interactions between different farming systems and distant poultry populations, and amplification of the viral circulation along the live poultry trade network. Interventions targeted at specific markets will now be developed that aimed at reducing the viral load in the entire network.

Keywords: Avian influenza; network; market; value chain

Oral Presentation: Emerging Infectious Diseases & Zoonosis-1**Screening of Avian Influenza Virus in Dhaka and Chittagong Live Bird Markets, Bangladesh**

Paritosh K. Biswas¹, Mohammed Giasuddin², Younjung Kim³, Md. Ahasanul Hoque⁴, Mahmudul Hasan², Rashed Mahmud⁴, Guillaume Fournié³, Nitish C Debnath⁵, Dirk Pfeiffer³

¹Department of Microbiology and Veterinary Public Health, Chittagong Veterinary and Animal Sciences University (CVASU), Chittagong, Bangladesh, ²Bangladesh Livestock Research Institute (BLRI), Dhaka, Bangladesh, ³ Department of Pathobiology and Populations Sciences, Royal Veterinary College, London, UK, ⁴Department of Medicine and Surgery, CVASU, Chittagong, Bangladesh, ⁵FAO ECTAD Bangladesh, Farmgate, Dhaka, Bangladesh

A cross-sectional survey was undertaken to assess the extent of circulation of avian influenza virus (AIV) subtypes H5 and H9 in live bird markets (LBMs) in Dhaka and Chittagong, Bangladesh. In total, 40 LBMs were randomly selected, 26 in Dhaka and 14 in Chittagong. In each LBM, oropharyngeal and cloacal samples were collected from 60 birds - broiler, Sonali, desi chickens and waterfowls. We also sampled 50 environmental sites, from poultry stalls and slaughtering areas. Samples were screened at first for the presence of the M gene of AIV by real-time reverse transcription polymerase chain reaction (rRT-PCR). Those which tested positive were further screened for the presence of H5 and H9 genes. Bayesian hierarchical regression models with different combinations of swab- and market-level variables were developed. The results revealed that 64% (95% Confidence Interval: 39%-84%) and 93% (66%-100%) LBMs in Chittagong were positive for AIV H5 and H9, respectively. In Dhaka, market-level prevalence reached 88% (70%-97%) and 100% (95%CI: 85%-100%) for AIV H5 and H9. Irrespective of location discrimination, the prevalence estimates for AIV H5 vs.H9 were 0.8% (0.3%-1.7%) vs. 10% (7.8%-12.7%) for broilers, 1.3% (0.6%-2.6%) vs.7.4% (5.3%-10%) for Sonali, 1.3% (0.6%-2.5%) vs. 8.2%(6%-10.8%) for desi, and 7.8% (5.1%-11.3%) vs. 4% (2.2%-6.7%) for waterfowls. According to the best fitted model, AIV H5 prevalence was significantly higher in retail in than in wholesale markets, and AIV H9 prevalence increased with the number of poultry sold. Sequencing of some representative isolates of subtype H5 and H9 obtained from the survey is underway to assess their genetic relatedness and evolution over time in the country. In conclusion, the findings of this study showed different levels of AIV prevalence between cities, markets and poultry types.

Association Between Biosecurity Measures and Environmental Contamination with Avian Influenza Viruses in Live Bird Markets, Bangladesh

Sukanta Chowdhury¹, Eduardo Azziz-Baumgartner², Susan C. Trock², Ahasanul Hoque³, Nord Zeidner^{1,2}, Ziaur Rahman¹, S.M. Nazrul Islam⁴, Enayet Hossain¹, Syed Sayeem Uddin Ahmed¹, Katharine Sturm-Ramirez^{1,2}, Erin D. Kennedy^{1,2} and Emily S. Gurley¹

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Live bird market (LBM) environments can be contaminated with avian influenza (AI) viruses. To determine if certain biosecurity practices could mitigate AI contamination in LBM settings in Bangladesh, during March 2015 we enrolled 10 randomly selected shops from each of 80 LBMs. We collected information about biosecurity practices and a pooled environmental specimen from each shop. Samples testing positive for AI viral RNA were subtyped for H5 using rRT-PCR. We performed a multivariable logistic regression analysis using a backward stepwise procedure to measure the association between biosecurity practices and environmental contamination with AI using prevalence ratios (PR). Samples from 205 (26%) of the 800 shops were positive for AI viral RNA; 60 (8%) were positive for H5 RNA. Shops that slaughtered poultry (PR 1.8, CI: 1.2-2.5) and/or those that did not sell all of their poultry every business day (PR 1.5, CI: 1.2-1.7) were more likely to harbour detectable AI RNA. Daily cleaning and weekly disinfection of poultry areas without a poultry-free rest day were associated with decreased AI detection but the association was insignificant. Our study provides evidence of LBM contamination with AI and suggests that slaughtering and/or keeping poultry overnight could be targets for interventions to reduce contamination.

Recent H9N2 Avian Influenza Viruses Revealed Genetic Evolution of the Virus in Bangladesh

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H9N2 avian influenza virus (AIV) has become wide spread since mid-1980s affecting chickens, ducks, turkeys, pheasants, quails, ostrich and migratory birds across the world and generally causes mild illness. In Bangladesh, AIV H9N2 was first isolated during a retrospective analysis of a sample from a poultry farm collected in September 2006. Since then H9N2 viruses have been isolated from commercial poultry flocks, live bird markets and also from environment. On the other hand H5N1 highly pathogenic AIV was introduced in Bangladesh in 2007. Since then both H9N2 and highly pathogenic H5N1 AIVs are co-circulating and causing serious damage to the poultry industry of Bangladesh. The co-circulation also raises the possibility of generation of new pandemic strain. Thus it is important to regularly monitor the genetic features of the circulating AIVs. In this study, recently isolated H9N2 viruses were characterized genetically and compared with previous Bangladeshi H9N2 sequences available in GenBank and also with the representatives H9N2 AIV sequences from elsewhere. The protein sequences of these isolates were analyzed, especially with regard to important genetic motifs. Phylogenetic analyses of HA and NA genes revealed that studied isolates belong to G1 lineage but they formed several subgroups. The HA cleavage site of the recently isolated viruses showed KSKR (dibasic) motif whereas the older Bangladeshi isolates exhibited KSSR (monobasic) motif indicating genetic evolution of the virus. Analysis of NA protein revealed that the viruses showed acquisition of mutations in three loops associated with resistance to neuraminidase inhibitor drugs. Multiple mammalian-host-associated mutations were also detected in internal protein analysis, which might favor to create a new pathogenic strain.

Keywords: H9N2, Avian influenza virus, Bangladesh, Evolution, Mutation

Initial Results of the Cross-sectional Survey of Live Bird Market Hygiene and Respiratory Contamination among Live Bird Market Workers in Bangladesh

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Zoonotic avian influenza A virus subtypes H5N1 and H9N2 are endemic in Bangladesh where poultry consumption via live bird markets (LBMs) is usual and very popular. We aimed to assess the presence of aerosolized AIVs at LBMs, as well as their presence in respiratory samples of workers to evaluate risk and inform future biosecurity related interventions.

A cross-sectional survey of workers in 42 LBMs, with sampling probability proportional to market size, was carried out, collecting nasal and throat swabs and information on high risk practices. In each market, air samples were collected together with market-level hygiene assessments. Data from initial 13 markets has been analyzed for this abstract.

While 85% LBMs had official weekly market closure day, none practiced it. Eight had open drainage system, while solid waste was removed from 11 LBMs daily. Only two LBMs had separate central slaughter house. In 95% cases stalls were used for slaughtering or butchering of birds and 41% stalls used defeathering machine. Among 13 collected air samples, 38% were positive for Influenza A. A total of 232 workers with mean age of 33 years were recruited among 615 eligible adult workers with a response rate of 87%. Average working experience in LBM was 12.8 years and 88% were involved in slaughtering and 81% in defeathering activity. With one step rRT-PCR, 25 (11%) LBM workers were tested Influenza A positive with nasal and/or throat swab. Among them, 8% were positive for H5, 40% were positive for H9, 8% had both H5 and H9 and rest 44% were unsubtypable. Acute and convalescent serum samples were obtained for subsequent testing.

The study provides evidence of aerosolization of avian influenza in LBMs and its presence in respiratory passages of workers, adding to our understanding of mode of transmission for AI to humans. A risk of spillover of AIVs has been detected to people working in live bird markets. These findings will support moving from emergency response to prevention of AIV spillover by investigating methods to assess improvements in market hygiene and biosecurity.

Keywords: Live bird market, Avian Influenza, Air sample, Live bird market workers, Market hygiene, Bangladesh

Outbreak Investigation of Avian Influenza in a Turkey Farm at Northern Dhaka and Trace of Possible Human Contacts

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Avian influenza is a potential threat of human health and if it crosses the species barrier and infect human, it will cause serious human mortality and morbidity due to lack of immunity among humans. The turkey farm was situated in northern part of Dhaka city where around 80 turkeys and 120 of local variety chickens reared.

The aim of the investigation was to identify the aetiologic agent, extend of the outbreak and possible associated human infections.

The occurrences of turkey death started four days before the outbreak investigation and continued dying of birds following three days. The drowsy and last 27 remaining turkeys were slaughtered, de-feathered by farm workers and was kept in freezer. During the investigation some chicks were found grazing around, two were drowsy and a fond dead. 14 people were found to have direct contact with sick or dead poultry. The oral secretions from the moribund and dead chickens were taken along with 14 oro and naso-pharyngeal swabs from exposed human.

Three samples from chickens were tested for HPAI and found positive. The rest of the flocked were culled. Human samples were tested for influenza in the IEDCR lab and found negative and they were followed up for following two weeks. One frozen turkey carcass was post-mortem and the organ tissue sample were collected and tested in CDIL and found positive for H5. There were concerns of gross breach of bio-safety and cross species mixing in the farm.

Government should ensure and educate the farm owners about bio-safety measures to prevent further AI outbreak and safe handling of dead and infected birds.

One Health Investigation of a Crow Mortality Event Linked to Potential Circulation of Highly Pathogenic Avian Influenza Virus at Live Bird Markets in Bangladesh

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Highly pathogenic avian influenza H5N1 has caused 500 or more reported outbreaks in poultry and wild birds in Bangladesh since 2007. Responding to reports of a crow mortality in Dhaka and Rajshahi city, a multidisciplinary One Health team including epidemiologists, veterinarians, and anthropologists investigated crow mortalities between 15 January to 20 February 2017. The aim was to identify the etiologic agent, source of the infection, and characterize the extent of the outbreak. The One Health team collected cloacal and oropharyngeal swabs from moribund and dead crows (n=228) and environmental samples from neighbouring Live bird Markets (LBMs; n=311) where crows were observed feeding from within a 7 km radius surrounding the crow roosts of the reported crow mortality. All samples were using a pan-influenza A consensus PCR assay as well as specific q-PCR for influenza A (M gene) H5/H7/H9/N1. PCR-positive samples were further cultured and stored the samples for sequencing. The team observed crows feeding on poultry offal and wastage in neighboring LBMs and sharing the roost site with other wild birds. Ninety percent of the sampled crows (n=205; 95% confidence interval (CI): 86-94) were positive for Influenza A/H5 and 3% for Influenza A/untypable (n=6; 95%CI:1-6). Among LBMs samples, 31% were positive to A/H5 (n=97; 95%CI: 26-37), 5% for A/H9 (n=15; 95%CI: 3-8), 3% had a co-infection with both A/H5 and H9 (n=10; 95%CI:2-6), and 14% for influenza A/untypable (n=44; 95%CI:10-19). None of the crow samples were positive for H7 or H9 and in LBMs no samples tested positive for H7. H5 positive crows and LBM samples were tested for N1; results revealed that 57%, H5 crows (n=205) and 66%, H5 LBMs (n=97) samples were positive for N1. The remaining were negative which suggests that other N types might be co-circulating in both crows and LBMs. Phylogenetic analysis based on partial sequence of the HA gene suggests that sub-type found in the crows is similar to the Bangladeshi 2.3.2.1a clade that were circulating since 2011. The findings suggest that highly pathogenic H5N1 is present in the LBMs in Bangladesh, and may have been transmitted to crows while they were feeding on poultry waste in the LBM. Improved LBMs biosecurity measures are therefore needed to reduce the risk of influenza virus spillover to wild birds or people in Bangladesh.

Key Words: One Health, Outbreak Investigation, Crow, H5N1, LBM, Bangladesh

Thematic Paper: Emerging Infectious Diseases & Zoonosis-2**Making the Case for Integrating Risk Communication and Community Engagement into Routine Public Health Programs: Lessons Learned from Ebola, Zika and Measles Outbreaks****Mario Mosquera-Vasquez**

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The effects of climate change, globalization and rapid urbanization increase the chances for human, animal and zoonotic diseases to spread globally. This presentation looks at the significant role that risk communication and community engagement played during three different outbreaks with different epidemiological and social contexts and distinct institutional capacity. It builds on the communication lessons learned from the Ebola Response in West Africa, Zika Virus outbreak response in Latin America and Caribbean Region and Measles outbreak response in Ukraine. It examines the challenges and the strategies used to communicate with various publics to address risk perceptions and sociocultural factors. The presentation emphasizes the importance of mainstreaming communication for Humanitarian Action, Community Engagement and Risk Communication in emergency preparedness structures in Government systems. It also highlights the critical role of social science research to understand the drivers of the outbreak to inform communication interventions taking into account a range of contextual, cultural and communication dynamics and processes.

Oral presentation: Emerging Infectious Diseases & Zoonosis-2**Epidemiological Investigation and Molecular Characterization of *Bacillus anthracis* from Soils in Selected Districts of Bangladesh**

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Anthrax has become a potential issue in public health sector of Bangladesh since last few years. A cross-sectional survey was conducted to assess the risk factors among the people at risk in selected areas of Bangladesh, considering awareness, attitudes and management practices towards anthrax. Molecular techniques were used to confirm the presence of *Bacillus anthracis* bacteria in soil. Administrative areas of Bangladesh had been classified into high, medium, and low-risk anthrax areas by assessing the risk of anthrax based on the reports published in daily newspapers and scientific journals. The selected high, medium and low-risk areas were Kushtia, Pabna and Mymensingh district respectively. A total of 622 data were collected and uploaded to the data collection tools "Magpi", and the data were analyzed using Epi Info™. In the study areas, it was found that about half of the people had no institutional formal education (46.46%; n=289/622). The farmers at high-risk districts were significantly ($p=0.000$) aware to anthrax as compared to those from medium- and low-risk districts. In our study, improper washing of grass and occurrence of flood in the study areas were significantly ($p=0.000$) correlated with anthrax outbreak. Soils (n= 128), blood (n= 1), meat (n= 2) samples from anthrax affected areas were tested of which the bacterium was isolated from 21 soils and all the blood and meat samples by standard cultural, morphological, and molecular techniques (PCR) in the period of June 2016 to May 2017. Gene sequencing of one isolate was done commercially and phylogenetic trees were constructed with the MEGA5 (www.megasoftware.net) software. After genome sequencing it resembles with full length 16S rRNA gene from *Bacillus anthracis*. Phylogenetic analysis of 16S rRNA gene of *B. anthracis* Sirajganj-1 revealed that the organism is almost similar to other established strains of *B. anthracis*. Genbank accession no. MF353929. Based on findings, it can be concluded that increasing awareness towards zoonosis of anthrax, proper vaccination and treatment of diseased animals by registered veterinarians may help to reduce the anthrax outbreak in Bangladesh and the molecular techniques help to detect the virulent genes of *Bacillus anthracis* in future.

Isolation and Molecular Detection of *Brucella* spp. in Bovine Milk from Some Selected Areas of Bangladesh

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The aim of the study was to isolate and identify *Brucella* spp. from bovine milk samples by bacteriological and molecular methods. This study also determined the prevalence of *Brucella* spp. in milk samples obtained from various dairy farms located at Mymensingh, Jamalpur, Bogra and Dhaka. Milk samples (n=200) were collected from the CCBDF, Savar, Dhaka; Nirala dairy farm, Mymensingh; BAU dairy farm, BAU, Mymensingh; Uzzal dairy farm, amalpur; Hasan dairy farm, Gabtali, Bogra; Agragati dairy farm, Naruli, Bogra, and some local markets at Mymensingh, Jamalpur and Bogra districts. A structured questionnaire was used to collect information on animal's status which include breed, age, pregnancy status, some reproductive disorders eg., abortion status; repeat breeding; retention placenta, and rearing system. Samples were processed and inoculated onto both *Brucella* selective agar and blood agar media and incubated at 37°C for 3-5 days under the supplement with 5% CO₂. Identification of *Brucella* spp. was performed by colonial morphology, Gram's staining and biochemical tests. Molecular detection of *Brucella* spp. at genus level was performed by polymerase chain reaction (PCR) assay targeting 16SrRNA gene. Overall prevalence of brucellosis in dairy farm was (10.47%). Prevalence recorded in milk sample collected from local market was (4.21%). Cross breed showed higher prevalence of brucellosis (11.11%) as compared to local breed (9.09%). Prevalence of brucellosis in >4 years age group was (12.00%) which is more than ≤4 years group (6.66%). Pregnant cows exhibited more prevalence of brucellosis (16.12%) as compared to non pregnant cows (8.11%). The

prevalence of brucellosis was 41.67%, 40.00% and 23.07% in cows with the previous history of abortion, repeat breeding and retention of placenta respectively. Cows reared under semi-intensive condition showed higher prevalence of brucellosis (17.86%) as compared to cows reared under intensive condition (7.79%). It may be concluded from this study that *Brucella* spp. is endemic in the study areas. Since *Brucella* spp. was detected in milk sample, affected dairy cattle a great threat to public health.

Key words: *Brucella* spp., Dairy farm, Local market, Milk sample, Prevalence, PCR.

Evaluation of Hospital Based Surveillance for Japanese Encephalitis in Bangladesh, 2007 to 2015

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Hospital based surveillance for Japanese encephalitis (JE) was established in Bangladesh in 2007 with the aim of describing the epidemiology and detecting outbreaks. Based on evidence from this system, the Government of Bangladesh is considering introducing JE vaccination. We evaluated the timeliness and data quality from the surveillance system to suggest improvements in performance using surveillance data collected from 2007 to 2015 at four surveillance hospitals. Patient enrollment was defined as timely if samples were collected ≤ 24 hours from patient admission. We reviewed lab reports for 2015 and estimated the time lag between patient enrollment and testing. We assessed data quality by calculating the percentage of missing values for dates of admission, serum sample collection, and onset of 1st symptom. Ninety-five percent of serum samples were collected ≤ 24 hours of patient admission. The time between patient enrollment and lab-test ranged from 1 week to >6 months (mean: 11 weeks; SD: ± 2); the surveillance guideline included no recommended standard timeline for lab reporting. Among 5,567 cases in the dataset, data were missing in 56(1%) for date of admission, 55(1%) for date of onset of 1st symptom and 1,256 (22%) for date of serum sample collection. The complete data on relevant dates makes the surveillance useful for estimating epidemiologic curves retrospectively, using lab findings; however, the delays in lab testing and reporting mean that outbreaks may not be identified soon enough to permit a public health response. We recommend including a standard timeline for lab reporting in the surveillance guideline to make the surveillance more useful for identifying cases and outbreaks in real-time, which would be important to track, particularly once vaccine is being used.

Keywords: Japanese encephalitis, surveillance, timeliness, data quality, lab reporting

Sero-prevalence and Determinants of Q Fever in Dairy Cattle

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Q fever is an emerging infectious disease with zoonotic potential caused by *Coxiella burnetii*. Little is known about status of Q fever in Bangladesh. The aims of the present study were to estimate the prevalence and to identify the determinants of Q fever in dairy cattle in Sylhet Division. To ascertain study objectives a cross sectional study was carried out from July 1 through December 31 2016. 1763 individual animals from 925 farms were enrolled using multistage random sampling. A face to face interview was performed with the 925 farm owners by filling up pretested questionnaire contained individual animal and farm level information's. For the diagnosis of disease, Enzyme-linked Immunosorbent Assay (ELISA) was conducted on milk samples from all enrolled animals (n=1763). Based on the laboratory result, individual animal and farm level prevalence been calculated with confidence interval. Multivariable logistic regression was performed for determining the farm level factors associated with Q fever. A total of 100 sample tested positive from 1763 individual cow milk samples for *Coxiella burnetii* by ELISA. An individual animal level prevalence was estimated 5.67 % (CI; 4.69% - 6.85%). Farm level prevalence was 9.62% (CI; 7.88%-11.69%). From multivariable logistic regression, herd size (OR=2.09 (CI; 1.13-3.88)) and rearing other farm animals along with dairy cattle (OR=2.56 (CI; 1.38-4.78)) were determined as risk factors for farm level Coxiellosis. This study explored prevalence and risk factors of Q fever among dairy cattle in Sylhet Division. We suggest further investigations to explore other epidemiological indices like transmissibility. Besides, epidemiological investigations on sheep, goat as well as human are also needed.

Keywords: *Coxiella burnetii*, Dairy cattle, Prevalence, Determinants, ELISA

Anthrax Outbreak Investigation in Pabna and Sirajganj, 2017

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In Bangladesh, outbreaks of cutaneous anthrax are reported commonly during monsoon season - May to November. On June 2017, the Institute of Epidemiology, Disease control and Research (IEDCR) initiated an outbreak response from the reporting of cutaneous anthrax patients admitted in a sub district hospital of Pabna district for containment of the outbreak and prevent future outbreaks.

The investigation was conducted from 2nd to 7th June, 2017 following the standard steps of outbreak investigation. The patient of cutaneous anthrax was defined as any patient developed an acute illness, or post-mortem examination revealing a painless skin lesion developing from a papular through a vesicular stage into a depressed black eschar with surrounding oedema with/without Fever, malaise and lymphadenopathy living in Pabna and neighbouring Sirajgonj district from 18th May to 2nd June, 2017. Patients were interviewed for clinical history, possible source and date of exposure. The investigation was conducted through One Health approach both from local and national level.

Out of 6 cows developed and died from mid-May due to suspected anthrax, 3 were slaughtered locally and sold in two neighboring villages -- where total 67 patients developed cutaneous anthrax - 37 (55.2%) in Jontiahar, Pabna and 30 (44.8%) in Kaliakor, Sirajganj. Among them, 24 (35.8%) were exposed from the cow slaughtered on 25th May, 18 (26.9%) on 27th May and 25 (37.3%) on 29th May. The incubation period was 2-7 days. Male (56.7%) were affected more than female (43.3%). Patients' age range were 2-95 years (median: 30 years) with highest occurrence among 16-45 years (62.7%). Patients had different stages of skin lesions. Out of 18 samples collected from skin lesions, none was positive for *Bacillus anthracis*. Health messages were delivered regarding regular vaccination of cattle and handling the carcass of dead animal. Approximately 800 cattle of these villages were vaccinated.

Despite of laboratory confirmation, the classical clinical features and exposure history confirmed the cutaneous anthrax outbreak. Sample collection and transport techniques need to be improved for laboratory confirmation of anthrax. Yearly cattle vaccination for anthrax was recommended in the affected villages to control future outbreaks.

Thematic Paper: Antimicrobial Resistance and Its containment -1**Containment of Antimicrobial Resistance: Potential Crossroads of One Health in Bangladesh****Md Sayedur Rahman**

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Emergence of antimicrobial resistance (AMR) in the microbes causing disease in humans is inter-linked with bacterial population in other populations, especially farm animals and environment. In Bangladesh, the veterinary sector is flourishing quickly and therefore use of antimicrobials in those sectors is increasing with its consequential impact on human health. In order to formulate and implement an effective strategy to contain antimicrobial resistance, adequate research in the related fields is required. In human sector, antimicrobial prescribing is extensively studied both in the community and hospitals. Sensitivity pattern of the causative microbes has also been studied for both clinical as well as research purpose. On the other hand, limited information is available about the consumption of antimicrobials in veterinary sector. Nevertheless, sensitivity pattern of the microbes causing disease in livestock is elaborately studied. The role of environment, the interface platform for interaction of these different microbes is inadequately investigated in Bangladesh. As there is a global consensus that exposure to antimicrobial is the principal contributor in emergence of resistance, reduction of exposure may reduce or slow the pace of development as well as transfer of resistance. In order to achieve that, quantification of consumption of individual antimicrobial at particular level and sector has become an impending necessity. Understanding about the consumption pattern of antimicrobials in human and veterinary sector will enable researchers and policy makers to identify and target specific antimicrobial, which needs to be conserved from indiscriminate use. The established methodology for investigating antimicrobial consumption is too robust for a country like Bangladesh. Therefore, a rational and scientific customization of the global methodology incorporating the contextual perspectives of Bangladesh without compromising the accuracy and precision of the result of the study has become the imminent issue to be addressed.

Oral Presentations: Antimicrobial Resistance and Its containment -1**Prevalence of multi-drug resistant ESBL- producing *Escherichia coli* isolated from broiler chicken at Sylhet division of Bangladesh**

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Antimicrobial resistance, a major health problem for both human and animals throughout the world, is leading to treatment failure after administering antimicrobial drugs. The current study was conducted to determine the susceptibility and multi drug resistance (MDR) patterns in *Escherichia coli* isolated from broiler chickens. A total of 250 cloacal swabs from 250 individual broiler chickens were collected from 25 different broiler farms located at Sylhet division of Bangladesh. Isolation and identification of *E. coli* was done by bacteriological culturing and specific biochemical tests. Antimicrobial susceptibility and MDR among the isolates against nine selected antimicrobial agents namely ampicillin, colistin, gentamicin, streptomycin, ciprofloxacin, levofloxacin, erythromycin, trimethoprim-sulfamethoxazole and tetracycline were performed on Muller-Hinton agar plate by the Kirby-Bauer disc diffusion method according to the Clinical and Laboratory Standards Institute (CLSI) guidelines. Extended spectrum beta lactamase (ESBL) productivity of the isolates against two specific antimicrobial agents (cefotaxime and ceftriaxone) was also determined according to the CLSI guidelines. Results showed that all swab samples were positive for *E. coli* and the isolates were 100%, 75% and 53% resistant to ampicillin, erythromycin, trimethoprim-sulfamethoxazole respectively. Highest sensitivity was shown to colistin sulphate (93%), gentamicin (87%), and levofloxacin (79%). Furthermore, 97%, 62% and 37% of *E. coli* isolates were resistant to 3 classes, 4 classes, and 5 classes of antibiotics respectively and considered as MDR strains. Out of 250 *E. coli* isolates 18 (7.2%) were ESBL positive in broiler chickens. Our data stress the importance of surveillance of MDR and ESBL production in bacteria to optimize empiric treatment and to prevent the introduction of MDR bacteria in human food chain from food animals. Also, prudent use of antibiotics and further search to alternative agents are warned.

Keywords: *E. coli*, antibiotics, multi-drug resistance, broiler and layer chicken, Bangladesh

Epidemiology of Antimicrobial Resistance of *Salmonella* and *Staphylococcus* Isolated from Free-ranging Rhesus macaque (*Macaca mulatta*) in Bangladesh

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Antimicrobial resistance (AMR) is a growing public health threat globally both for human and animal health due to indiscriminate or inappropriate use of antibiotics. Further, environmental contamination of antimicrobial residues by people or livestock may lead to AMR in peri-domestic wildlife, such as the Rhesus macaque. This study was conducted to characterize the epidemiology of AMR of *Salmonella* spp. and *Staphylococcus* spp. in macaques, and how exposure might occur. We collected 399 non-invasive fecal samples from free-ranging Rhesus macaques at different land gradient of Bangladesh. Fecal samples were collected in buffered peptone water for *Salmonella* spp. and Mueller Hinton broth for *Staphylococcus* spp. using selective media, biochemical test and PCR for confirmation of specific organism followed standard microbiological procedure. AMR profiling was assessed by disc diffusion method of 12 antimicrobials. 5% (n=18; 95% CI: 3-7) of macaques were positive for *Salmonella* spp. and 26% (n=103; 95% CI: 22-30) for *Staphylococcus* spp. Rhesus macaques from urban area were significantly more (8%; n=11; 95% CI: 4-14) infected with *Salmonella* spp. than rural and peri-urban areas. There was no significant differences in *salmonella* infection according to sex, but adult macaques had a higher prevalence (6%; n=11; 95% CI: 3-11) than other age groups (sub adult and baby). Female macaques (30%; n=71; 95% CI: 24-36) were more infected with *Staphylococcus* spp. than that of male. Macaques from different locations (urban 31%, peri-urban 16%, rural 29%) showed the significant variation in the infection of *Staphylococcus* spp. Partial results revealed; *Salmonella* spp. (n=18) is resistant to Tetracycline (89%), Azithromycin (83%), Sulfamethoxazole-Trimethoprim (50%), Nalidixic acid (44%) and sensitive to Ciprofloxacin (94%), Gentamicin (94%), Imipenem (94%), Cefixime (78%), Ceftriaxone (72%), Cefotaxime (61%), Amoxicillin (61%) and Chloramphenicol (56%). Close interaction with human and livestock for water resources might be one the reasons of increased antimicrobial resistance in Rhesus macaque against of *Salmonella* and *Staphylococcus*. However this findings suggest that need for genetic analysis of these pathogens in Rhesus macaque that might be spread out in the environment.

Keywords: AMR, Rhesus macaque, *Salmonella*, *Staphylococcus*, Bangladesh

Occurrence and Anti-biogram of *shiga* Toxin-producing *Escherichia coli* in Domestic Buffaloes of Bangladesh

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Escherichia coli (*E. coli*) are normal gut flora in warm-blooded animals and are usually harmless. However, some *E. coli* serotypes may cause food-borne illness in humans. Among them, Shiga-toxin producing *E. coli* (STEC) has recently emerged as significant food-borne pathogens. Ruminants are the major reservoir of the zoonotic STEC. Previous studies reported the presence STEC in cattle, goat and sheep in Bangladesh. However, healthy buffaloes in Bangladesh have apparently not been investigated for the presence of the zoonotic STEC. This study carried out to assess the presence of STEC and anti-biogram pattern in buffaloes of Bangladesh. A total of 100 buffaloes in Chittagong district were opportunistically sampled for faecal materials originated from recto anal junction (RAJ). Collected faecal samples were inoculated into MacConkey agar, a selective medium where *E. coli* produce pink-colored colonies. Isolates producing pink-colored colonies eventually re-inoculated in Eosin Methylene Blue (EMB) agar and isolates producing characteristic metallic green sheen colonies on EMB agar were confirmed to *E. coli* positive. The STEC was diagnosed with exploring the presence of any of the two shiga toxin-producing genes – *stx1* and *stx2* in *E. coli* isolates using polymerase chain reaction (PCR). The anti-biogram profiles of STEC against 10 commonly used antimicrobials were investigated by the disk-diffusion method. Results show 77 faecal samples were positive for *E. coli* in bacteriological screening. The proportion of buffaloes harbouring STEC isolates were 11% (11/100) [95% confidence interval (CI) 6.1-18.8], of which 7% (7/100) [95%CI 3.2-13.9] and 4% (4/100) [95%CI 1.2-10.2] carried *Stx1* and *Stx2* genes, respectively. Antibigram revealed 91% (10/11), 73% (8/11), 55% (6/11) and 55% (6/11) STEC isolates were resistance to tetracycline, sulfamethoxazole-trimethoprim, erythromycin and ampicillin, respectively. In contrast, 91% (10/11) STEC isolates were sensitive to ciprofloxacin, chloramphenicol and gentamycin, whereas 73% (8/11) isolates were sensitive to ceftriaxone. This study is first to reveal a significant proportion of direct faecal samples from domestic buffaloes of Bangladesh harbouring antimicrobial resistant STEC. Transmission of antimicrobial resistant STEC from buffaloes to humans could pose a potential threat to public health in Bangladesh.

Keywords: Buffalo, *E. coli*, Shiga Toxin, Anti-biogram, Bangladesh

An Investigation of Plasmid-mediated Colistin Resistance Gene, MCR in *Escherichia coli* of Human, Veterinary and Environmental Origin

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Unprecedented increase in the emergence of different antimicrobial resistance mechanism occurred in last few decades. New plasmid-mediated colistin resistance gene (MCR) has been emerged in China and reported in many countries of the world. Due to unavailability of any published information regarding its occurrence in Bangladesh the present study was designed to reveal the existing situation in the country. A total of 810 samples were collected from human, cattle, goat, poultry, poultry farm environment and street foods of Chittagong Metropolitan Area. Total 368 *E. coli* isolates were confirmed using cultural and biochemical tests and tested against 7 antimicrobials of six different groups namely Amoxicillin, Cephalixin, Gentamycin, Tetracycline, Colistin, Ciprofloxacin and Sulfamethoxazole-trimethoprim using disc diffusion technique. Colistin-resistant isolates were further investigated for the presence of plasmid-mediated colistin resistance gene, *mcr-1* and *mcr-2* by polymerase chain reaction (PCR). Among all the isolates 13.32% (49 out of 368) were found resistant to colistin. The prevalence of *mcr-1* and *mcr-2* genes was 6.12% (3 out of 49) and 4.08% (2 out of 49) respectively. None of the isolates harbored both *mcr-1* and *mcr-2*. 10.20% colistin-resistant isolates possessed either *mcr-1* or *mcr-2* gene whereas 89.80% isolates had none of above tested genes. All MCR positive were poultry and street food isolates. Resistance in MCR gene lacking isolates may be due to any other mechanism not investigated here. Since this plasmid-mediated, MCR gene is highly transmissible it'll lead to the development untreatable superbug, resulting an unbeatable catastrophe. Henceforth authorities should pay attention immediately to resolve the issue.

Key words: Antimicrobial-resistance, *E. coli*, colistin, MCR

Epidemiological Assessment of Anti-Microbial Residues in Poultry and Fish in Chittagong, Bangladesh

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Antimicrobial residues in animal products, sold for human consumption, can have harmful effects to human. To identify prevalence and concentration of antimicrobials residues in broiler chicken and fishes, a repeated cross-sectional study was conducted in Metropolitan area and one sub-district of Chittagong, during July to December 2015. Residues were extracted from pooled chicken tissue (N=182) and fish flesh (N=153) and tested for five common antimicrobials using Thin Layer Chromatography (TLC) followed by Ultra-High Performance Liquid Chromatography (UHPLC) for quantification of amoxicillin residues. The TLC-based point prevalence of residues in chicken in June (N=91) and October (N=91) respectively was 91.5% and 83.5% (amoxicillin/ampicillin), 1.1% and 1.1% (Ciprofloxacin), 1.1% and 0% (Enrofloxacin), 0% and 6.6% (Oxytetracycline). In fish, the prevalence of antimicrobial residue in September (N=74) and October (N=79) respectively was 52.7% and 44.3% (amoxicillin/ampicillin) and 1.4% and 27.8% (Oxytetracycline). Other antibiotics were undetectable in fish. The mean and median concentration of amoxicillin residue in raw samples was 508.4 mg/kg and 480.9 mg/kg, respectively in chicken and 515.4 mg/kg and 65.2 mg/kg in fish. Random effect model identified market (Chawkbazar vs. Boalkhali; OR 5.7; CI 1.22-26.9; $p=0.02$; Steel Mill Bazar vs. Boalkhali: OR 5.6; CI 1.22-26.1; $p=0.02$) and Generalized Linear Model identified market (Kazir hat $\beta= -1.4$; $p=0.015$ and Chawkbazar $\beta= -1.17$; $p=0.04$) and month (October $\beta=0.77$; $p=0.003$) as potential factors for amoxicillin residue in chicken. This variation may be attributable to the difference in the poultry supply chain in those markets. Climbing perch fish (*Anabas testudineus; koi*) had more risk of having antimicrobial residue than that of Bombay duck (*Harpadon nehereus/Loitta*) (OR=0.05; $p=0.000$). All samples were then treated by washing (for chicken samples), boiling and cooking with spices and extracted for TLC. A sub-set of each treated group was evaluated by UHPLC. The prevalence and concentration of amoxicillin residues significantly reduced in chicken (87.4-23.2%; 188.3-16.2 mg/kg) and in fish samples (48.4-18.9%; 515.4 to 49.4 mg/kg) with different treatments. The results suggest that different treatment measures are effective in reducing prevalence and concentration of amoxicillin residues but the concentration still remains above the threshold level which poses risk to human health.

Keywords: Antimicrobials residues, Chicken, Fish, Chittagong, Bangladesh, TLC, UHPLC.

Prevalence of Multi-drug Resistant Genes and Virulence Factors in *Enterococcus faecalis* Isolated from Poultry in Bangladesh

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E. faecalis has been emerged as leading causes of hospital infection, surgical sepsis, and urinary tract infection (UTI) due to their harsh environment tolerance and intrinsic multi-drug resistance. Current study focused on determination of antimicrobial tolerance and molecular characterization of *E. faecalis* isolates. Pure-culture of *E. faecalis* was isolated and maintained using 5% Sheep Blood Agar, KAA agar and *sodA* gene specific PCR. CLSI antimicrobial susceptibility testing (AST) standards M02-A12 and M07-A10 was followed in antimicrobial tolerance study. Partial sequencing was done using Applied Biosystems 3130 Genetic Analyzers and phylogenetic analysis was inferred using the Neighbor-Joining method in MEGA6. We have collected 136 samples from commercial broiler, layer and broiler breeder from July, 2016 to June, 2017. Among these, 35% commercial broiler (n=10; 95% CI: 20-50%), 25% layer (n=15; 95% CI: 15-35%) and 13% broiler breeder (n=04; 95% CI: 2-24%) were infected with *E. faecalis*. and 29 isolates were confirmed as *E. faecalis*. In phylogenetic analysis of partially sequenced *sodA* gene, increased level of sequence similarity among the isolates and virulent strains (NCBI database) was observed with overall mean distance; d=0.004. All *E. faecalis* isolates harbored genes coding for virulence factors *agg*, *esp*, *fsr* *gelE* alone or in combinations with the high prevalence of *esp* gene. In disk diffusion test, 96% isolates (n=28) were multi-drug resistant (MDR) according to analysis software WHONET-2017. Among 13 tested antibiotics, 96% isolates were resistant against streptomycin and tetracycline (n=28, 95% CI: 79-100%), followed by erythromycin 83% (n=24, 95% CI: 61-93%), penicillin G 70% (n=20, 95% CI: 50-86%), amoxicillin 63% (n=18, 95% CI: 43-80%), ciprofloxacin & vancomycin 31% (n=9, 95% CI: 15-50%), linezolid 28% (n=8, 95% CI: 12-47%) where only imipenem showed high sensitivity (89%) with zero resistance. Higher MIC value (MIC₅₀/MIC₉₀) was observed against ceftriaxone (≥1024/≥1024) and gentamycin (8/128). The alarming MDR and virulence profile of isolated *E. faecalis* is utterly threatening. The resistance of *E. faecalis* to multiple antibiotics especially to vancomycin, streptomycin, gentamicin and linezolid will allow them to survive and proliferate in patients receiving multiple antimicrobials and will cause superinfection.

Keywords: *Enterococcus faecalis*, Nosocomial, Multi-drug resistance and Poultry

Thematic Paper I: One Health Governance, Advocacy, Communication & Policy**One Health Journey in Bangladesh: from Advocacy to Action**

Meerjady Sabrina Flora, Director IEDCR

Bangladesh has been encountering health problems at human, animal, environment interface for long and considered as hot spot for the emergence of diseases which may create public health emergencies of international concern. Zoonotic diseases like Avian Influenza, Nipah, Anthrax, leptospirosis, Rabies, etc are common in the country putting the population at risk. At the outset of Avian Influenza outbreaks in the country, a group of visionary professionals formed One Health Bangladesh in 2007. The forum started advocacy with the government, development partners, NGO, civil society organizations, professional bodies, research institutions, academic institution to promote one health concept. As a result, Government of Bangladesh developed a National One Health Strategy in 2012 and later endorsed by relevant ministries. Coordinated one health actions were at the heart of the national strategy and the strategy suggested for institutionalization of one health among others. While informal sectoral collaboration in the field of outbreak investigation, surveillance, workforce development, communication continued, strive to formalize the coordination mechanism also continued in parallel. As a result an inter-ministerial meeting held in June, 2016 decided to establish One Health Secretariat and Inter-ministerial Steering Committee on One Health. Government of Bangladesh with the support from development partners developed the Terms of Reference of One Health platforms and those later endorsed by the Inter-ministerial Steering Committee on One Health in March 2017. The leadership of these of these entities will rotate among the Ministries at an interval of every three years. Government has already mobilized resources from the 4th Health Population & Nutrition Sector Strategic Plan. The One Health Secretariat with seconded staff from three ministries with the backstopping of development partners has started functioning at Institute of Epidemiology, Disease Control & Research within the Ministry of Health and Family Welfare. One Health Secretariat has already assessed the performance of one health mechanisms for future planning, supported revision of One Health Strategy and prioritized zoonotic diseases. Functional One Health Platforms will help strengthening coordination, collaboration, networking, joint surveillance, preparedness and response to counteract health hazards and thus be able in contributing to achieving Sustainable Development Goals (SDG).

Thematic Paper II: One Health Governance, Advocacy, Communication & Policy**The Global Virome Project: The *Beginning of the End* of the Pandemic Era**

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Emerging infectious diseases (EIDs) are rising in frequency, leading to an exponential rise in their economic impacts, and threatening global health, livestock production and food security. Zoonotic viruses from mammalian and water bird hosts are a particular threat, and the Global Virome Project (GVP) has been launched to strategically address this. The GVP aims to identify and characterize the majority of currently-unknown viruses in wildlife that have potential for zoonotic infection. Based on patterns of viral discovery in wildlife, we estimate that there are around 1.6 million as-yet undiscovered viruses in wildlife from viral families known to infect humans, and more than 500,000 likely to have the potential to become zoonotic. The GVP sampling can be targeted to geographical hotspots of EIDs to the species most likely to harbor zoonoses, and to those for which we can calculate a high proportion of 'missing zoonoses'. This would mean that a 10 year GVP program would discover the majority of unknown viruses, and a disproportionately high percentage of the global zoonotic risk.

Key Words: Emerging infectious diseases, zoonotic viruses, global health

Oral Presentations: One Health Governance, Advocacy, Communication & Policy**Embracing the One Health Paradigm to increasing Awareness, Prevention & Control of Zoonoses in Bangladesh**

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As a part of EU One Health Programme in Asia, Fighting Zoonoses in Afghanistan, Bangladesh and Nepal (ABN), Sher-e-Bangla Agricultural University (SAU) of Bangladesh came in agreement with Relief International-UK, Bangladesh to embrace one health paradigm to increasing awareness, prevention & control of zoonoses in the country. The agreement focused on the development of zoonoses related course curriculum for post graduate study, establishment of a zoonoses resource center/research unit in the university and conducting researches on economic impact and other important issues related to zoonoses or one Health. Accordingly, a Zoonotic Diseases Research and Information Centre (ZDRIC) was established at SAU under collaboration with RI, Bangladesh, that facilitated the development of course curriculum related to zoonoses for MS course in the Department of Medicine and Public Health, SAU. Besides ZDRIC facilitated five research grants awarded to Bangladeshi researchers to encourage researches on zoonoses including situation assessment, intensive field investigation, laboratory analysis of important bacterial and parasitic zoonoses in some selected areas. Studies on zoonotic gastrointestinal parasites in cattle, poultry slaughter food borne zoonotic diseases, milk-borne zoonotic *Staphylococcus aureus*, zoonotic potential of campylobacteriosis and socio-economic impact of anthrax in some selected areas in Bangladesh were performed. The research projects were conducted for one year and completed successfully with potential research findings for the community stakeholders. The emergence of MDR superbugs, presence of zoonotic bacterial and parasitic pathogens and high economic burden due to recurrent and up streaming outbreak of anthrax seeking urgent control action to be implemented. In addition to providing useful epidemiological information for control policy design and evaluation through the researches, ZDRIC promoted One Health concept by organizing students' seminar on zoonoses and public health, observing important days related to one health, hosting consultation workshop, arranging field trips to understand wild life zoonoses and their impact on one health. Thus, ZDRIC contributed to the advocacy of one health concept to different corners. ZDRIC will continue its activities to promote one health concept in Bangladesh by disseminating zoonoses related information and facilitating researches. Agencies working on one health in Bangladesh can find a good workplace here in ZDRIC for future one health related activities.

Keywords: Zoonoses Resource Center, One Health Approach in Bangladesh, Zoonoses Courses, etc.

One Health Institute at CVASU: Creating Opportunities for Interdisciplinary Education, Research and Policy Dialogue to Resolve One Health Issues

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One Health is a well-known multidisciplinary, cross-cultural and collaborative effort to attain optimal health for all the inhabitants in the planet earth. It is founded on the need for a more integrated understanding of the connections among humans, animals, and the environment within the political, economic, and social systems in which they operate. Over the years, the One Health has gained significant international attention and endorsed by the World Health Organization, the World Organization for Animal Health, and the Food and Agriculture Organization. Many countries are now developing national One Health platforms to bring together government and nongovernment agencies to implement their disease preparedness and response plans. Each platform is established under unique circumstances and has its own components and mandates. Bangladesh, considering its high population density, fragile ecosystems and rapid growth of livestock industry, is vulnerable to the emergence of infectious diseases with potentials of igniting pandemics. Predicting the significance of the One Health in the country, Chittagong Veterinary and Animal Sciences University (CVASU), Bangladesh has recently established a dedicated “One Health Institute” in its Chittagong campus to facilitate institutionalization of One Health theme. The new Institute will closely collaborate with national and international One Health agencies towards successful implementation of the agenda through a range of activities. The prevention of emerging infectious diseases (EIDs) is in the forefront of One Health Institute goals. It is expected that through better understanding the disease transmission comprehensively, the public health, veterinary, agriculture, and environmental communities can work together to identify more effective solutions for any relevant issues to control and prevent EIDs. Further terms of references and activity plan are under development to promote One Health Institute into a centre of excellence in South Asia which can be model for other developing nations of the world.

Keywords: Bangladesh, One Health, Policy, dissemination, institutionalization, education

Improving Competencies of the Veterinary Workforce to Strengthen Public Health and Food Security in Bangladesh

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A reform is underway in Bangladesh to better train the veterinary workforce to meet the emerging demand of improved veterinary services for both public health and food security. All nine veterinary schools, the Department of Livestock Services (DLS), the Food and Agriculture Organization of the United Nations (FAO), and the Bangladesh Veterinary Council (BVC) are making a joint effort to introduce continuing education (CE) for the existing veterinary workforce, establish a national veterinary accreditation system, revise the disease control curriculum, and improve teaching and learning in veterinary schools. Prior to that, a National Veterinary Dean Council (NVDC) was formed in order to better prepare veterinary students to meet current needs and respond to the demand of the future veterinary services. Subsequently, a tripartite forum involving the BVC, NVDC and DLS has been formed with FAO facilitation to work together to enhance the competencies of veterinary workforce. FAO is also providing specialized technical support to the nine veterinary schools for improving pedagogic skills of the teaching faculty and revising the disease control curriculum. Similarly, the BVC accreditation standard is being reviewed and a national veterinary accreditation framework will be established with technical support from FAO. As a result, better trained graduates is expected to be produced, an effective veterinary accreditation system will be in place, and a CE programme combined with in-service training for DLS veterinary services will be established. A better trained veterinary workforce will thus emerge which will work within disease control programmes developed by DLS and FAO to implement an integrated suite of disease control interventions, including value chain-based surveillance to monitor control progress and detect novel diseases, and live animal market interventions to enable market vendors to produce and sell safer food, thereby reducing the risk of pathogen spill-over.

Prioritizing Zoonotic Diseases: Going Forward with One-Health Approach in Bangladesh 2017

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Zoonotic diseases have tremendous impact on public health and economy. Because of lack of coordination between human and animal health agencies, effective public health interventions are often ineffective. Thus, to facilitate multi-sectorial collaboration and to prioritize endemic and emerging zoonotic diseases a One Health Zoonotic Disease Prioritization workshop (OHZDPW) was held on July, 2017 in Bangladesh.

We used a semi-quantitative tool (OHZDP tool) by Centers for Disease Control and Prevention, USA. Workshop participants were the core policy making group from human, animal, and forest ministries. As first step, an extensive literature review of over 400 articles were performed to evaluate existing country-specific data on zoonotic diseases. During the workshop, participants create criterion, develop questions, individually ranked each criterion to generate a final weighted disease list. Participants and subject matter experts (as observer) evaluated 42 zoonotic diseases for Bangladesh. A decision tree was designed using Microsoft excel and used to determine disease ranking. Each weighted criterion were applied, scores were assigned based on participants' response. Scores were summarized and normalized so that the highest score was 1.

The workshop included 12 participants and 17 subject matter experts. In second step of group work, they approve the disease list, choose five disease ranking criteria e.g., Intervention availability, severity of disease, economic burden, response capacity and transmissibility of the disease. According to the questions and individual ranking, the weightage of the criterion were 0.20, 0.41, 0.14, 0.11 and 0.14 respectively. The decision tree analysis showed Rabies (normalized score 1.00), Zoonotic influenza (1.00), Anthrax (0.85), Japanese Encephalitis (0.81) and Nipah (0.76). The list of these diseases was presented to the group for discussion. The group decided that Japanese Encephalitis should go down to the list and Brucellosis (0.63) and Zoonotic Tuberculosis (0.20) should be the top six zoonotic diseases of concern.

Ministry representatives and observers suggested to enhance the capacity building among every stakeholders under one health platform. The existing One Health secretariat could help to establish multi-sectoral surveillance, laboratory capacity, develop prevention and control strategies and conduct joint outbreak investigations. Thus the country would certainly be prepared to effectively address these identified diseases.

Key words: One health; Zoonotic Disease; Prioritization

Thematic paper: Food Safety and Security**Nutrition and food security: what does the future hold for us?****Tahmeed Ahmed**

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Despite being the most densely populated countries in the world, Bangladesh has done quite well in terms of public health. For example, infant mortality rate is lower and immunization and ORS coverage rates are much better than in the region. Compared to a decade ago, rates of malnutrition among children and women have decreased. Yet, 40-50% of the population suffers from one kind or the other of malnutrition. Food insecurity still ravages 20-30% of the households. By 2050, the population of the country will have stabilized to more than 200 million. This huge population density is likely to have its toll on food security, water, sanitation and hygiene. Migration to cities, unplanned urbanization, and climate change will compound the problem. Self-sufficiency in food is estimated to be reduced.

These may sound provocative, but if we do not prepare from now onwards, the future may not be good for us. Prudent planning, population control, thinking out of the box for improving food security and nutrition – these are now the ‘must do’ elements for the future.

Oral Presentations: Food Safety and Security**Arsenic mitigation in Rice (BRRI-28) through association of an aquatic fern *Marsilea minuta* L.**

Ummehani Hassi, Md. Tawhid Hossain, Monira Begum and Dr. S.M. Imamul Huq

Arsenic (As) contamination has been a burning issue in causing severe health problems to human being. The impact is vast when arsenic is accumulated in food especially in staple foods like rice. Hence it is important that effect of arsenic to be mitigated up to maximum level. This paper discusses about the process of reducing the level of arsenic in rice (BRRI-28) with the association of an aquatic fern *Marsilea minuta* L. A pot experiment was carried out to study the possibility of using an aquatic fern (*Marsilea minuta*) as a phytoremediator of arsenic. Rice and the selected fern (*Marsilea minuta*) were allowed to grow in soils together. To compare the results, *Marsilea minuta* was also cultured alone in presence and absence of arsenic (applied at 1mg/L As as irrigation water). The process caused no significant change in growth of rice due to the association of *Marsilea minuta*. The result showed a reduction of approximately 58.64% arsenic accumulated in the roots of rice grown in presence of fern compared to that grown without fern. The bioaccumulation factor (BF) of >1 indicated that *Marsilea minuta* could be a good phytoremediator of arsenic and it also showed a positive allelopathic relationship between roots of rice and *Marsilea minuta*.

Keywords: *Marsilea minuta*, Rice, Arsenic, Phytoremediation, Allelopathy

Use of Untreated Poultry Waste in Agricultural Farms Causes Microbial Contamination of Vegetables

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Poultry generate huge amount of wastes which are used in agricultural farms, pond water, biogas plants etc. These wastes can contain potential pathogens which may affect man and animal health and environment. However, proper waste disposal can eliminate such problem. Our preliminary survey revealed that 69% of the poultry farmers are unaware of the health and environmental problems of the poultry waste. It is noteworthy that majority of the small scale farmers dispose their droppings to fish ponds (31%) and agricultural farms (16%) directly, while only 3% farmers use that in biogas plant. Such contaminated and untreated poultry waste can serve as potential source of pathogen entry into food chain and may create serious environmental and public health concerns. The present study aimed to investigate the presence of *Escherichia coli* and *Salmonella* species in the poultry litter, soil, pond water and vegetables obtained directly from farms using poultry litter as fertilizer, as well as from market. A total of 28 samples were collected from vegetable gardens of three poultry farm areas and one market in Mymensingh district during the period from May to August 2016. Isolation and identification of *Escherichia coli* and *Salmonella* were performed by culturing in selective media and by Gram's staining. The prevalence of *E.coli* was found in 2 samples (litter and pond water), while *Salmonella* sp. were detected in 14 samples including litter, contaminated soil and common vegetables such as sponge gourd, spinach, taro, brinjal, bottle gourd, wax gourd, cucumber, bitter gourd and carrot. Moreover, both *E. coli* and *Salmonella* were found in 10 samples tested. However, one litter samples from biogas plant showed no growth of the bacteria. The results may suggest that untreated poultry litter used in agricultural farms and ponds is an environmental and public health hazard.

Key words: Poultry waste management, food safety, vegetables, microbial contamination

Effects of Food Borne *Mycotoxins* on Toll Like Receptor**Mohammad Rafiqul Islam¹ and Bumseok Kim²**

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Mycotoxins are structurally diverse toxic secondary metabolites produced by the organisms of the Fungus kingdom. Due to the widespread presence of fungi in the environment, mycotoxins are regarded as an unavoidable contaminant in food products. Mycotoxins can cause mycotoxic nephropathy, hepatotoxicity, cytotoxicity, genotoxicity and induce dysregulation of the immune response and are able to either enhance or suppress resistance to pathogens. Toll-like receptors (TLRs) are a class of proteins that play a key role in the innate immune system. Once microbes have breached physical barriers such as the skin or intestinal tract mucosa, they are recognized by TLRs, which activate immune cell responses. In the present study, the effects of food borne mycotoxins on TLRs have investigated in the female BALB/c mice. Mycotoxins (citrinin, deoxynivalenol, zearalenone) were orally administered to seven weeks old female BALB/c mice at different dose rate for 14 days, and several immunotoxicity tests were performed. Normalized fold expression of TLRs in immune organs were differentially expressed. After priming of RAW 264.7 macrophage cell line by different TLR ligands, it was observed that mycotoxins differentially modulated TLR signaling by increased or decreased production of IL-1 β , IL-10 and TNF- α . These results indicate that mycotoxins have multiple immune modulatory effects on TLRs in mice that may alter normal functions of immune system.

Keywords: Mycotoxins, Toll-like receptors, IL-1 β , IL-10 and TNF- α

Characterization of *Staphylococcus aureus* From Milk and Dairy Products Sold in Some Local Markets of Mymensingh District of Bangladesh

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Staphylococcus aureus is an important foodborne pathogen which can be found in a good extent in milk as it is a nutrient enriched medium for their rapid growth. The main objective of this study was to determine the prevalence of *Staphylococcus aureus* in raw milk and some dairy products sold in the local markets of Mymensingh by using conventional and molecular techniques. Raw milk, pasteurized milk, curd, cheese, lassi, matha, milk shake, roshmalai, custard, faluda, pudding and borhani were sampled from the local markets of Mymensingh. The prevalence and bacterial load of *S. aureus* in the samples were determined using the most probable number (MPN) method according to the International Commission on Microbiological Specifications for Foods (ICMSF, 1996) by using a surface plate technique. Out of 72 samples tested, all the samples were positive for *Staphylococcus spp.* and 57 isolates were coagulase positive *S. aureus*. The antimicrobial susceptibility of the pathogenic isolates were determined using 10 commercially available antimicrobial drugs by disk diffusion assay. The resistance pattern of coagulase positive *S. aureus* isolates of this study revealed that the most of the isolates (79.16%) were resistant to more than three antimicrobial agents. Some isolates (24.56%) showed resistance against both methicillin and oxacillin and intermediately resistant against vancomycin. In conclusion, our findings revealed that the milk and dairy product sold at local markets of Mymensingh are contaminated with multidrug resistant *S. aureus* which are very alarming for both human and animal health.

Keywords: Foodborne, Pathogen, *S. aureus*, Multidrug resistant.

Use of Detoxified Sulphur as a Feed Supplement for Methane Mitigation of Ruminant**Ashraf A Biswas** and Sung Suk Lee

This study was conducted to evaluate the effect of adding detoxified sulphur powder on ruminal fermentation parameters using *in vitro* fermentation technique. Ruminal samples were collected from ruminally cannulated Holstein Friesian cow, and grind commercial concentrate with or without addition of detoxified sulphur powder was used as substrate at 1g dry matter (DM). The treatments were: non addition, 0.2, 0.4, 0.6, 0.8, and 1.0% of detoxified sulphur powder and, hereafter referred to as control, T1, T2, T3, T4, and T5, respectively. Each serum bottle was filled anaerobically with 100 ml buffered rumen fluid (1:3 rumen fluid-buffer ratio) and sealed prior to incubation at 0, 3, 6, 12, and 24 h. pH, total gas (TG), ammonia nitrogen (NH₃-N), methane (CH₄), DM digestibility, organic matter (OM) digestibility, and volatile fatty acids (VFA) production were analyzed. Result showed that after 12 h of incubation, CH₄ production was significantly lowest in T1 (13.78 ml) highest was in control (20.16 ml). Non significantly highest total VFA was in T1 (64.28 mM) among the treatments after 12 h incubation but it was significantly highest in T1 (63.15 mM) after 24 h of incubation. After 2 h of incubation period, significant different was observed in case of A/P where lowest was in T1 (1.90) and highest was in T4 (2.44) among the treatments, but no significant difference was in pH, total gas, NH₃-N, DM digestibility, OM digestibility, acetate, propionate and butyrate within the control and T1 treatment group. Total bacterial DNA copies were significantly lower in treatment group than the control. From this *in vitro* experimental trial, it was observed that detoxified sulphur at 0.2% inclusion level is competent for production performance and ruminal CH₄ mitigation.

Key words: Detoxified sulphur, *In vitro*, Methane, Ruminant

Devil in the milk: relevant genetic makeup of cattle in Bangladesh

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Milk is considered as most nutritious, perishable and nature's almost complete food. It contains all the nutrients required for normal functioning of our body system. However, consumption of dairy products reported to play a role in the development ischemic heart disease, insulin dependent diabetes, atherosclerosis, schizophrenia, infant sudden death syndrome, gastrointestinal dysfunction and immune/inflammation related disorders, etc. β -casomorphine-7 (BCM-7) derived from digestion of A1 milk in human intestine, has opioid and cytomodulatory properties, is attributed as accountable agent. BCM-7 can potentially affect numerous opioid receptors in the cardiovascular, respiratory, nervous system and immune system in human. It is reported that the populations consume A2 milk have a lower incidence of cardiovascular disease and type-1 diabetes. Classification of A2 or A1 milk is based on β -casein gene variants. A2 β -casein is recognized as the original β -casein protein because it existed before a mutation caused the appearance of A1 β -casein in European cattle (*Bos taurus*) a few thousand years ago. The difference between A2 & A1 β -casein variants is a single nucleotide CCT to CAT which alter amino acid P at proline to histidine at 67th position of β -casein peptide chain. Present research focuses to determine genetic composition of cattle in Bangladesh in terms of A1/A2 β -casein. For this purpose a total of 300 blood samples were collected from three different regions of the country. Of these, 140 samples were derived from local and 160 from crossbred animal. DNA was extracted from blood and tested by polymerase chain reaction using allele specific primer. Of the tested samples, 44.0% (132/300) samples were found homozygous A2A2 (A2 milk producer), 49.0% (147/300) heterozygous A1A2 (Mixed A1A2 milk producer) and 7.0% (21/300) homozygous A1A1 allelic (A1 milk producer). Homozygous A1A1 allelic gene was not found in local animals tested but A1A2 was detected from them. A1A2 gene allele was found higher in crossbred animals. From the study it is evident that A1 milk, reported as devil in the milk, producing animal is available in Bangladesh.

Keywords: Beta-casein gene, A1/A2 milk, Cattle, Bangladesh

Thematic Paper: Ecosystem Health & Conservation-1**City Slickers: the reality of an urban ecosystem**

Paul Reiter, Professor of Medical Entomology at the Pasteur Institute in Paris, France

In Africa, ceramic pottery dates back at least 10,000 years. An important application was probably for pots used to carry and store water. At some stage, the mosquito *Aedes aegypti*, a forest species, adopted the village environment by breeding in such pots—a substitute for tree-holes or other natural containers—and by switching diet from rodent to human blood. This adaptation gained strength as the size of human communities increased. By now, the species is rarely found much more than 100m from human habitation and we must recognize that we have become the perfect host: we provide the adult mosquito with shelter, minimal exposure to predators, easy access to an abundance of blood and an enormous variety of artificial containers for their aquatic stages. Moreover, in the immensity of modern cities, the high density of the human population and the abundance and ubiquity of such containers offer a paradise for the mosquito and for the viruses it can transmit. Nevertheless, for more than half a century and despite major efforts and expenditure, this seemingly simple, man-made ecosystem defies our attempts to disrupt it. What is more, the recent emergence of Zika virus teaches us that, in addition to the long-recognized urban transmission of Yellow Fever, dengue and chikungunya, “new” viruses are waiting in the wings, perhaps ready to be transmitted in an urban cycle by *Ae. aegypti*. We have long been aware of several of these but have given them little attention. More undoubtedly await discovery. We must not ignore them as rural Hillbillies: they have the potential to become City Slickers.

Oral Presentations: Ecosystem Health & Conservation-1**Infection Dynamics and Viral Diversity in Bats Influence Nipah virus Encephalitis Outbreaks in Bangladesh**

Jonathan H. Epstein¹, Ariful Islam*¹, Simon J. Anthony², A. Marm Kilpatrick³, Shahneaz Ali Khan^{1,4}, Noam Ross¹, Ina Smith⁶, Carlos Zambrana-Torrel¹, Ausraful Islam⁵, Kevin J. Olival¹, Emily S. Gurley⁵, M. Jahangir Hossein⁵, Thomas Briese⁴, Mahmudur Rahman⁷, Gary Crameri⁶, Lin-Fa Wang⁶, Stephen P. Luby^{5,8}, W. Ian Lipkin², and Peter Daszak¹

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Nipah virus (NiV) is an emerging zoonotic virus that has caused seasonal outbreaks of encephalitis in Bangladesh with greater than 75% mortality. *Pteropus medius* is the putative reservoir in Bangladesh, though little is understood about NiV in these bats or their ecology. The primary route of transmission to humans appears to be date palm sap consumption. Between 2006 and 2012 we collected urine, blood, feces and saliva from 100 wild-caught *P. medius* from each of four districts inside and four districts outside the “Nipah Belt.” 100 bats were also sampled quarterly over six years from a population near recurring outbreaks. Urine, saliva and fecal samples were screened for NiV RNA by nested PCR. Serum was screened for anti-NiV IgG antibodies using an indirect ELISA, a recombinant expressed NiV-N antigen ELISA, and Luminex. We modeled serological data from the longitudinal study to identify seasonal trends. Nipah virus RNA was detected in 0-4% of bats, depending on time and location of sample collection, which included locations outside the Nipah Belt and times of year beyond human NiV season. IgG-positive bats were found throughout Bangladesh (seroprevalence: 20% - 56%). All SIR models show recurring outbreaks within a single bat population approximately every two years, following periods of waning immunity. Adults drive outbreaks in bats, and appear to become susceptible to reinfection after approximately 7 years. Phylogenetic analysis of a 224bp segment in the NiV N-gene from 13 samples from the same population but across different time points showed >98% sequence homology. A divergent strain of NiV was identified in eastern Bangladesh. The divergent N gene sequences in different locations, but N gene stability in one location over time, suggests that there may be localized strains persistently circulating in bats. Telemetry studies show limited long-range movement of these bats, suggesting that there is limited connectivity among distant colonies in Bangladesh, which may relate to observed viral strain diversity. However, NiV detection in bats was not restricted to the Nipah belt, suggesting spillover would be possible anywhere in Bangladesh if a suitable strain and bat-human interface was present. Our data support the conclusion that *P. medius* is the reservoir for Nipah virus in Bangladesh and likely to be an ongoing source of human infection. Seasonal and location-specific human activities such as date palm sap harvesting, concurrent with viral circulation within local bat populations is likely to be the major driver of human outbreaks in Bangladesh.

Key words: Nipah, Bats, Telemetry, Ecology, Outbreaks, Viral diversity

Day 2

Second noon Session

Ecosystem Health & Conservation-1

Antimicrobial Resistance Pattern of *Salmonella* spp. Isolated from Resident Wild birds and Environment of Bangladesh

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Salmonellosis is one of the most common zoonotic diseases, and the presence of antimicrobial resistant *Salmonella* in wild birds and environment are the global public health threat. Throughout the last decades, multidrug resistance of *Salmonella* spp. has increased, particularly in developing countries. Therefore, a cross-sectional study was conducted to investigate antimicrobial resistance of *Salmonella* spp. isolated from two species of resident wild birds namely house crow (*Corvus splendens*) and Asian pied starling (*Gracupica contra*), and from the environmental sample (especially slaughter house, human medical and veterinary hospital effluent). Isolation of *Salmonella* spp. were done from the cloacal swab sample house crows and Asian pied starling whereas environment effluents were taken from the common drainage of slaughter house, medical and veterinary hospital. The salmonella were isolated based on standard bacteriological culture method and susceptibility tests were performed by using disc diffusion method. The results showed that isolated *Salmonella* spp. were 100% resistance to Penicillin, Oxacillin, and Clindamycin followed by Erythromycin (50-93%), Kanamycin (7-20%), and Cephalothin (30-67%) of both wild birds' species. Furthermore, the level of resistance of *Salmonella* spp. positive isolates were found 100% to Ampicillin, Enrofloxacin, Pefloxacin, Gentamycin and Erythromycin followed by Ciprofloxacin (67%), Oxytetracycline (33%) for positive effluent samples but Colistin and Neomycin were remained sensitive. Remarkably, resident wild birds and the hospitals and slaughter houses waste effluents has multidrug resistance *Salmonella* spp. In conclusion, wild birds and effluents could create a potential threat to human and animal health by transmitting AMR bacteria to the water body and other environmental resources through contamination. This finding is of public health importance as these wild birds and effluents might be reservoirs for transmission of AMR bacteria to human and animal.

Key words: *Salmonella*, AMR, resident wild birds, hospital, slaughterhouse, effluents

Poultry Farm Biosecurity and Bioexclusion: Poultry Delivery Practices between Farmers and Traders in Chittagong, Bangladesh

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Agriculture, including crop cultivation, livestock, and fishery, holds a key position in the 2030 Agenda for Sustainable Development. Meanwhile, the poultry industry, which has grown extensively over several decades and continues to be a major contributor to food security and livelihoods of local populations, stays under the threat of avian influenza in Bangladesh. In fact, Bangladesh is considered an avian influenza hot spot, as highly pathogenic avian influenza H5N1 is endemic in poultry within the country. Starting from the aftermath of the 2007 outbreak, the number of farms has been reduced to 55,000 in 2013 from 115,000 in 2007. Reactive behaviours have been preferred to preventive behaviours: An unsustainable policy of bird culling and an unsuccessful compensation policy in response to HPAI H5N1 outbreaks stand against investment in biosecurity as an effective form of protection against this poultry disease. Biosecurity has been and is still being neglected in Bangladesh. In particular, the delivery of poultry from farmers to traders requires high biosecurity standards; however, no systemic study has previously been conducted to explore biosecurity status in this regard. Therefore, a cross-sectional study was undertaken during May-June 2017 with a view to investigating the current status of biosecurity practices in commercial farms and assessing the farmers' knowledge and attitudes mainly on poultry rearing and trading in response to avian influenza in Chittagong region. The preliminary data analysis of the present study revealed most of the farms maintained the expected distance from the neighbouring farms according to the FAO biosecurity guideline. Contrarily, distance of residential area, trees hosting wild birds etc. from the study farms were strongly violated from the recommended distance. More than half of the farms were lack of protective fence and safe disposal system of sick and dead birds. Using footbath was the least practiced personnel hygiene. However, the goals like ensure good health and sustainable economic growth may turn out to be mere utopian dreams unless addressing this biosecurity issue with a view to producing safe food and combat HPAI zoonoses in compliance with one health approaches.

Keywords: Bangladesh, poultry farms, biosecurity, avian influenza, knowledge and attitudes

Save Life from Slow Death Trap: Case of Environmental Health of Bangladesh

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Environmental Health is a critical issue for Bangladesh being a country with extremely high population density. This issue in global context as estimated by WHO highlighted that about a quarter of the world's disease burden can be mitigated by minimizing environmental and related social risk factors. Hence, controlling air, water and soil pollution is increasingly getting priority in the development goals and plans of the country but needs much more attention. Moreover, environmental pollution control for safeguarding the environmental quality is associated with Sustainable Development Goal for ensuring environmental sustainability. Yale University's *2014 Environmental Performance Index* (EPI) covering two key policy areas: (i) protection of human health from environmental harm and (ii) protection of ecosystems. South Asia as a region has low EPI scores – and Bangladesh has a low EPI even within South Asia.

Bangladesh could avoid 10,000 deaths and save between 200 and 500 million dollars a year if indoor air pollution in four major cities can be reduced to acceptable limits.² Air pollution kills 15,000 Bangladeshi each year, according to a World Bank report. An annual government health survey has found that pesticide-related poisoning may be responsible for several thousand deaths each year in Bangladesh. There is no updated data and regular monitoring on environmental health statistics. The 2009 Health Bulletin recorded 7,438 pesticide-related poisoning deaths at more than 400 hospitals nationwide amongst men and women aged 15-49. BCAS reported more than 50% of waste generated by the industries goes to the rivers untreated³. Bangladesh is currently facing a serious threat to public health, with 85 million people at risk from arsenic (As) in drinking water and in food crops.

It is high time for human beings to take the 'right' action towards saving lives from such environmental death trap. One Health Action Platform for multi-disciplinary team with policy advocacy and program can play an effective role for an integrated approach to address this environmental health issues. If ignored today, these ill effects are sure to curb human existence in the near future. Existing national policies lacks integrated pollution control program action. There is a need for effective consolidated policy or act for controlling air, water, land and soil pollution. Coordinated research based program with adequate financial support and powerful enforcement with people's participation can bring a win-win situation.

Key words: Environmental Health, Human Health, Ecosystems, Pollution, Policy

² <http://www.bangladeshenvironment.com/index.php/polution-s/294-environmental-pollution-of-bangladesh-it-s-effect-and-control>

³ <http://fairbd.net/water-pollution-of-most-of-the-water-sources-in-bangladesh/>

Emergence of Multidrug Resistant *Enterococcus* in free range wildlife in Bangladesh

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There has been an increase in the emergence and reemergence of zoonoses and antimicrobial-resistant (AMR) in which wildlife serves as the reservoir. Evolving land use increases the interactions among people and animals and persuades bacterial resistance which has serious implications for human and animal health. The aims of this study were to determine the prevalence and AMR profile of *E. faecalis* and *E. faecium* in wildlife, and phenotypic and genotypic relevance among the isolates. We collected 777 fecal samples from Rhesus macaques (n=288), Bats (n=369) and Rodents (n=120) from 12 different area of Bangladesh. *Enterococcus spp.* were isolated using selective broth, KAA agar and PCR. *Enterococcus faecalis* & *E. faecium* prevalence rate were 39% (n=303; 95% CI:28-50%) and 20% (n=155; 95% CI:11-29%) respectively where prevalence of coinfection was 7% (n=54; 95% CI:18-35%). *Enterococcus faecium* infection was significantly higher in Rhesus macaques (33%) than Bats (10%) and Rodents (11%) (P<0.05). Nonetheless, there was no significant difference in the prevalence of *E. faecalis* among the three species. In disk diffusion test, 63%(n=71) of the tested isolates were multidrug resistance (MDR). Prevalence of vancomycin and gentamicin resistance (GR) enterococci were 26% (n=29; 95% CI:18-35%) and 23% (n=26; 95% CI:16-32%) respectively where 21% (n=24; 95% CI:13.5-28.5%) isolates demonstrated resistance for both. Vancomycin resistant (VR) genes *vanA*, *vanB* and/or *vanC₂* detected in phenotypically resistant *E. faecalis* & *E. faecium*, among them *vanC₂* were present in 59% (n=17) of VR isolates. Bifunctional *aac(6')-Ie-aph(2'')-Ia* gene was detected in 26/26 GR Enterococcal strains. Among other tested antibiotics (n=10); 95.5% (95% CI:89-98%) strains were streptomycin resistant followed by tetracycline 63%, erythromycin 61%, linezolid 30%, ampicillin 29% and ciprofloxacin 25%. However, imipenem, chloramphenicol and amoxicillin/clavulanic acid showed high sensitivity 78%, 83% & 96% respectively. Higher MIC value (MIC₅₀/MIC₉₀) was observed against ceftriaxone (≥1024/≥1024) and gentamicin (16/128). Alarming MDR profile of enterococci in wildlife of Bangladesh might be due to coexistence of human-animal ecosystems. Antibiotic resistant enterococci in wildlife species closely associated with people suggests that environmental contamination may be responsible for wildlife infections. Continued surveillance for AMR organisms in people and wildlife will improve our understanding of prevalence and transmission patterns.

Keywords: Wildlife, Zoonosis, Antimicrobial-resistant, Enterococcus and Multi-drug Resistance

Thematic Paper: Ecosystem Health and Conservation-2

The Global Virome Project: The *Beginning of the End of the Pandemic Era*

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Emerging infectious diseases (EIDs) are rising in frequency, leading to an exponential rise in their economic impacts, and threatening global health, livestock production and food security. Zoonotic viruses from mammalian and water bird hosts are a particular threat, and the Global Virome Project (GVP) has been launched to strategically address this. The GVP aims to identify and characterize the majority of currently-unknown viruses in wildlife that have potential for zoonotic infection. Based on patterns of viral discovery in wildlife, we estimate that there are around 1.6 million as-yet undiscovered viruses in wildlife from viral families known to infect humans, and more than 500,000 likely to have the potential to become zoonotic. The GVP sampling can be targeted to geographical hotspots of EIDs to the species most likely to harbor zoonoses, and to those for which we can calculate a high proportion of 'missing zoonoses'. This would mean that a 10 year GVP program would discover the majority of unknown viruses, and a disproportionately high percentage of the global zoonotic risk.

Key Words: Emerging infectious diseases, zoonotic viruses, global health.

Oral Presentations: Ecosystem Health and Conservation-2**Diversity of Gastrointestinal parasite in rhesus macaque (*Macaca mulatta*) in human-wild life ecosystem in Bangladesh**

Shariful Islam^{1,2}, Md Kaisar Rahman^{1,2}, Md. Helal Uddin³, Md. Mustafizur Rahman⁴, Mohammad Nizam Uddin Chowdhury⁴, Mohammad Mahmudul Hassan³, Meerjady Sabrina Flora² and Ariful Islam^{1*}

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Anthropogenic environmental changes influence the diversity, alteration of ecology and infection risk in the particular species. Parasitism in wildlife influenced by host ranging patterns, density, intraspecific and interspecific contact rates and diet. Rhesus macaque is widely distributed in Asia and accustomed to coexist with humans and flourish near human settlement, in both urban and rural areas. From 2015 to 2016, we collected 182 non-invasive fecal samples at different land gradient to examine parasite prevalence, helminth eggs in the feces, and number of parasitic taxa by direct smear, sodium nitrate flotation and fecal sedimentation, with respect to the annual cycle, sex and age. We identified 12 taxa of GI parasites, consisting of seven nematodes (*Toxocara* sp., *Trichuris* sp., *Strongyloides* sp., *Trichostrongylus* sp., *Dictyocaulus* sp., *Enterobius* sp., and *Ascaris* sp.), 4 cestode (*Hymenolepis nana*, *Monizia* sp., *Diphylobothrium* sp., *Taenia* sp.) and 1 trematode (*Fasciola buski*). We observed high prevalence of parasites (55%; n=100; 95%CI: 47-62), with the most prevalent being *Strongyloides* sp. (26%), *Trichuris* sp. (21%) and *Trichostrongylus* sp. (17%). The higher prevalence was in rural area (43%) where the macaques mixing with livestock's and human; and get easy access to dumping areas compared to urban area (16%). The adult macaques were more prevalent (45%) to GI parasites infection than sub-adults and neonates. Our results demonstrate macaques infected with divers species of GI parasites, with high prevalence and zoonotic potential. Living close to human activities should consider when evaluating the maintenance of GI parasites and its transmission between reservoirs and humans.

Key words: Ecology, Gastro-intestinal, Parasites, Macaques, Bangladesh

Determining hotspots of human exposure to rodents, bats and monkeys in Bangladesh

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Bangladesh is at risk for emerging infectious disease transmission from wildlife to humans because of its extremely dense human population, wildlife diversity, deforestation, urbanization and habitat migration. There are some known examples of diseases that have been transmitted to humans from wildlife in Bangladesh, however, efforts to identify new emerging threats should be pursued. The objectives of this study were to identify the frequency of human exposures to rodents, bats and monkeys and to map human exposure to these animals across Bangladesh, their seasonal variation, and to inform in-depth studies of disease transmission.

From 2013 through 2016, we conducted a cross sectional survey in a nationally representative sample of 9,512 households from 952 randomly selected urban and rural communities. The most senior household member between 18 to 60 years of age was interviewed about any household members' exposures to rodents, bats and monkeys within the past month. We performed kernel density estimation to measure intensity of each exposure geographically. The spatial dependence between exposure and longitude was examined by scatter plot and correlation coefficient.

Throughout the country, 90% (95%CI: 89-91) of respondents reported observing rats/mice in their households, 51% (95%CI: 50-52) reported observing bats and 2% (95%CI: 1.6-2.2) reported observing monkeys close to their households. Among all households, 8.5% (95%CI: 7.9-9.1) reported direct contact with rodents, 0.5% (95%CI: 0.4-0.7) with bats and 0.05% (95%CI: 0.022-0.13) with monkeys. Contact with rodents was more commonly reported in the two largest metropolitan areas and their surroundings. Human exposure to bats was more common in the southwest and northern part of the country and exposure to monkeys was primarily clustered in the southwest and northeast. There was no seasonality in exposures.

Of the 160 million people in Bangladesh, 13.6 million are exposed to rodents every month, 800,000 to bats and 80,000 to monkeys. Diseases known to be transmitted through these exposure routes could be prevented by targeting high contact areas for surveillance and prevention efforts. Information about where these exposures cluster could be used to inform studies aimed at identifying emerging disease from rodents, bats and monkeys.

Keywords: Human exposure, rodents, bats, monkeys, Bangladesh

Assessing Viral Diversity in Peridomestic Small Mammals, Bangladesh.

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Rodents and shrews live in close proximity to humans and have been identified as important hosts of zoonotic pathogens. The results of viral family-level PCR testing performed on rectal and throat swab collected from 427 rodents and shrews from 10 districts in Bangladesh between June 2011 and October 2013 are presented. All samples were screened for 10 viral families (adenoviruses, arenaviruses, astroviruses, bunyaviruses, coronaviruses, flaviviruses, hantaviruses, influenzas, paramyxoviruses, and rhabdoviruses) using consensus PCR. PCR products were sequenced to confirm positive. A subset of the multiple PCR bands were cloned and sequenced. Based on a BLASTN search, 52 viruses were identified including 5 influenza A viruses, 45 novel adenoviruses, 1 novel mamastrovirus and 1 novel West Nile strain. Influenza-A viruses were present in 1.3% (n=150, 95%CI: 0.4-5.7) of *Suncus murinus*; 4.6% (n=22; 95%CI: 0.1-22.8) of *Mus musculus* and 2.2% (n=90; 95% CI 0.3-7.8) of *Rattus rattus*. Novel adenoviruses were present in 6% (n=150, 95% CI: 2.8-11.) of *S. murinus*; 15.8% (n=76; 95%CI: 8.4-26) of *Bandicota bengalensis*, 11.4% (n=9; 95%CI: 3.4-20.5%) of *Bandicota indica* and 16.7% (n=15; 95%CI: 9.6-26.0) of *R. rattus*. The novel mamastrovirus, a new astrovirus, was detected from *B. bengalensis* and the virus related to West Nile was identified in *R. rattus*. These findings represent the first description of viral diversity in apparently healthy wild peridomestic small mammals in Bangladesh and form a basis for understanding the types of viruses circulating among small mammals. Additional genomic and experimental studies are required to ascertain the zoonotic potential of novel viruses.

Key words: Novel virus, Diversity, Rodents, Shrews, Zoonotic

Nesting Ecology and Biomorphometry of Yellow-wattled Lapwing (*Vanellus malabaricus*) nearby a Protected area at Gazipur District in Bangladesh

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Yellow-wattled Lapwing (*Vanellus malabaricus*), an uncommon village bird, inhabit mostly in the grasslands, agricultural fields and drier parts of the country recently became Near Threatened in Bangladesh. Breeding ecology of this bird was not studied earlier in the country. This study was, therefore, aimed to investigate the nesting ecology and biomorphometry of Yellow-wattled Lapwing in Bangabandhu Sheikh Mujibur Rahman Agricultural University and adjacent areas nearby a Protected area named Bhawal National Park, a deciduous forest, at Gazipur district. Breeding birds were searched, identified and photographed in this study. Nesting ecology and natural history including habitat type, mating, nesting behavior, egg and nestling characteristics were recorded. Biomorphometric parameters of eggs (n=14 from 4 nests, yr-1 and n=22 from 6 nests, yr-2) and nestlings (n=6 from 4 nests, yr-1 and n=15 from 6 nests, yr-2) were also recorded. The length and width of eggs were measured by venire calipers and measuring scale. Weight of eggs and nestlings were taken using a mobile digital balance. Results of the study indicated that the mean±SD length and width of *Vanellus malabaricus* eggs at lay for yr-1 and yr-2 were 3.34±0.16 cm & 3.32±0.15 cm; and 2.51±0.13 cm & 2.51±0.17 cm, respectively. The mean±SD weight of eggs at lay was 13.70±0.46 g & 13.64±0.44 g, respectively for yr-1 and yr-2. Mean egg lay per bird and hatching rates were 3.50 & 42.86% and 3.67 & 68.18%, respectively for yr-1 and yr-2. On the other hand, mean±SD weight of nestlings at hatching for yr-1 and yr-2 was 9.27±0.50 g & 9.12±0.61 g, respectively. In conclusion, nesting ecology and biomorphometry of eggs and nestlings of *Vanellus malabaricus* are figured out. The less hatchability of *Vanellus malabaricus* eggs might be due to their open nesting behavior that favors disturbances in incubation by small boys, workers and animals like jakals, mongooses, monitor lizards etc as well as natural disasters like excessive rain and flood. Further detailed investigation is needed to study breeding, nesting & hatching behavior and conservation of this bird in Bangladesh.

Keywords: *Vanellus malabaricus*, Nesting ecology, Eggs, Nestlings, Biomorphometry

Poster Presentation: Emerging Infectious Diseases and Zoonosis**Prevalence of immune escape highly pathogenic avian influenza virus A/H5N1 in the vaccinated poultry in Bangladesh**

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Highly pathogenic avian influenza virus (HPAIV) A/H5N1 subtype is a major issue for the poultry industry in Bangladesh during first incursion of HPAIV. Vaccination is one of the tools implementing in Bangladesh since 2013 including OIE classical methods to control HPAIV. Vaccination splits the scientific community, due to the risk of it being a potential driving force in HPAIV evolution through the selection of mutants able to escape vaccination-induced immunity. It is therefore essential to monitor the shading of HPAIV in vaccinated flock. Considering the facts, we supervised commercial (n=60) and breeder (n=8) farms having different husbandry and receiving AIV (H5N1) vaccine, with filling a pretested questionnaire in a face-to-face interview of farm owner and/or designated workers to verify the hygienic practice and biosecurity. Cloacal and oropharyngeal swabs in case of live birds and morbid materials such as trachea have collected thrice yearly. Virus was isolated from the samples and performed rRT-PCR for influenza type A and subtype specific primers. Complete HA gene of selected isolates have sequenced and analyzed. In biosecurity scoring test, most of the farms has poor biosecurity score of <17 followed by moderate and good biosecurity an average score of 27.40 and 35.97 respectively, from total score of 42. There were low (<log₂⁴), moderately low (≥log₂⁴) and protective (≥log₂⁶) level of mean HI titer in 30% (n=18; 95% C.I. 19.25-40.8%), 23% (n=14; 95% C.I. 13.1-32.9%) and 47% (n=36; 95% C.I. 35.3-58.7%) farms respectively against HPAI vaccine. During active surveillance, 34% (n=23; 95% C.I. 22.9-44.1%) farms were shading AIV presumably allied with farm's bio-security and birds acquired immunity. Among vaccinated farms, 4.4% (n=3, 95% C.I. 0-9.2%) and 22% (n=15, 95% C.I.12.3-31.7) were shading H5N1 and H9N2 respectively. Coinfection of H5N1 and H9N2 were persist in 7.4% (n=5, 95% C.I. 1.2-13.5%) farms. Complete HA gene sequence data of H5N1 isolates revealed that shading virus strains are similar to 2.3.2.1a clade that circulated since 2015 in Bangladesh. Our findings suggest that LPAI and HPAI viruses are circulating in vaccinated flocks might be due to vaccine strain variants, cutting vaccine dose or coverage that could result in enhanced antigenic drift.

Keywords:Avian influenza, Vaccine, Biosecurity and Evolution

Circulation of Highly Pathogenic Avian Influenza A/H5N1 in Dhamrai and Savar Upazila, Bangladesh

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Bangladesh has experienced outbreaks of avian influenza (AI) frequently from 2007 until 2012 and thereafter only sporadic outbreaks were reported. In January 2017, a cluster of sick and dead poultry in Dhamrai Upazila was reported to Department of Livestock Services (DLS). DLS confirmed Influenza A (H5N1) and notified to OIE. Subsequently, an investigation was conducted in Savar and Dhamrai to determine the extent of the outbreak and whether HPAI, including other subtypes, has been circulating in LBMs and among the wild birds and to identify the possible sources of AI for the reported event. The team surveyed nearby all live bird markets (LBM) in Savar and Dhamrai Upazila in Dhaka District and extended up to 24km radius in outbreak areas. Oropharyngeal and cloacal swab samples from dead crows (N=3) and environmental swab samples from LBMs (N=77) were collected. All swabs tested by real-time RT-PCR for Influenza-A (M gene), H5/H7/H9/N1. Samples are also being tested using PREDICT's pan-influenza consensus PCR to detect any additional subtypes that may be circulating. The team observed crows feeding on poultry wastage in neighboring LBMs and results expressed that, in crow 100% (n=3; 95%CI: 29-100) were positive for influenza A/H5N1. None of the LBM and crow samples were positive for H7 subtypes. Of the 77 environmental samples, 40% (95%CI: 29-52) were positive for influenza-A, including: A/H5 8% (n=6; 95%CI:3-16), A/H9 9% (n=7; 95%CI: 4-18) and A/untypable 23% (n=18; 95%CI:14-34). Twenty six percent of urban LBMs (n=23; 95%CI:10.2-48.4) were positive for influenza A/H5 and none of rural (n=22) LBMs were positive for A/H5. Presence of waterfowl having higher (75%; n=4; 95%CI:19- 99) A/H5 positive than others (7%; n=41; 95%CI: 2-20). H5 positive LBM samples were tested for N1; results revealed that 50% H5 (n=6; 95%CI: 12-89) were positive for N1 and the remaining were negative which indicates that other N types might be co-circulating in LBMs. No human cases were reported. Our findings suggest that low pathogenicity and highly pathogenic avian influenza viruses are circulating in LBMs. In a response to an outbreak of influenza A on a farm, we found that influenza A appears to be circulating in LBMs and crows. Consensus PCR assays that detect all Influenza A subtypes may be useful in identifying novel or less common subtypes.

Key words: Outbreak Investigation, Avian influenza, LBM, Crow

Surveillance for avian influenza among crows in Bangladesh

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Earlier studies have demonstrated that domestic poultry sold in the live markets throughout Bangladesh carry a wide range of avian influenza virus (AIV) strains. Poultry sold at the market are usually slaughtered on site, and the offal is disposed of without any containment. As a result, crows get exposed to this potentially infected waste. Our objective was to assess the presence of AIV among crows associated with these markets. We sampled crows from April through May, 2014 from Dhaka, the capital of Bangladesh. We collected 5000 crow fecal environmental swabs and made a pool of 10 (total 500 pool) in viral transport media for testing of AIV using real time reverse transcriptase polymerase chain reaction. Partial sequencing of all eight segments of AIV was conducted for strain identification. A single pool was tested positive for AIV and the sequence data identified it as H9N2. From 1998 to 2016, 28 laboratory confirmed human cases of H9N2 virus was reported to WHO of which three were from Bangladesh. As this strain has the potential to reassort with H5N1, H7N9 and H10N8 viruses, and can cause human infections, presence in a ubiquitous bird(s) as crows can potentially be a significant public health risk.

Key words: Avian influenza, crows, H9N2, Bangladesh

What perceptions, knowledge and attitudes guide backyard poultry farmers to implement Avian Influenza control measures in Bangladesh?

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Effective control of HPAI outbreaks on backyard poultry farmers is influenced by farmer's perceptions, knowledge and attitudes. We used the Health Belief Model and the Snyder Hope Scale framework, to explore determinants of HPAI preventive measures conducted by 108 poultry farmers in the Chittagong district of Bangladesh. Almost all farmers (>94%) acknowledged the severity of HPAI infection in poultry and the contagiousness of HPAI virus infection in poultry. Farmers were aware of interventions to minimise the risk of infection to their flocks and themselves. Using Structural Equation Modelling we were able to identify that farmer's perceptions on the susceptibility of poultry and people to become infected with HPAI virus increased their likelihood to implement preventive actions to reduce HPAI infections and spread. Perceived barriers to HPAI control (e.g. cost associated with building poultry houses) refrained farmers from taking preventive actions. Surprisingly, perceived severity of HPAI infection in poultry and people, perceived benefits to farmers when implementing preventive actions and activities to motivate farmers to implement HPAI control (e.g. training or information campaigns) did not influence the likelihood of HPAI control measures. Thus, HPAI control actions by backyard poultry farmers in Bangladesh are mainly driven by the perceived possibility of infection and perceived obstacles to disease control. Used the Snyder Hope Scale, a cognitive model describing the farmer's capacity to initiate actions (for example to explore multiple options to reach the goal of controlling HPAI), we identified more two 'hopeful' groups: 1) farmers who were aware of HPAI occurring and 2) members of certain religious groups. Our research highlights that behavioural and social determinants of poultry farmers need to be considered for the development of successful HPAI control programs.

Key Words: Avian Influenza, Backyard poultry farmers, Health Belief Model, Hope Scale, Bangladesh

High mortality with nervous signs in young ducks in 2017 due to H5N1 highly pathogenic avian influenza virus

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In Bangladesh, highly pathogenic avian influenza virus (HPAIV) of subtype H5N1 was first detected in chickens in February 2007. HPAIV of clade 2.2 were circulating among poultry in Bangladesh before the introduction of clade 2.3.2.1 in 2011. Majority of the avian influenza outbreaks were limited to chickens with occasional spill-over to feral crows; however following the introduction of clade 2.3.2.1 virus few outbreaks in other avian species such as ducks, quails and migratory birds were also recorded. Clinical outbreaks of HPAIV in ducks are relatively rare in Bangladesh, although the virus is frequently detected in apparently healthy ducks. Here we performed pathological and molecular phylogenetic analysis of six outbreaks of HPAIV in ducks. Six freshly dead or sick ducks from 6 farms of 4 Upazilla (Sadar, Bhaluka, Tarakanda and Issorgonj) of Mymensingh district were submitted to the Department of Pathology, Bangladesh Agricultural University for routine diagnosis during the period from April to June 2017. The ducks were of 4-9 weeks of age. The farm size varied from 150-1550. Clinically, the affected ducks showed severe nervous signs, such as shaking of head and twisting of neck. The morbidity ranged from 13-100% (average 43%) and the case fatality ranged from 15-91% (average 50%) at the time of investigation. At necropsy, congestion in brain was found consistently in all affected ducks. In addition, congestion and/or haemorrhages were found in trachea, lungs and other visceral organs. The presence of influenza A virus in the affected ducks were detected by a matrix gene specific RT-PCR. The complete coding region of both hemagglutinin and neuraminidase gene was amplified and sequenced from all six samples. BLAST search in the GenBank revealed that all six isolates belonged to the H5N1 subtype of HPAIV. Phylogenetic analysis showed that the present isolates clustered with the previously reported clade 2.3.2.1a viruses. Full length amplification and characterization of internal genes are in progress.

Keywords: HPAI, H5N1, ducks, clade 2.3.2.1, nervous signs, Bangladesh

Poultry trading networks in Bangladesh: implications for control and surveillance of avian influenza.

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Highly pathogenic avian influenza subtype H5N1 has been considered endemic in Bangladesh for ten years now. Live bird trading and marketing play a major role in the maintenance of avian influenza viruses (AIVs). In Bangladesh, live bird trading is ubiquitous, more than 90% of poultry are marketed through live bird markets (LBMs). Yet, national poultry trading networks and patterns have scarcely been described, nor have their potential role in virus spread and maintenance been assessed. This study aimed at assessing the potential of poultry trading networks to facilitate AIV spread and maintenance, and to identify suitable targets for control and surveillance programs. Data on poultry trading practices in Bangladesh was collected during two cross-sectional questionnaire surveys. A first survey, conducted in 2014, included 849 poultry traders from 138 LBMs in 17 districts. A second survey, conducted in 2015, included over 2,000 poultry traders from 159 LBMs in 3 sub-districts. The network of contacts between farms and LBMs resulting from commercial movements of live poultry across Bangladesh were constructed according to poultry types and their key characteristics were compared. Poultry trading routes were compared according to their relative importance and the type of intermediates involved in the poultry transaction chain. Poultry trading practices and routes varied according to poultry type. Industrial broiler chickens, the most commonly traded poultry, were generally sold in LBMs close to their production areas, whereas ducks and backyard chickens were moved over longer distances, and their transportation involved a greater number of actors. They also spent more time in transport between their farm of origin and the consumer than broilers. Although trading routes differed according to poultry types, they interacted in LBMs, shaping a highly connected and disassortative poultry trading network that could promote AIV spread and maintenance. The removal of small number of LBMs significantly reduced its connectedness, and the maximum size of potential epidemics. Knowledge of trading patterns could be used to target control and surveillance interventions.

Key words: Avian Influenza, surveillance, poultry network, Bangladesh

The source-sink model and its implications for spillover risk to humans and detection of rare pathogens – what the patterns of human H5N1 and H7N9 cases tell us about emerging spillover risk

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For emerging diseases such as avian influenza (AI), traditional surveillance systems may not be able to detect disease events due to low prevalence, low surveillance intensity, and barriers to reporting. Sink surveillance utilizes a source-sink ecological model that predicts the accumulation of pathogens of interest from various sources (production areas) in a common location called the sink as a result of movement of pathogen hosts. Poultry are most sinked into mega-urban cities which have very high demand for poultry from outside areas. To meet this high poultry meat demand, live birds, along with any pathogens they are carrying, are brought from various farms in different regions into mega-urban LBMs. As a result of accumulating very large numbers of poultry, live bird markets (LBMs) in mega-urban sink areas also accumulate AI viruses, thereby greatly increase the spill-over risk to humans who enter these LBMs as either consumers or traders. Patterns of the emergence of H5N1 and H7N9 human cases in mega-urban areas support the source-sink model and should be further investigated. The source-sink model and its implications for emerging disease accumulation, amplification, and spill-over to human populations should be further studied in order to better inform surveillance and public health risk mitigation strategies.

Genetic diversity of zoonotic *Echinococcus* species in Buffalo, Sheep and Human in Bangladesh as revealed through phylogenetic analyses**M O Faruk,^{1*}** M F Karim,² M Masduzzaman,¹ S Chowdhury,¹ M A Hossain,¹ and AMAM Z Siddiki¹

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The dog tapeworm *Echinococcus granulosus* causes cystic echinococcosis (CE) in humans and many domestic animals all over the world including Bangladesh. Until now limited molecular data are available on this important zoonotic cestode of significant public health importance. We attempted to identify circulating genotypes of *E. granulosus* isolated from buffalo, sheep and human using DNA based molecular tools. Two genetic marker namely, 12S rRNA and Cytochrome oxidase 1 (COX 1) gene were used for this study that successfully identified *E. granulosus sensu stricto* G1, G3 strain and *E. ortleppi* (G5 strains). Twenty eight hydatid cyst samples were collected from a total of 727 buffalo and sheep from local slaughterhouses in Chittagong. Four human samples were collected from the Hepatology Unit of Sir Salimullah Medical College and Hospital (Mitford) based in Dhaka, Bangladesh. Germinal membrane and protoscoleces were used for genomic DNA extraction by using commercial DNA extraction kit. Two strains namely *E. granulosus* G1 strain and G3 strain were amplified successfully through conventional PCR and four amplified products were sequenced for further bioinformatics analyses. Sequences derived from three buffalo samples and one sheep samples were submitted to publicly accessible GenBank databases. Phylogenetic analyses revealed that these sequences were aligned with common sheep strain G1 and buffalo strain G3 of reference sequence of NCBI BLASTn search. Present study documented the presence of common sheep strain G1 and Buffalo strain G3 of *E. granulosus* in this geographical area.

Keywords: *Echinococcus granulosus*, Cox1, 12S rRNA, molecular characterization, Bangladesh

Molecular Epidemiology of Anthrax in Domestic Animals of Bangladesh

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Bovine anthrax, locally known as 'Torka', is believed to be enzootic for long in Bangladesh. A series of anthrax outbreaks infecting over 140 cattle and goats have been reported in different districts of Bangladesh since 2009. The reports on anthrax after the series outbreaks since 2010 indicate that the disease remains a serious problem in Bangladesh. Considering the emerging threat of anthrax to the veterinary and public health in Bangladesh, few molecular studies on the isolates from this country have been carried out recently. The present research work was designed to explore the genetic diversity of *B. anthracis* circulating in Bangladesh based on hierarchical fingerprinting system PHRANA: CanSNP and Multiple Locus Variable Number Tandem Repeat Analysis (MLVA) using 31VNTRs which exhibits greater resolving power and allows differentiation between closely related strains of the same CanSNP group. This study was carried out by bridging collaboration among the Chittagong Veterinary and Animal Sciences University, the University of Dhaka, the Bundeswehr Institute of Microbiology, Munich, Germany, the Istituto Zooprofilattico Sperimentale of Puglia and Basilicata, Italy and the Louisiana State University, USA. The first investigation was conducted to isolate *B. anthracis* from 169 samples (73 soil, 1 tissue, 4 bone and 91 bone meal samples) collected from 12 different districts of Bangladesh in 2012 – 2015, by sending the samples to the Istituto Zooprofilattico Sperimentale of Puglia and Basilicata, Italy. In the second investigation, 24 samples including 16 soils, 6 swabs and 2 water were collected between July and September 2013 from different cattle farms in the anthrax reported areas in the districts of Sirajganj and Tangail and shipped to Bundeswehr Institute of Microbiology, Munich, Germany. To detect *Bacillus anthracis* from the samples the Ground Anthrax Bacillus Refined Isolation (GABRI) method was used. Molecular investigation on the isolates obtained was conducted by CanSNP to analyse the phylogenetic origin of strains, MLVA with the analysis of 15 Variable Number Tandem Repeats (VNTR) (for the isolates obtained from the 1st investigation), 31VNTR based MLVA (for the isolates obtained from the 2nd investigation) and Single Nucleotide Repeats (SNR) analysis. Whole-genome sequencing was also performed for five isolates isolated from the districts of Sirajganj and Tangail. All the bone meal samples were negative for *B. anthracis*. CanSNP analyses for the phylogenetic clustering showed that all the isolates (10) obtained from the 1st investigation belonged to the lineage A major subgroup A.Br.001/002, which represent the same group circulating in China and other countries in South-East Asia. The MLVA-15 loci analysis of the isolates demonstrated the presence of four genotypes; two of them were previously identified in the district of Sirajganj. The sub-genotyping, conducted with SNR analysis, revealed the presence of eight subgenotypes. All the strains (8) of the 2nd investigation also belonged to CanSNP group A.Br.001/002 differing only in a few of the 31 VNTR-markers. Whole genome sequences were obtained from five of these strains and compared with genomic information of *B. anthracis* strains originating from various geographical locations. Characteristic signatures were detected defining two

“Bangladesh “clusters potentially useful for rapid molecular epidemiology. Not importation of bone meal from abroad but the practice of burial of dead animals and the improper removal of infected carcasses could be the mainstay of causes that determine the contamination and persistence of *B.anthraxis* in the environments of anthrax-prone districts in Bangladesh. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. CP015777 (pXO1), CP015778 (pXO2), and CP015779 (chromosome).

Investigation on Brucellosis associated with reproductive disorders in small ruminants

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A seroepidemiological study of Brucella infections was conducted in small ruminants at northern barind tract in Bangladesh between January 2012 and July 2015. A cross-sectional multi-stage sampling technique was employed to select 475 small ruminants, 396 goats and 79 sheep from the target populations. Sera were collected from the animals, and serially tested using Rose Bengal test and iELISA according to the protocol recommended by the manufacturer. Overall prevalence and prevalence with respect to explanatory variables were established, and potential risk factors for seropositivity were analyzed using a crosstab, Chi square, student t test, correlation and binary logistic regression. The results showed that 12.0%, 9.3%, and 2.7% of the tested small ruminants and goats, sheep, respectively, had antibodies to Brucella antigen. Brucellosis was insignificantly highest positive reactors value in species, age, parity, density of population and location were 5.6%, 8.9% in older goat and sheep; 7.6%, 5.5% and 15.7% first parity in small ruminants, goat and sheep, 8.2% small flock of small ruminants; 5.9%, 1.5%, 2.3% and 2.3% into Rajshahi, Chapainawabgonj, Natore and Naogaon district at northern barind tract in Bangladesh. The brucellosis has higher insignificant negative correlation with local breed (6.9%); heavy body weight (6.1%) and rainy seasons (6.1%) of small ruminants in study area. Brucellosis was positive and highly ($p < 0.01$) significant effect on sex value in female (9.5%) but negative effect with biosecurity on traditional (8.2%) and feed habit on grazing (8%) in small ruminants. The seropositive rate of brucella in coordination with cervicities, abortion, retained placenta, anoestrus, repeat breeding, dystocia, stillbirth, vaginal prolapse or uterine prolapse, endometritis or pyometra, orchitis, postitis, urinary tract infection and epededymitis were 1.9%, 2.1%, 1.7%, 1.1%, 0.6%, 0.6%, 0.4%, 0.6%, 0.4%, 0.2%, 0.2%, 1.7% & 0.4% , respectively. The overall prevalence of brucellosis in relation with pregnant status of SR was recorded as 12.6% but pregnant 4% and in non-pregnant 8.6%.

Key words: Brucellosis, small ruminant, Barind tract and risk factors.

Retrospective Clinical Follow-up of Post Exposure Prophylaxis with Injection ARV or Injection ARV & Injection Equine RIG in Animal Bite Patients Attending at BITID

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Rabies is a fatal but preventable zoonotic disease.. Bangladesh Institute of Tropical & Infectious Diseases (BITID) is the national institute for tropical-infectious diseases in the country which is working as a center for rabies control under the Rabies Elimination Program of the CDC. This report is about the cumulative follow-up of patients inflicted with animal bites who had attended the institute during the period of September 2014 till the end of December 2015. It is important to understand the characteristics of animal bite and subsequent clinical outcome of the post-exposure prophylaxis that was provided, to those patients to assess the situations of the logistics supply and demand as well as the relative efficacy of the ARV and ARV+ RIG in the prevention of Rabies. Data from all the patients who attended the BITID for post-exposure prophylaxis following animal bite had been recorded in the register. Patient confidentiality had been strictly maintained. Retrospective clinical follow up of post exposure prophylaxis with ARV or ARV +RIG among animal bite patients attending the BITID during the mentioned period, all the available patient information from rabies vaccination register had been compiled with a data table. Then data analysis was done. A total of 1708 persons received vaccination during the mentioned period. The data of 1398 patients had been analyzed and the rest 310 patients were excluded from the analysis because of the incompleteness of the information in the register book or any other reasons. The 1398 patients were analyzed in two groups, Group A comprised of 886 patients receiving Inj ARV only and the Group B included 512 patients who received both of Inj ARV and RIG. Among the analyzed patients, CAT- III bites were more prevalent at 54.7%. The total of 84% of the patients who attended for rabies PEP completed the vaccination schedule. Most of the CAT- III patients attended the institute within 2 days of the animal bites. Among the patients, all of the CAT- II & CAT- III bite cases received ARV vaccination but RIG could not be provided to all CAT- III patients as govt. supply was insufficient. No patients had any adverse effect following vaccination or RIG and none had developed Rabies.

Key words :ARV, RIG, BITID, CDC, PEP

Rabies Prevention Awareness Building Among Students to Eliminate it from Bangladesh

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Rabies is an acute viral encephalomyelitis caused by Rabies virus. It is 100% fatal zoonoses that causes numerous death in human and animal every year in Bangladesh. Ignorance is one of the main cause for high rate of rabies incidence in Bangladesh. Rabies is 100% preventable disease with timely proper medical care and many of its prevention tools are simple and available everywhere. But due to ignorance people cannot use these properly after being exposed to suspected rabid animal. The current program is a pilot project that was implemented in two school and college in Gazipur district, Bangladesh from the month, January 2017 to March 2017. The objective of the program was to improve the knowledge of the student on (a) How to avoid rabies exposure, (b) How to apply post exposure treatment, (c) How to do animal rabies control, (d) How to motivate community people to prevent rabies. The program was implemented among the students of selected school and college by rabies prevention experts, trained teachers and students from the institutions on the selected topics. The present status of knowledge of the students was measured by pre-KAP (knowledge, attitude and practice) study with pre-designed and pre-tested questionnaire regarding various aspects of rabies and its prevention. The students got training in two months using different training instruments. The development of knowledge was measured by post KAP study after training. Data was collected for analysis to evaluate the development of knowledge the students on prevention and control of rabies. Analysis of pre-KAP and post KAP study showed very nice development of knowledge of the selected students on fundamental methodologies of prevention and control of rabies. The data was preserved for publication. Students are the representatives of millions of families from every nook and corner in Bangladesh. Getting training the students are capable to disseminate the knowledge on rabies and its prevention measures to their family members and other people, wherever they go throughout their life and thus it will reflect very good impact on the subject. The achieved success of the program will encourage the donors and other authorities to expand it throughout the country and it will be an effective strategy for prevention and control of rabies in Bangladesh.

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Characterization of *staphylococcus* species isolated from laboratory animals and human**Sushanta Das¹**, Dr. Mst. Minara Khatun²¹Upazila Livestock Office, Hizla, Barisal ²Professor, Department of Microbiology and Hygiene, Faculty of Veterinary Science (FVS), Bangladesh Agricultural University, Mymensingh

The research was designed to characterize *Staphylococcus* spp. isolated from laboratory animals and human. A total of 100 samples were collected from different species of laboratory healthy animal mice (n=30), guinea pig (n=30), rabbit (n=30), and human (n= 10). The all nasal swabs samples were transferred to the laboratory, Department of Microbiology and Hygiene, BAU, Mymensingh. The samples were enriched in nutrient broth at 37°C for 24 hours overnight incubation. Enriched cultures were streaked onto different type of solid media like nutrient agar, mannitol salt agar, and blood agar and incubated at 37°C for 24 hrs. The isolated and identified *Staphylococcus* spp. were tested for antibiotic sensitivity to methicillin and vancomycin. A total of 100 *Staphylococci* spp. were isolated among them 100 were coagulase-negative *Staphylococcus epidermidis* (CNSE) produced whitish pigments in mannitol salt agar media. A total of 100 (100%) *S. epidermidis* were non-hemolytic on the blood agar media. Antibiotic sensitivity pattern of the CNSE were highly resistant to methicillin but these isolates were highly sensitive to vancomycin. The organisms were established as opportunistic pathogen producing abscess in mice. Nosocomial airborne contamination is now new thinking globally. Coagulase-negative *Staphylococcus* spp. are now new emerging threat to the world.

Keywords: CNSE, Laboratory animals, Methicillin-resistance, Vancomycin-sensitive

Blood feeding mechanism in the ixodid ticks, the potent vectors of microbial diseases of humans and animals

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The ticks are obligate haematophagous ectoparasites distributed worldwide and suck blood from almost all terrestrial vertebrates including humans. Ticks are voracious blood suckers and blood feeding is obligatory in ticks for their development and reproduction. Ticks are second only to the mosquitoes for transmitting microbial diseases as vectors to humans and animals. Depending on the species and stage of development, ticks feed blood for 3-12 days on host to reach repletion. During sucking blood for long time they need to counteract the host homeostasis. For successful blood feeding ticks need to perform three important biological events; creating a blood pool and maintenance of the wound of the pool, preventing blood coagulation and digestion of blood. We have unveiled the molecular basis of successful blood feeding by the ixodid tick, *Haemaphysalis longicornis* as a model, where a number of tick bioactive molecules counteract the host defense mechanism. The salivary gland derived Kunitz-BPTI serine protease inhibitor, haemangin of the *H. longicornis* prevents angiogenesis and thus, wound healing where the blood pool persists as long as the ticks remain attached on hosts. Longistatin, a salivary gland derived unconventional serine protease activates the plasminogen and keeps blood in flood state preventing coagulation of blood that facilitates blood acquisition for long time by the ticks. The midgut derived serine protease causes hemolysis and breakdown of hemoglobin into large peptides and finally to absorbable amino acids takes place by the action of different proteases. The asparaginyl endopeptidases, legumains (HLLgm and HLLgm2) from the midgut take part in final stage of blood digestion into absorbable amino acids and modulate midgut remodeling and embryogenesis in ticks. The molecular basis of successful blood feeding would lead to development of novel control strategies of ticks and tick-borne microbial diseases of humans and animals.

Key Words: Ticks, Blood feeding mechanism, Bioactive molecules

Quail selling practices in pet-bird wholesale markets in Dhaka, Bangladesh and the potential for cross-species transmission of avian influenza viruses

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Quails are a potential source of avian influenza (AI) exposure for other domestic poultry and humans. Between February and September 2014, the icddr,b influenza surveillance in pet-bird wholesale markets in Dhaka, Bangladesh identified 36 quails of which 6 were positive with influenza A/H5 and 31 with influenza A/H9. In February 2015, icddr,b in collaboration with the Institute of Epidemiology Disease Control and Research, identified a human infection of influenza A/H9 virus in a person with exposure to sick quails purchased from a pet-bird wholesale market. A team of social scientists conducted a qualitative study to explore the sources, supply chain and storing of quails along with bio-security practices; and workers everyday exposures to birds. Following convenient sampling, we conducted 30 in-depth interviews with pet-bird shop workers and mobile quail vendors, 5 key-informant interviews with quail wholesale businessmen and one group discussion with pet-bird shop workers. Quail farmers from 23 districts of Bangladesh provided about 12,000 quails daily to 2 pet-bird wholesale markets. Retail pet-bird shop owners and mobile vendors bought quails from these markets for resale to household and restaurants. Workers reported housing quails in cages with other birds up to 30 days before selling. Workers also fed the quails, cleaned feeding pots and cages by removing quail feces and discarded the wastes in front of shops. Workers slaughtered sick and moribund quails and discarded quails found dead inside the cage in waste receptacles. Workers washed their hands with stored water after cleaning waste, slaughtering quail and disposing of dead quails. Workers did not use any PPE and a few used cloth mask to avoid dust generated during cleaning waste and handling birds. Wholesale pet-bird markets located in Dhaka receive a large number of quails from many districts, store them for long time with other birds, and slaughter and handle sick quails with limited infection control practices, all providing opportunities for cross-species transmission of AI. Infection control interventions that currently focus only on poultry markets should be broadened to include pet-bird shops to monitor virus circulation and reduce risk of AI transmission from quails to humans and other animal species.

Keywords: Quail, Avian Influenza, Pet-bird wholesale market, Infection control

Survey of Coxiellosis related to reproductive disorders in small ruminantMd. Jalal Uddin Sarder¹; Md. Hemayeatul Islam¹; Mst. Ishrat Zerin Moni¹; Md. Siddiqur Rahman²¹Department of Veterinary and Animal Sciences, University of Rajshahi, Bangladesh¹Department of Medicine, Bangladesh Agricultural University, Mymensingh, Bangladesh

The zoonosis Q fever, caused by *Coxiella burnetii*, is typically associated with small ruminants. In January 2012 to July 2015 the positive brucella, common brucella and toxoplasma ELISA positive samples with some negative samples were sent to National reference laboratory in Germany. The investigation involved public health and animal field epidemiological investigations. Serological test was performed by iELISA on goat and sheep. The results compiled in a database created with Microsoft Office software Excel 2007 (Microsoft®, Redmond) and statistical package for social science program. To evaluate significant differences

between the tabulated and calculated value at specific degrees of freedom obtained from cross tab analysis, correlation and binary regression of coefficient and p value $< 0.05/ 0.01/ 0.1$ considered statistically significant. An overall seroprevalence of 11% was found. Goats had a significantly ($P < 0.01$) lower seroprevalence than sheep, respectively 5.6% and 30.0%. Small ruminants had significantly ($p < 0.05$) higher chance in animals reared at smaller 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 (7.7%) sex, older (6.6) age, 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 of small ruminants was negative correlation but significant ($P < 0.01$) effect with Q fever infection in experimental area. The lower to higher gradation in parity and pregnancy were observed in greater than third parity to first parity and pregnant to non pregnant. Animals from the stall feeding (4.4%) had negative insignificant ($P > 0.01$) effect and lower seroprevalence than animals from the grazing on field (6.6%). The binary logistic regression of anestrus, repeat breeding, stillbirth and orchitis were found to be positive and statistically significant ($P < 0.01$), cervicitis, retained placenta, dystocia, vaginal prolapsed/uterine prolapse & pyometra significant at ($P < 0.05$) and abortion, & urinary tract infection had significant ($P < 0.10$) effect on Q fever at northern barind tract in Bangladesh. First report, the seroprevalence of Q fever on goat and sheep in Bangladesh was established now. Female local breed goat and sheep having lower body weight, older age, greater than third parity, traditional biosecurity farms and grazing in field were more chance to Q fever in.

Key words: Seroprevalence, Q fever, northern barind tract, goat and sheep

Inter-subunit interaction and arrangement of the central stalk subunits of***Enterococcus hirae* V-ATPase**K. M. Mozaffor Hossain¹ and Ichiro Yamato²

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V-ATPases function as ATP-dependent ion pumps in various membrane systems of living organisms. ATP hydrolysis causes rotation of the central rotor complex, which is composed of NtpC, NtpD, and NtpG subunits. We successfully cloned, expressed, and purified the central stalk subunits of Na⁺-translocating V-type ATPase from *E. hirae*. Full length DNAs for genes of NtpC, NtpD, and NtpG subunits were amplified by conventional PCR method and cloned into the plasmid vector pET23d. Recombinant DNA transformed *E. coli* (JM109) cells were grown in LB agar plate containing ampicillin. NtpC and NtpG subunit proteins were expressed as separate His-tagged soluble proteins in *E. coli* BL21(DE3) cells at 30°C and NtpD subunit protein was stably expressed in *E. coli* BL21(DE3) cells at 16°C. Expressed central stalk subunit proteins were purified by affinity chromatography followed by gel-filtration method. The amount of purified NtpC, NtpD, and NtpG subunit proteins were 13.8 mg/1 liter culture, 16.6 mg/1 liter culture, and 15.2 mg/1 liter culture, respectively. Here, we report the stable interaction and the complex formation mechanisms of the central stalk subunits of *E. hirae* V-ATPase. The purified NtpD could interact directly with NtpG and NtpC could bind directly to NtpD-G complex and these three subunits could form NtpD-G-C complex. NtpD could bind to NtpG and formed NtpD-G complex. NtpD or NtpD-G complex could bind to NtpA₃-B₃ and formed NtpA₃-B₃-D or NtpA₃-B₃-D-G complex, respectively. NtpC could bind to NtpA₃-B₃-D-G and formed NtpA₃-B₃-D-G-C complex but could not bind to NtpA₃-B₃, NtpA₃-B₃-D, NtpD, or NtpG.

Keywords: *Enterococcus hirae*; V-ATPase; central stalk subunit proteins; interaction.

Small commercial poultry farmers' perception about avian influenza and biosecurity, Bangladesh 2011-12

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Highly pathogenic avian influenza A (H5N1) virus is endemic in Bangladesh. Small-scale commercial farms accounted for 44% of 549 H5N1-confirmed outbreaks in poultry farms. Biosecurity measures may reduce the spread of avian influenza. Understanding farmers' perceived risks and identifying their motivation to adopt preventive measures can help develop interventions to reduce the risk of avian influenza transmission. This exploratory study aimed to understand small commercial poultry raisers' perception of bird flu and biosecurity. During 2011-12, our qualitative research team conducted in-depth interviews and group discussions with poultry farmers in 16 purposively selected small commercial farms from two districts. We reviewed and summarized emerging themes from data. Few (4/16) farmers mentioned knowing the term 'biosecurity' and related it with bird flu. Farmers, who had experienced an H5N1 outbreak in their flock, equated 'biosecurity' with fencing. Farmers perceived bird flu as a disease that occurred at a distant time or place that could not affect their farm. More than half of the farmers either did not know or did not believe that bird flu could be transmitted to humans. Farmers were more concerned about Newcastle and infectious bursal disease, which caused mortality in their flock, than bird flu. They reported practices to prevent disease, germs and cold. Although they did not explicitly mention 'bird flu prevention' or 'biosecurity', many of these practices, such as using footbath before entering the shed and keeping gap between batches, partially or fully matched with standard biosecurity measures. Only to prevent cold, which they considered to trigger other disease and weight loss, farmers reported aerating the litter to release gas and keeping the litter dry, since they considered damp litter or gas as the source of cold. Their main motivation was to reduce mortality and raise healthy chickens. Bangladeshi small commercial farmers are more concerned about diseases that are more common in their flocks and were less concerned about bird flu. Interventions that consider promoting biosecurity to prevent not only bird flu but also other infectious diseases they consider harmful and to keep their flock healthy may motivate these farmers to change practices.

Keywords: Avian influenza, H5N1, Small commercial poultry, perception, biosecurity

An outbreak of Classical Swine Fever (CSF) in native pigs of Kurigram District of Bangladesh in 2015

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Pigs are a minor domestic animal species in Bangladesh that are largely reared by some ethnic communities and tribal people through mostly free roaming system. The present study was conducted in Kurigram district in the North-Eastern part of Bangladesh near the Indian border. Unusual deaths of native scavenging pigs were reported in the mid-November 2015 by the local pig farmers. The objectives of the study were to describe the outbreak in terms of animal, time, place and the disease agent, and to describe the impact of the disease. A descriptive epidemiological study was conducted. A survey questionnaire was developed to capture a detailed history of the feed and housing, number of pigs affected, mortality pattern, vaccination and treatment status and clinical findings were recorded where the unit of interest was a household. Outcome variable include results of post mortem examination and diagnostic tests results from the collected samples. Two hundred and sixty-three (263) pigs out of a total of 592 pigs ranging from 6 months to 2 years 6 months died over a period of 4 weeks with a peak mortality occurring during the second week from the date of onset. The mortality and case fatality rates were 66.22% and 66.41% respectively. Isolates from nasal swabs and tissue samples (spleen, lung, liver) were tested using RT-PCR showed positive for CSF virus. BLAST analysis revealed the highest similarity to CSF virus sequences from India and the first reported case in Bangladesh. The government should take special program for assessing and controlling diseases of pigs being reared by certain ethnic minority communities of Bangladesh bordering India.

Key Words: Outbreak investigation, Classical Swine Fever (CSF), Native scavenging pigs; Bangladesh.

Current Biosafety and Biosecurity Status in Microbiology Laboratories of Govt. Medical College Hospitals in Bangladesh: Preliminary Findings from On-going Assessment

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Biosafety and Biosecurity- the current burning-issues remain the basis of global public health under one health-concept that encompass biocontainment in laboratories/ hospitals including infection control. Biosafety/biosecurity remain the essential pillars of global health security that address cross-cutting elements of biological non-proliferation and spill management of potentially-dangerous pathogens in laboratories. Here, we report some preliminary finding on Bio-safety/security from IEDCR-led on-going project 'Global Health Security Agenda (GHTSA)' in collaboration with US-CDC's and Government of Bangladesh (GOB). The aim was to assess Biosafety and biosecurity capacities in microbiological laboratories of government-ran medical college hospitals towards strengthening public health actions in Bangladesh. Employing a pre-tested assessment tool, a survey team comprised of public health and one-health experts conducted the Biosafety/biosecurity activities in seven GoB-ran microbiological-laboratories located in IEDCR's sentinel-surveillance sites. The assessment was comprised of 4 phases. First phase comprised of direct interview of hospital deputy/directors to record information on policy implications/planning strategies that directly/indirectly affect biosafety/security component(s). Second phase: interviewing vice/principals/Head, Microbiology to record laboratory-associated information/data affecting biosafety/security-activities, directly. Third phase: Faculty/MT-assisted laboratory-rounds to check laboratory-data and video/photography of specific bio-safety/security component. Fourth phase: hospital -round (OPDs/indoor-wards/OTs) to document infection-control activities (6-steps of handwashing, using disposable-gloves and colour-coded-bins) along with infection control issues (hospital-acquired-infections).Physical-infrastructure (labs/wards, lightings/ventilations/air-conditioning, stair-cases/lifts, fire-fighting-measures/fire-extinguishers) were not adequately-built in all MCHs, except Chittagong BITID to meet standard Biosafety/security levels, while Uttara-Adhunik hospital lacked in certain structural designs. Laboratory-facilities (sample-collection/space, processing/labelling, clean-bench/sample-preservations, PPE, instruments/reagents/media, biosafety-cabinets) were found inadequate and lacked BSL-II-Laboratories. Overall-scenario of waste disposal-methods (waste-collection, sorting/segregation, autoclaving/chemical treatment, final-dumping), revealed limited capacity. Incongruities yielded in infection control activities, too in these laboratories and hospitals. The infectious-disease wards in Chittagong-BITID also require renovation. These remain major warning-signs as limitations of biosafety/security practices that may potentially hinder combatting dangerous re/emerging infections through hazardous human-animal-interface.Current state of limitations in biosafety/biosecurity measures in most GoB-ran MCHs, assessed preliminarily, require essential improvements and plausible alterations. These inadequacies seized biosafety/biosecurity issues prudently enough. Lacking policy-implications, imparting proper-trainings and inadequate funding remain main challenges in establishing biosafety and biosecurity in these hospitals towards ensuring a country wide robust public health.

Determination of Bovine Rotavirus G and P genotypes in some selective areas of Bangladesh

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Rotavirus is distributed worldwide as an enteric pathogen in man, animal and poultry. Bovine rotavirus (BRV) has been detected in both dairy and beef cattle herds worldwide. A total of 200 faecal samples were collected from diarrheic calves of the dairy region of Barisal, Madaripur and Sirajgonj districts during the period from July 2015 to December 2016. These 200 faecal samples were consisted of 68 from Barisal, 92 from Madaripur and 40 from Sirajgonj. The collected stool samples were screened using rapid test- strips BioK 152 to determine the presence of BRV. Group A BRV was detected in 22.50% of faecal samples (45/200). The highest rate of BRV infection was detected in the Barisal (26.47%) and Madaripur (26.08%) while the lowest detection rate was in Sirajgonj (7.5%). The detected positive rotavirus samples by rapid test- strips BioK 152 were also examined by Polyacrylamide Gel Electrophoresis and Silver Staining (PAGE-SS) technique for the detection of presence of rotavirus dsRNA. About 70% of positive rotavirus samples by rapid test- strips BioK 152 was found positive in PAGE. All the electropherotypes were long pattern. RT-PCR and sequencing were applied to determine the distribution of G and P serotypes of bovine rotaviruses are circulating in Bangladesh. Genotyping analysis of rotavirus (G & P) in 30 positive samples indicated that G6P[11] was the most prevalent genotype (56.70%) followed by G10P[11] (3.3 %). This study demonstrates that BRV is a contributing pathogen to diarrhoeal disease in calves of different three district of Bangladesh. In the present study, it was not investigated that bacteria, parasites or any other pathogens responsible for causing diarrhea or not.

Key Words: Bovine Rotavirus, Molecular Characterization, Severe Diarrhea & Ca

Perceived Knowledge of Medical Technologists on Laboratory Biosafety Varies Among Government and Private Health Care Institutions in Dhaka, Bangladesh

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Medical technologists (MT) remain integral part of health-care service delivery. MTs must possess sound-knowledge in handling biosafety issues in laboratories, properly. It is thus important to assess MT's perceived knowledge on biosafety. Determine level of perceived knowledge on biosafety if varies between MTs working in GoB and private health-care institutions. This cross-sectional study was conducted in 12 health-care institutions (5-GoB and 7-private). Data were collected employing face to face interview using semi-structured questionnaire and analyzed on SPSS/Win-V.16 using *Chi-square* accepting $p < .05$ as significant. More MTs (35%) from private laboratories defined BS correctly than GoB (33%, $p < .04$) but more GoB-MTs (59%) than private (4%) was exposed to BSL type-II-Cabinets ($p < .001$). Overall, 62% MTs had no training on BS but GoB-MTs (60%) had it (3-4 day-long) more than private-MTs (12%, $p < .001$). All MTs remain aware of "No eating, drinking and smoking" in the lab except 9% GoB-MTs ($p < .001$). Although 63% MTs knew 'infection spreading is the main bio-hazard in laboratories, 44% could identify bio-hazard-risk categories correctly having no difference in groups ($p = .61$). MTs from private-institutions knew it better than GoB-MTs, that: i) personal protective equipment (PPE) prevents from infections ($p > .31$), mouth-pipetting remains prohibited ($p = .04$) and removing of PPEs before going out of lab is mandatory ($p < .01$). GoB-MTs ticked-out bar-soaps, private-MTs marked liquid-soap for hand washing ($p < .001$) though designated sinks were as ticked by GoB-MTs ($p < .03$). Shockingly, no MTs knew WHO's 6-steps of hand-washing ($p > .59$). Despite all MTs having acceptable knowledge on waste-disposal methods: private-MTs exhibited it better in: i) using color-coded waste-bins ($p < .03$), ii) auto-clave/chemical-treating bio-hazardous wastes ($p < .01$), iii) using waste-specific color-coded bins for pre-dumping segregation ($p < .02$), iv) prior to final disposal; incineration being favorite among private but 'burn-and-burry' among GoB-MTs ($p < .05$). Private-sector-MTs knew measures to take during accidental spillage of toxic/corrosive-chemicals/dangerous -pathogens, better ($p < .02$). Though no MT were aware on 'Emergency Response Team', they knew about 'First-Aid Kit-Box' though, more being among private-MTs than GoB-ones ($p < .02$). Since all MTs should possess detailed knowledge on biosafety-issues it is imperative that they undergo in-depth training to keep laboratories infection-free towards keeping our environment safer & better.

Key words: Biosafety, Knowledge, Medical technologists, Dhaka, Bangladesh

Characterization and Antibigram of Selective Pathogens in Pneumo-Enteritic Goats

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Pneumonia and enteritis are among the common diseases affecting small ruminants. Indiscriminate use of antibiotics in animals against bacterial infections has led to emergence of multidrug-resistant strains. The sensitivity and resistance of antimicrobials to different drug with associate risk factors in pneumo-enteritic goats is crucial to ensure effective treatment as well as taking necessary steps for minimizing the antimicrobial resistance. Hence, the cross sectional study was conducted to characterize the selective pathogens of pneumo-enteritis in goat along with their antibiogram over a one year period from September 2013 through September 2014. A pre-tested questionnaire was used for farm level risk factor analysis. One hundred and fifty goats (n=150) were sampled having pneumonia and/or enteritis. Both nasal and fecal swabs were collected from each goat and the samples were subjected to culturing using a series of agar and broth. Biochemical tests were done and finally PCR was done for *Salmonella sp* targeting TetA and blaTEM gene. The prevalence of *Staphylococcus spp* in pneumoenteritic goats was 28%. Among the *Staphylococcus spp*, the coagulase positive *Staphylococcus* was 43% whereas the coagulase negative *Staphylococcus aureus* was 57%. The prevalence of *Salmonella spp* was 16.7% in pneumoenteritic goats. The percentage of TetA gene and blaTEM genes among *Salmonella spp.* were 50% and 72% respectively. Commonly used antibacterials in the field except cefotaxime and sulfamethoxazole with trimethoprim combination were found resistant in comparative antibiogram of coagulase positive and coagulase negative *staphylococcus spp*

Keywords: *Pneumoenteritis, Antibiogram, Staphylococcus spp, Salmonella spp.goats*

AMU reality check: documenting the widespread use of critically important human antimicrobials in livestock in Bangladesh

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Fluoroquinolones are broad-spectrum antimicrobials and are an important class of drugs to both human and animal health, including ciprofloxacin, levofloxacin, and moxifloxacin in human medicine, and enrofloxacin and danofloxacin in animal medicine. In Bangladesh, ciprofloxacin, a WHO critically important drug for human medicine, is now being used regularly as a preventative and growth promoting antimicrobial in food producing animals. In February 2017, a collaborative FAO, Department of Livestock Services, pharmacy, poultry breeder, and medicine company assessment of the extent of use of this drug was conducted in five districts of Bangladesh. A total of 55 different liquid formulations of ciprofloxacin were found formulated for use in food animals with instructions for use in drinking water. Of the 55 products identified, 20 products were combined with other antimicrobials, including enrofloxacin and colistin sulphate. The products ranged in retail price from US\$ 0.13 -0.45 per gram. Some products also specifically advised to administer the ciprofloxacin via feed and as a growth promoter. In addition to increasing antimicrobial resistance (AMR) to ciprofloxacin, the widespread availability and use of ciprofloxacin products increases the risk of the drug residue in poultry products. In January and February 2017, 26 dressed chicken carcasses were collected from various markets throughout Dhaka and tested for ciprofloxacin residues via high performance and ultra-high performance liquid chromatography. Of the 26 samples tested, seven (27%) were positive for ciprofloxacin and three (12%) were classified as suspected ciprofloxacin residues. The availability of ciprofloxacin products marketed for use in food animals and the lack of awareness of the implications of misuse of this critically important human drug contribute to the increasing risks of AMR in Bangladesh. It is critical to assess the full extent of use of ciprofloxacin in food animals to enable the development and implementation of appropriate mitigation measures and policies.

Eco-epidemiology of Antimicrobial Resistance pattern of *Staphylococcus spp.*, *E. coli* and *Salmonella spp.*, isolated from Small Mammals of Bangladesh

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Antimicrobial resistance is a global concern and is extremely important for human health where wild animals provide a biological mechanism for the spread of antibiotics emerging resistant pathogens. Small mammals may act as a bioindicator for the environment that lives in close proximity to human may influence the antibiotic resistance profile of wildlife. This study aimed to determine the prevalence of *Staphylococcus spp.*, *E. coli* and *Salmonella spp.* and multi-drug resistance level in small mammals. Between January and June, 2017 we captured 200 small mammals consisted of 42 Mice (*Mus musculus*), 73 Rat (*Rattus rattus*, *Bandicota indica* and *Bandicota bengalensis*) and 85 House Shrew (*Suncus murinus*) from thirty different location of Chittagong, Bangladesh. Oral and rectal swab samples were collected and preserved in BPW. The samples were then tested in the laboratory for *Staphylococcus spp.*, *E. coli* and *Salmonella spp.* by using standard bacteriological tests, selective biochemical tests and PCR for confirmation of the each species of bacteria. Based on the seven interface, the small mammals of residential area possess 54.72%, 50% and 45.53% of *Staphylococcus sp.*, *Salmonella spp.* and *E. coli* respectively than others types of areas ($P < 0.05$). The isolated *Staphylococcus spp.*, ($n=53$), *Escherichia coli* ($n=99$) and *Salmonella spp.* ($n=112$) were then assessed for antimicrobial susceptibility test (AST) by Kirby-Bauer disk diffusion method using fourteen different types of the antibiotic disc on the Muller-Hinton agar. The AST result for *Staphylococcus sp.* showed 100% resistant to Oxacillin, Cefixime, and Metronidazole followed by Ceftriaxone (30.0%), Ciprofloxacin and Doxycycline (10.0%), Erythromycin and Gentamycin (05.0%). Moreover, *Salmonella sp.*, exhibited 100% resistant to Sulphamethoxazole and Trimethoprim, Ceftriaxone, Ampicillin, Oxacillin, Doxycycline, Cefixime, Amoxicillin, Erythromycin and Metronidazole followed by others. Furthermore, *E. coli* isolates presented 100% resistant to Oxacillin, Erythromycin and Metronidazole followed by Cefixime, Sulphamethoxazole, and Ampicillin (98.57%) and others. Our study reveal that, close proximity to human dwellings, food animal and agriculture increases the likelihood of selected micro-organisms isolated are resistant more than three antibiotics. We need further study and attention needed for proper use of antimicrobial in food animals and agricultural products to reduce multidrug resistant pattern and transmission of resistance bacteria from human animal to the environment and vice versa.

Keywords: Small mammals, Antibiotics, Resistance, *Staphylococcus spp.*, *E. coli*, *Salmonella spp.*

Prevalence and Antimicrobial Resistance patterns of *Salmonella* spp. Isolated from various street food items

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Salmonellosis is zoonotic disease and during the last decade, multi-resistance of *Salmonella* spp. has increased a great deal, especially in developing countries due to an increased and indiscriminate use of antibiotics in food animals, environments and human. Therefore, a cross sectional study was conducted to investigate the multidrug resistance pattern in *Salmonella* isolated from various street food samples. Standard microbiological methods was used for isolation and identification of *Salmonella* spp. The antibiotic susceptibility tests was conducted by using disc diffusion method with commercially available eleven antibiotics. *Salmonella* spp. was isolated from fuska surface water (around 73%), sugarcane juice (around 78%) and Borhani (60%). We found multidrug resistance from each of the items tested. Higher (100%) resistance was found in fuska surface water for Ampicillin and Amoxicillin followed by others and lowest for Pefloxacin (around 13%). Moreover, we found higher (100%) multidrug resistance in sugarcane juice for Ampicillin, Amoxicillin and Erythromycin followed by others and lowest for Pefloxacin (around 13%). We also found higher (100%) multidrug resistance in Borhani for Ampicillin, Amoxicillin, Azithromycin, Oxytetracycline, Tetracycline and Erythromycin followed by others and lowest for Ceftriaxone (0%, i.e. 100% sensitive). *Salmonella* isolates were multidrug resistance up to six of the eleven antimicrobials tested. In conclusion, it can be said that the rational use of antibiotics need to be adopted in food animal and agricultural production system and human practice of Bangladesh to prevent the emergence of multi-drug resistance *Salmonella*. In addition, appropriate hygienic measures should be taken in the process of preparation and before taking the street foods to prevent occurrence of zoonotic *Salmonella* spp. in human infection.

Key words: Antimicrobial, prevalence, resistance, street foods, *Salmonella* spp.

An Eco-Epidemiological Assessment of Antimicrobial Resistance of *Salmonella* and *Staphylococcus* in Bats of Bangladesh

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Antimicrobial resistance (AMR) is currently one of the greatest challenges to global health. The prevalence of resistant microbes in wildlife are poorly understood. Bats are a diverse and highly mobile taxon that often live in close proximity to people and livestock. Bats use of shared environments may contribute to their exposure to AMR enteric pathogens. The identification of zoonotic and anthroozoonotic agents carried by bats is critical for understanding the ecology of zoonotic pathogens. This study aimed to identify antimicrobial resistance in *Salmonella* spp. and *Staphylococcus* spp. isolated from bats and test the hypothesis that drinking behavior of bats may result in their infection with AMR bacteria. We collected fecal samples (N=369) from free-ranging bats and 21 water samples from different water bodies in Dhaka city between December 2016 and June 2017. Pre-enrichment was done in buffered peptone water for *Salmonella* spp. and in Mueller Hinton broth for *Staphylococcus* spp. Selective culture media, biochemical test and PCR were done to confirm bacterial isolates. Culture sensitivity was determined using disc diffusion technique of 12 antibiotics. Seven percent (n=27; 95% CI: 5-11) and 49% (n=182; 95% CI: 44-55) bats were positive for *Salmonella* spp. and *Staphylococcus* spp. respectively and 4% (n=21, 95 % CI: 18-62) of water samples were positive for *Salmonella* spp. *P. medius* (8.55%; n=269; 95 % CI: 7-14) were more infected with *Salmonella* spp. than *R. leschenaulti* (4.00%; n=100). Bats from urban areas (11 %) had higher infection rates with *Salmonella* spp., compared to bats from rural areas (4 %) (p<0.05). Preliminary results reveal all isolates developed multiple resistance to antibiotics to varying degrees; *Salmonella* spp. are resistant to tetracycline (93%; n=27), sulphamethoxazole-trimethoprim (79%; n=23), chloramphenicol (62%; n=18) cefotaxime (41%; n=12), amoxicillin-Clavulanic acid (42%; n=12), azithromycin (76%; n=22) and sensitive to nalidixic Acid (86%; n=25), ceftriaxone (66%; n=19), gentamicin (72%; n=21), imipinem (69%; n=20), cefixim (62%; n=18) and Intermediate to ciprofloxacin (76%; n=22). The study results indicate presence of AMR *Salmonella* spp. and *Staphylococcus* spp. in bats. It is unclear how bats were infected with AMR bacteria, however water contaminated by people and/or livestock may be a source of infection. Screening people and livestock for similar resistant bacterial species will improve our understanding of pathogen transmission among wildlife, livestock and people.

Keywords: AMR, Bat, Prevalence, *Salmonella*, *Staphylococcus*

Poster Presentation

Antimicrobial Resistance and its containment

Isolation and molecular identification of antimicrobial resistant *Campylobacter* species from poultry value chains and screening of antibiotics residue

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This study was conducted with a view to isolate, identify, antibiogram study of *Campylobacter* spp. and screening of antibiotics residue during the period of October 2015 to May 2016. A total of 153 samples (meat samples, cloacal swabs, chick meconium, transport swabs, feed samples, water samples and floor swabs) were collected from 7 broiler farms and 2 live bird markets of different upazilla of Gazipur and Tangail districts of Bangladesh and subjected to bacteriological isolation and identification by using cultural, biochemical and molecular techniques. Furthermore, the isolated bacteria were characterized by antimicrobial susceptibility test. Moreover, a total of 46 samples (meat and liver) were collected for the screening of antibiotics residue by using TLC and HPLC. Out of 153 samples, 32 (20.78%) isolates of *Campylobacter* spp. were identified and among 32 isolates 24 (75%) isolates were *Campylobacter jejuni* and 8 (25%) isolates were *Campylobacter coli*. In this study, amoxicillin, azithromycin and erythromycin displayed significantly higher resistance to *Campylobacter jejuni* and *Campylobacter coli*. Out of 32 *Campylobacter* isolates, 45.83% *Campylobacter jejuni* and 37.50% *Campylobacter coli* were detected as multidrug resistant. In this study, highest rate of residue in liver tissue was oxytetracycline (44.44%) followed by ciprofloxacin (22.22%) and enrofloxacin (11.11%) respectively as estimated by TLC. In muscle, highest rate was oxytetracycline (33.33%) followed by ciprofloxacin (20%) and enrofloxacin (13.33%) respectively as estimated by TLC. The mean concentration of oxytetracycline, ciprofloxacin and enrofloxacin in muscle were 113.25 µg/kg, 18.29 µg/kg and 93.28 µg/kg respectively. The findings of present study have revealed the presence of antimicrobial resistant *Campylobacter* spp. in broiler farms and dangers of antibiotic residues in edible poultry tissues.

Keywords: *Campylobacter* spp., broiler, multidrug resistant and antibiotics residue

Poster Presentation

Antimicrobial Resistance and its containment

Isolation and molecular characterization of shiga toxin producing *escherichia coli*(stec) from betel leaves (*piper betle*)

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Shiga toxin-producing *Escherichia coli* (STEC) is an important pathogen which may leads to watery to bloody diarrhea, hemorrhagic colitis and hemolytic uremic syndrome in humans. This study was designed to determine the shigatoxin producing genes and investigate antibiotic sensitivity or resistant patterns of the *E. coli* isolated from ready to eat betel leaf from different road side vendors . A total of 100 samples were collected and screened for the detection of *E. coli* on the basis of cultural, staining and biochemical properties followed by molecular characterization using genus specific 16SrRNA primers by Polymerase Chain Reaction. According to the study, 44 out of 100 samples, were confirmed as *E. coli*. Again, those 44 positive *E. coli* were analyzed for the presence of *Stx-1* and *Stx-2* genes by duplex PCR. From the results, two isolates were confirmed to be positive for the presence of the *Stx-1* gene but no isolate was found to be positive for the *Stx-2* gene. Antimicrobial sensitivity and resistant pattern of *Stx-1* positive *E. coli* was determined by disc diffusion method against 10 different antimicrobial agents. Ciprofloxacin shows the highest susceptibility pattern followed by the Ceftriaxone and Levofloxacin than Azithromycin, Cefixime, Gentamicin and Tetracycline. Highest resistant pattern was showed by Amoxicillin and Cephradine than Moxifloxacin. From the study, it was concluded that Levofloxacin and Ciprofloxacin may be effective drugs to control STEC infections now a days.

Poster Presentation

Antimicrobial Resistance and its containment

Screening for Antimicrobial Activity of Some Selected Medicinal Plants: A Possible Alternative of Commercially Available Antibiotics to Treat *E. coli* and *Salmonella* sp. Infections in Poultry

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The antimicrobial resistance of pathogenic bacteria is a great public health concern globally for indiscriminate use of antimicrobials in veterinary and human health practices. The development of drug resistance as well as appearance of undesirable side effects of certain antibiotics has led to the search of new antibacterial agents in particular from medicinal plants. The aim of the study was to assess the antibacterial effect of some selected medicinal plant extracts at different concentrations against *E. coli* and *Salmonella* sp., and to evaluate the antimicrobial sensitivity of different commercial antibiotics against selected organism. A total of 90 broiler liver samples were collected from six Live Bird Markets (LBM) of Chittagong metro from September, 2015 to February, 2016. The isolation and identification of *E. coli* and *Salmonella* sp. from liver samples were done following conventional bacteriological techniques. The extracts of Neem (*Azadirchta indica* A. Juss), Tulsi (*Ocimum sanctum*), Durba grass (*Cynodontoctylon*), Thankuni (*Centella asiatica*), Sajna (*Moringa oleifera*) and Garlic (*Allium sativum*) were prepared using water reflux. The antibacterial activities of plant extracts and commercially available 04 antibiotics (enrofloxacin, ciprofloxacin, trimethoprim and oxytetracyclin) in market were evaluated using the disk diffusion method. The minimum inhibitory concentration (MIC) of the plant extracts against *E. coli*, and *Salmonella* sp. were assessed using micro-dilution method at 5% and 10% concentrations. The overall prevalence of *E. coli* and *Salmonella* sp. in broiler liver samples were 74% (n=67; 95%CI: 64-83) and 26% (n=23; 95%CI: 17-36), respectively. In anti-biogram study, *E. coli* were more resistant to enrofloxacin (75%) and ciprofloxacin (72%) where *Salmonella* sp. was mostly resistant to oxytetracyclin (80%). *E. coli* was sensitive to Tulsi (*Ocimum sanctum*) among the selected medicinal plants at 10% MIC. None of the other plants extracts were sensitive to *E. coli* and *Salmonella* sp. neither at 5% nor 10% MIC. The study provides scientific rationalities of Tulsi extracts for treatment of poultry diseases where the commercially available antibiotics are resistant.

Keywords: Antimicrobial Resistance, *E. coli*, Poultry, Plant extracts, *Salmonella* sp.

Poster Presentation

Antimicrobial Resistance and its containment

Determination of Antimicrobial Resistance in the Bacteria Isolated from Waste Water of Pharmaceuticals

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Antibiotic resistance is one of the biggest threats to global health, food security, and development today. Antibiotic resistance can affect anyone, of any age, in any country. Antibiotic resistance occurs naturally, but misuse of antibiotics in humans and animals is accelerating the process. A growing number of infections – such as pneumonia, tuberculosis, and gonorrhoea – are becoming harder to treat as the antibiotics used to treat them become less effective. Antibiotic resistance leads to longer hospital stays, higher medical costs and increased mortality. This study was carried out to highlight the incidence of antibiotic resistant bacteria in antibiotic producing plant generated waste water. The waste water samples were collected from the five established antibiotic producing plant situated in Dhaka and Savar. The laboratory works were conducted in the Department of Microbiology, Faculty of Veterinary and Animal Science, Hajee Mohammad Danesh science & Technology University (HSTU), Dinajpur. Spreadplate method was used for isolation of bacteria from the waste water. Isolated bacteria were identified on the basis of colony morphology, gram's staining, microscopic character and biochemical characteristics of the isolates. Among the samples 50% were *Bacillus spp.*, 35% were *Pseudomonas spp.*, 10% were *Staphylococcus spp.* and 5% were unidentified. Twelve antibiotics were selected for the antibiogram study. Antibiogram was determined by disc diffusion method. All of the isolates of *Bacillus spp.* were 100% resistant to Penicillin, Amoxicillin, Cephalexine, Cefixime, Cloxacillin, Tobramycin, Cefotaxime and Cephaclo and 75 % sensitive to Vancomycin, Sulphamethoxazole, and 25% sensitive to Cephadrin and Chloramphenicol. All of the isolates of *Pseudomonas spp.* were 100% resistant to Cefotaxime, Sulphamethoxazole, Vancomycin, Cephalexine, Tobramycin; Chloramphenicol, Cephadrin, Cephaclo, Amoxicillin and Penicillin; 66.66% sensitive to Cloxacillin and 33.33% sensitive to Cefixime. *Staphylococcus spp.* was 100% resistant to all antibiotics. The results showed that all samples contain multidrug resistant bacteria which indicate that the liquid waste of the plants may carry active antibiotics or ingredients.

Keywords: Antimicrobial resistance, Bacteria, Isolation, Pharmaceuticals, Multidrug resistance

AMR and strategic use of selected feed additives for sustainable animal production**H. M. Salim¹, M. R. Amin¹, M. A. Haque¹ and M. A. H. Beg²**

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The use of antibiotics in food animal production is a growing concern due to its potential adverse effects on human and animal health, food safety and the environment. Prophylactic use of antibiotics in human health care and animal production is a key driver for the rapid development of antimicrobial resistance (AMR), which urges the need for effective feeding strategies to reduce antibiotic use in animal production. The European Union, South Korea, Bangladesh and other countries have been implemented various feeding strategies in terms of regulatory affairs for reducing antibiotic uses in animal industry. The success of this reduction in antibiotic use in animal feed may be attributed to the wide application of selected feed additives and combinations for targeting optimum growth, intestinal integrity, gut health and immunity. Productivity and health well being can be obtained in animals similar to those reported for antimicrobial growth promoters by improving microbiological quality of drinking water and feed, stabilization of the intestinal microbiota and strengthening the mucosal barrier of the host. Regulatory recognition of the prophylactic use of feed additives in animal feed industry should further facilitate the progress to reduce AMR. Further research is needed on quality feed ingredients, diet composition and finding reliable and cost effective alternative feed additives in replacement of antibiotic growth promoters to combat the AMR.

Keywords: AMR, alternative feed additives, antibiotic growth promoters, animals and human

Poster Presentation

Antimicrobial resistance and its containment

Ecology and Epidemiology of Antimicrobial Resistance pattern of *E. coli* and *Staphylococcus* spp. isolated from Budgerigar (*Melopsittacus undulatus*) in Bangladesh

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Budgerigar (*Melopsittacus undulatus*) is commonly reared pet birds in Bangladesh. Generally, antimicrobials are commonly and indiscriminately used by pet bird owners by using their own idea. The bird keepers may have close contact with cage pet birds, and can be exposed to pathogenic organisms carried by them, those already resistant to specific pathogenic bacteria. Antimicrobial resistance is an emerging global public health threat for human and animals and is related to the inappropriate use of antimicrobials in humans and animals. This study was aimed to understand antimicrobial resistance patterns of *E. coli* and *Staphylococcus* spp. isolated from Budgerigar in Bangladesh. From December, 2016 to June, 2017, 100 cloacal swab samples were collected from Budgerigars in Chittagong, Bangladesh. A structured questionnaire survey was conducted on farm owners to know the management, disease ecology of Budgerigar at the farm level. The most common species found were Budgerigar (70%, 70/100). The standard microbiological procedure were followed for isolation of these zoonotic bacteria. The prevalence of *E. coli* and *Staphylococcus* sp. were 35% (n=30) and 26% (n=26), respectively. Susceptibility of *E. coli* and *Staphylococcus* spp. to antibiotics was conducted using disc diffusion method with nine commercially available antibiotics. All (100%, n=30) *E. coli* isolates were resistant against amoxicillin, sulfamethoxazole, trimethoprim, and cefixime but lowest resistant was found ciprofloxacin (4%). Moreover, we found higher (100%, n=26) multidrug resistance in *Staphylococcus* spp. ciprofloxacin and gentamycin followed by others and lowest for ciprofloxacin and azithromycin (2%). In conclusion, this study presented multidrug resistant in *E. coli* and *Staphylococcus* spp. isolated from the pet birds. The indiscriminate use of antibiotics on pet birds should be reduced to lessen the risk of public health importance multi-drug resistance bacteria.

Key words: Antimicrobial, ecology, epidemiology, resistance, *E. coli*, *Staphylococcus* sp.

The value of integrating different platforms to institutionalize the One Health approach in BangladeshNitish C Debnath¹, Meerzady Sabrina Flora², Mehedi Hossain³, Habibur Rahman¹, M A Kalam⁴, Eric Brum¹¹Emergency Centre for Transboundary Diseases (ECTAD), FAO Bangladesh²Institute of Epidemiology and Disease Control Research (IEDCR)³Department of Livestock Services, Ministry of Fisheries and Livestock, Dhaka, Bangladesh⁴Preparedness & Response Project, USAID, Development Alternative Incorporated (DAI)

A multi-disciplinary team including physicians, veterinarians, environmental scientists, civil society, and development practitioners formed an organization, 'One Health Bangladesh (OHB)' in 2008, that provided a forum for discussing the concept of One Health (OH) and its relevance for controlling emerging and re-emerging diseases in Bangladesh. As the advocacy continued through regular meetings, seminars and conferences by OHB, a phase emerged towards building effective relationship and ownership of collaborative effort to practice One Health approach through undertaking joint disease outbreak investigation, surveillance, prevention and control of avian influenza, Nipah, rabies, and anthrax. In this phase, the value of the special role of government partners in practicing the OH approach was recognized and a National One Health Strategic Framework and Action Plan were developed jointly by government partners, FAO, WHO, UNICEF, and other stakeholders. With the endorsement of the strategic framework, government took steps to institutionalize OH within government systems through creation of the One Health Secretariat (OHS). While OHB promotes a whole-of-a-society approach by connecting other health related forums, institutions and activities, OHS focuses on a whole-of-a-government approach to address interface issues related to human, animal, and environmental health. Development partners and UN agencies involved in implementing the Emerging Pandemic Threat programme and Global Health Security Agenda have developed OH coordination to promote collaborative activities and share information. Joint initiatives for OH capacity building through Field Epidemiology Training programmes by the Institute of Epidemiology and Disease Control Research, OH Postgraduate training by the Massey University in collaboration with local partners, and the creation of the One Health Institute at Chittagong Veterinary and Animal Sciences University to offer different forms of training have created a new momentum for developing OH workforces in Bangladesh. All these platforms work in close collaboration to institutionalize OH at all levels.

The veterinarian's role in animal welfare**Mohammad Rashedul Alam**

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Public concerns about animal welfare are well documented worldwide. The OIE has led the harmonization of animal welfare standards internationally. In Bangladesh the need for the scientific study of animal welfare was first identified in 2006. Veterinarians are well placed to positively influence the future health and welfare of all animals, including humans, which must be part of the one health approach. They have the pragmatism to examine and assess animal welfare and to make recommendations if necessary to improve welfare. Expansion of the role of veterinarians is becoming increasingly important as the human population expands and the earth's ecology appears to be veering towards a dangerous imbalance. Modern veterinarians are not only animal doctors and animal welfare advocates; they are also key public health stakeholders because of their role in reducing global hunger, controlling and preventing diseases in animals, promoting animal welfare, controlling zoonoses, monitoring food quality and safety, and protecting the environment and biodiversity. Veterinarians can also contribute to animal welfare in a number of ways such as addressing food security and animal welfare issues; human-animal interactions and their impact on animals; slaughter and pre-slaughter inspections; developing strategies to address painful husbandry procedures, and distress associated with transport, disaster preparedness, and human responsibilities to wild animals. To be able to do all these things, a veterinarian must be well versed in animal welfare science. They need to remain visible, active and relevant in this important part of animal welfare science as their professional responsibilities.

Keywords: Animal Welfare, Veterinary Profession and One Health

Telemedicine: an effective treatment support center for rural community in Bangladesh

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Telemedicine is playing a pivotal role in developing country. Realizing the fact, Government of Bangladesh has started its telemedicine journey in 2009 with 8 centers. By 2016 the number has been increased up to 84. Among these, 26 centers are service provider and rests are service recipient. Patients coming to Upazila Health Complex (UHC) or referred from community clinic get direct telemedicine services. These telemedicine centers are equipped with high Internet bandwidth, large screen display, quality telemedicine camera, digital medical equipment and telemedicine peripherals. It is a cross sectional study. Enrolled patient information for telemedicine health care service was collected from District Health Information Software² (DHIS2). DHIS2 is a web-based open-source information system keeping up regularly by Management Information System Department (MIS), Director General of Health service, Government of Bangladesh. In this study, five year's data were observed. In five years (2011to 2016) 36,442 patients enrolled. Among them 44% are male and 56% are female. 93% patient takes services from UHC. Intercommunication between UHCs and district level hospitals is 97% whereas it is less than 2% in case of super specialized and medical college hospitals. In 41 (34%) centers, patients come to receive service every day. Consultant doctors were available regularly in 46(38%) centers. However, comfortability of doctors and patients with the new intervention, consultant's busy schedule at hospitals and uninterrupted internet connectivity are identified as the main barriers to this intervention. In Bangladesh, most of the people are living in the villages and people are suffering due to lack of medical expertise and health care facilities. Telemedicine can play a pivotal role in our country by providing easier and cheaper way to connect healthcare facilities to the rural community and thereby it can reduce the huge healthcare cost and improve patient outcomes significantly and these telemedicine centers can play an important role in early detection of diseases and treatment support for rural community.

Keywords: Implementation Telemedicine, Rural community

Microbiological quality of street-vended foods sold at BAU campus and Mymensingh city

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The study was undertaken to determine the microbial load of street vended foods sold by different street vendors at Bangladesh Agricultural University (BAU) campus and Mymensingh city. A total number of 36 different samples such as phuska(n=6), chotpoti(n=6),samucha (n=6),dalpuri(n=6), pakura(n=6), noodles (n=6) were collected from 36 different vendors of BAU campus and Mymensingh city. Microbial quality was determined by Total Viable Count (TVC), Total Coliform Count (TCC) and Total Staphylococcal Count (TSC). Samples were inoculated into various selective media such as Eosin Methylene Blue (EMB) agar, Plate count (PC) agar and Mannitol Salt (MS) agar and incubated at 37^oC for 24 hours. *E. coli* and *Staphylococcus* spp.were isolated and identified from the samples. Identification of *Staphylococcus* spp. and *E.coli* were confirmed by sugar fermentation and biochemical tests.Total Viable Count (TVC) of bacteria in phuska ranged from 4.7×10^5 cfu/g to 0.23×10^5 cfu/g, in chotpoti 7×10^4 cfu/g to 0.225×10^4 cfu/g, in samucha 8×10^4 cfu/g to 1.360×10^4 cfu/g, in dalpuri 7.2×10^4 cfu/g to 0.52×10^4 cfu/g, in pakura 28.5×10^5 cfu/g to 0.32×10^5 cfu/g and in noodles 2.135×10^6 cfu/g to 0.155×10^6 cfu/g. Total Coliform Count (TCC) in phuska ranged from 3.85×10^2 cfu/g to 1.2×10^2 cfu/g, in chotpoti 30×10^2 cfu/g to 3.8×10^2 cfu/g, in samucha 17×10^2 cfu/g to 5.05×10^2 cfu/g, in dalpuri 3.4×10^2 cfu/g to 1.2×10^2 cfu/g and in pakura 0.46×10^2 cfu/g. Total Staphylococcal Count (TSC) in phuska ranged from 18.5×10^3 cfu/g to 5×10^3 cfu/g, in chotpoti 13×10^3 cfu/g to 0.35×10^3 cfu/g, in samucha 4.1×10^3 cfu/g to 2.0×10^3 cfu/g, in dalpuri 2.6×10^3 cfu/g to 0.28×10^3 cfu/g, in pakura 67.5×10^2 cfu/g to 1.1×10^2 cfu/g and in noodles 1.7×10^4 cfu/g to 0.165×10^4 cfu/g respectively. Antibiotic sensitivity test showed that *E. coli* were sensitive to gentamicin, ciprofloxacin, cephalixin and resistant to ampicillin and penicillin G. *Staphylococcus* spp.were sensitive to gentamicin, ciprofloxacin, cephalixin, vancomycin and resistant to ampicillin. Data of this study indicated that phuska, chotpoti, pakura, dalpuri, samucha and noodles sold by different street vendors at BAU campus and Mymensingh city may act as a source of multidrug resistant food borne bacteria which can contribute to potential health risks for consumers.

Keywords: Street food, microbial load, multidrug resistant, BAU campus, Mymensingh.

Use of the Mini Nutritional Assessment Short Form (MNA-SF) tool for assessing the nutritional status of the older people: A cross-sectional scenario in a rural area of Bangladesh**Sumon Chandra Debnath**, Ekramul Haque

Older people are potentially vulnerable group for malnutrition. It is important to obtain knowledge about the prevalence of nutritional risk and associated factors among older home-dwelling people in order to be able to meet nutritional challenges in this group in the future and to plan appropriate interventions. The present study was carried out to estimate the prevalence of malnutrition and at risk of malnutrition among older population. This rural-based cross-sectional study was carried out in Deora village under Comilla district of Bangladesh among 330 older individuals aged ≥ 60 years during January to December 2015 by applying Mini Nutritional Assessment Short Form (MNA-SF) tool. The Mini Nutritional Assessment (MNA-SF) is an instrument specially designed for assessing the nutritional status of the older people.

Three hundred thirty older (men, $n = 145$ and women, $n = 185$) were interviewed. According to MNA-SF, 33.0% were malnourished, 59.4% at risk of malnutrition and 7.6% well-nourished. The mean (\pm SD) score of MNA-SF was 7.9 ± 2.2 . A significant association was seen between malnutrition and age ($p < 0.001$), gender ($p < 0.001$), and occupation ($p < 0.001$).

Nutritional status of older subjects is very poor as detected in this study. Therefore, it is necessary to raise awareness among older and their caregivers about the quality, quantity and frequency of food intake of older persons. Those found to be at risk of malnutrition or malnourished were counselled and referred for appropriate intervention.

Key words: Mini Nutritional Assessment Short form, nutritional status, older people, rural area

Isolation and characterization of *vibrio* spp. from semiprocessed shrimp**Flora Chakma**

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Microbial safety is one of the public health issues associated with seafood consumption. The present study was conducted to determine the microbial load, isolation and identification of *Vibrio* spp. from semi processed shrimp collected from a processing plant located at Rupsha, Khulna. Furthermore, the isolated *Vibrio* spp. were tested for antimicrobial sensitivity. A total of 20 semi processed shrimp samples were collected after removal of head and tail from 20 different lots. Nutrient agar were used to determine the total viable count and thiosulphate citrate bile salt sucrose (TCBS) agar were used for *Vibrio* spp. isolation. All the samples were primarily enriched in alkaline peptone water (APW) and 2-3 loopful of overnight cultures were streaked onto thiosulphate citrate bile salt sucrose (TCBS) agar plates. Colony appearance on TCBS agar, followed by conventional biochemical tests including oxidase, catalase, sugar fermentation, methyl red (MR), vogesproskauer (VP) and salt tolerance tests were used for identification of *Vibrio* species. In addition, antimicrobial sensitivity testing was performed by disc diffusion method. The study revealed that total viable count (TVC) of semi processed shrimp samples ranged from 7.00×10^5 cfu/g to 4.90×10^6 cfu/g. Out of the 20 samples, five (25%) were found to be positive for *Vibrio* spp. Antibiotic sensitivity test showed that the isolates of *Vibrio* spp. were resistant to ampicillin, intermediate resistant to erythromycin and sensitive to gentamicin, streptomycin, azithromycin, tetracycline and chloramphenicol. The findings of this study revealed that semi processed shrimp samples under this study was more or less contaminated with *Vibrio* spp. which indicated the unhygienic condition of the shrimp culture and processing plant and the presence of antibiotic resistance bacteria in shrimp supposed to be a threat to food safety and might deteriorate the export quality.

Key words: TVC, *Vibrio* spp., semi processed shrimp, processing plant, antibiotic sensitivity test.

Arsenic and rice: Development of crop varieties safer for farming in arsenic-contaminated environments

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Ground water of Ganga-Brahmaputra delta region in West Bengal, India and also Bangladesh is highly contaminated with arsenic which is used for irrigating crops and vegetables. Rice is an efficient arsenic accumulator and thus irrigation with arsenic-contaminated groundwater and soil may induce human health hazard via water-soil-plant-human pathway. According to WHO, provisional maximum tolerable daily intake of arsenic of $2 \mu\text{g Kg}^{-1}$ body weight. Therefore, there is an urgent need to understand the mechanisms of As tolerance and accumulation in rice in order to develop strategies to reduce the risk of As contamination in soil. In this context, gene modification is an effective and practical approach to reduce As accumulation in rice grains. Our study offers an understanding the molecular basis of arsenic toxicity and accumulation in plant parts. We have identified several candidate genes that are involved in arsenic metabolism in rice. We have generated several transgenic rice plants that accumulate less arsenic in their grains. We describe a glutaredoxins (Grx) family protein designated as OsGrx_C7, and investigate the mechanism of glutaredoxin mediated arsenic tolerance and accumulation in rice grains. Overexpression of OsGrx_C7 conferred a markedly enhanced tolerance to arsenite and reduces arsenite accumulation in seeds and shoots of rice. Another potential strategy to alleviate arsenic effects is to generate genetically engineer plants to enable them to transform inorganic arsenic to methylated and volatile arsenic species. Recently, we reported an arsenic methyltransferase gene (*WaarsM*) of the soil fungus *Westerdykella aurantiaca* when expressed in rice able to convert more toxic inorganic arsenicals to methylated arsenic species therefore reduce arsenic accumulation in rice grains. This will have tremendous societal impact related to public health consequences.

Keywords: Arsenic, Glutaredoxin, Methyltransferase, Rice, Transgenic

Evaluation, characterization, and antibiogram study of bacteria isolated from slaughterhouse

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A slaughterhouse is a facility where animals are slaughtered for consumption as food. Meat is considered an important source of proteins, essential amino acids, vitamin B complex and minerals. Fresh meat is highly perishable due to its biological components. Due to this rich composition, it offers a highly favorable environment for the growth of pathogenic bacteria. Bacterial spoilage of meat depends on the initial number of microorganism, time/temperature combination of storage conditions and physicochemical properties of meat.

In this study the isolation and identification of bacteria were confirmed on the basis of their morphology, staining, cultural and biochemical properties and antibiotic sensitivity assay of the isolated bacteria were also studied. A total of 60 slaughterhouse samples were collected from Rajshahi and Gazipur City Corporation. Among 60 samples, 53 (88.33%) samples were positive for bacteria and 7 (11.66%) samples were negative for bacteria. The prevalence of bacteria in Rajshahi City Corporation and Gazipur City Corporation were 93.33% and 83.33%, respectively. The prevalence of *Streptococcus* sp., *Staphylococcus* sp., *Bacillus* sp., *E. coli*, and *Salmonella* sp. were 11.66%, 31.66%, 26.66%, 10.00%, 8.33%, respectively. Besides these 32.07% samples were found for mixed bacterial infection. The prevalence of bacteria were 24.52%, 22.64%, 16.98%, 15.09%, 13.20%, and 7.54% in floor washing, intestinal content, skin, blood, washing of employee's hands and instruments, and meat, respectively.

The antibiotic sensitivity patterns of *Streptococcus* sp. was 0.00%, 42.85%, 42.85%, 57.14%, 57.14%, and 71.43% sensitive to penicillin, gentamycin, tetracycline, amoxicillin, ampicillin and ciprofloxacin, respectively. Similarly, *Staphylococcus* sp. showed 0.00%, 30.00%, 40.00%, 40.00%, 50.00%, and 80.00% sensitive to penicillin, gentamycin, tetracycline, amoxicillin, ampicillin and ciprofloxacin, respectively. The *Bacillus* sp. also revealed 10.00%, 30.00%, 30.00%, 40.00%, 40.00% and 80.00% sensitive to penicillin, gentamycin, tetracycline, amoxicillin, ampicillin and ciprofloxacin, respectively. Similarly, *E. coli* revealed 00.00%, 33.33%, 33.33%, 50.00%, 50.00% and 83.33% sensitive to penicillin, gentamycin, tetracycline, amoxicillin, ampicillin and ciprofloxacin, respectively and *Salmonella* sp. showed 0.00%, 40.00%, 40.00%, 60.00% , 60.00%, and 80.00% sensitive to penicillin, gentamycin, tetracycline, amoxicillin, ampicillin and ciprofloxacin, respectively. Appropriate methods should be applied during slaughtering operations, using adequate water and disinfection to reduce the occurrence of bacteria in slaughterhouse.

Keyword: Evaluation, Characterization, Antibiogram study, Bacteria, Slaughterhouse

Implementation of food control guidelines across poultry value chain in Bangladesh

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The overuse of antibiotics, chemicals and as well as lack of farm biosecurity and good hygiene practices in poultry production are considered to be contributors for occurring foodborne illness and many significant public health threats reported in both developed and developing countries now a days. Considering the above, a piloted food safety activity was implemented jointly by Department of Livestock Services and FAO-Food Safety program, Bangladesh in twenty five selected poultry (broiler) dense areas of the country. Good Agricultural Practices (GAP) and Good Hygiene Practices (GHP) related five (microbial) plus five (chemical) control measures were adopted in the farm level (N=500) through farmers' motivation and intensive participatory training program. It was found that average production cost reduces, feed conversion ratio decreases and mortality rate decreases that induces increase farm profitability in the best practiced farms (n=81). In conclusion, Good Agricultural Practices (GAP) and Good Hygiene Practices (GHP) through ensuring key control measures can increase profitability in broiler farming and also reduces public health threats.

Key words: Food Safety; Poultry value chain; Bangladesh.

Should consumers purchase poultry from live bird markets or from door-to-door live bird traders - a comparative assessment of avian influenza spill-over risk in Dhaka, Bangladesh

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Live bird markets (LBMs) have been identified as a maintenance reservoir for viruses and found to be the most frequent source of infection for human cases of avian influenza. However, demand for live poultry remains high among residents in Asian cities and therefore it may be valuable to explore alternative trading and supply systems and the associated risks of human exposure to avian influenza (AI). Due to traffic congestion, mobile traders form an important source of live poultry supply to consumers in Dhaka, Bangladesh. These traders walk or ride modified rickshaws with a limited number of live poultry through the streets to the homes of both established clients and ad hoc customers. Slaughter and dressings are performed in customer's home, in front of the premises (e.g. street-side, corridor, veranda, garage, etc.), or in public areas for mobile consumers. Waste is disposed on the ground, into dust bins, or placed in a plastic bag for later disposal. Although studies have been initiated to estimate the movement details of these traders, much information is still unknown. Since these traders are less clustered than traders in a LBM, they may potentially be a safer alternative to the consumer than slaughtering of poultry in LBM which exposes the virus within tightly confined and poorly cleaned slaughter and sales areas. In this study, samples will be collected from mobile trading system to assess the probability of presence of viable H5N1 HPAI virus in the mobile trader environment. Data on trading and processing habits will also be collected through observations and interviews to assess consumer exposure and perceptions of traders and consumers alike. The results from this study will outline exposure pathways and estimate the risk of consumer exposure to H5N1 HPAI through purchase from mobile traders versus risk of consumer exposure through purchase of poultry from LBMs.

Effect of washing on reduction of pesticide residues in selected vegetables of Bangladesh

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To assess the effect of washing with tap water on removal of organophosphorous pesticide residues (Diazinon, Malathion, Cypermethrin, Dimethoate, Qunalphos & Chloropyrifos) in Tomato, Eggplant, Cauliflower, Country bean and Green chili, 150 samples were collected from 16 markets of Dhaka city and 18 markets of 06 Districts town during January'17 to march'17. Analysis of Pesticide residues was carried out in the National Food Safety Laboratory, Institute of Public Health, Mohakhali, Dhaka, Bangladesh, by using Gas Chromatograph equipped with Mass Spectrometry Detector (GCMSD). About 30% of tested samples showed contamination with different amount of pesticides residues. Positive samples were dipped in tap water for 5 minutes after an initial 15 sec. gentle rotation by hand followed by repetition of the process. About 40 -74% reduction of residues was observed after 1st wash. Only 02 cauliflower and 04 Green chili samples showed positive residues level even after 2nd wash. In case of Green chili, the residues level was found above MRL.

Key word: Vegetables, Pesticide residues, MRLs, washing.

Looking into farmer's mind: Perception towards bovine mastitis control and antibiotic uses in Bangladesh

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An ethnographic study nested within the Sweden funded project of “Bovine Udder Health Control Programme in Bangladesh” is being conducted to assess the perception of farmers about mastitis control and antibiotic use in Dairy cows at Chittagong, Bangladesh since February 2017. The study is based on “Theory of Planned Behavior” to measure the intention of the farmers behind their behavioral act with qualitative and semi-quantitative data, collected by a face-to-face questionnaire interview to 100 farmers. We have completed the interview of 25 farms so far. The belief on mastitis control was controlled by expensive mastitis treatment (% Weightage 80.7 and mean score 2.8). Farmers had a feeling that “Mastitis Milk” is safe for human consumption” (% Weightage 60 and mean score 3). Many farmers reported to use antibiotic or sulphur drugs irrationally in their farms and used to buy antimicrobials directly from drug shop without veterinarian prescription (% Weightage 72.6 and 66.6 and mean score 3.6 and 3.3, respectively). Insufficient field veterinarians to ask for a prescription was identified as an indicator of lacking farmers capability to use antibiotic rationally (% Weightage 56.3 and mean score 2.8). These findings could be used to identify the gap in farmer's knowledge and attitude and make them aware of preventive management practices rather than reactive behaviors or acts for mastitis control, public health consequences and rational use of antibiotic uses.

Keywords: Bovine mastitis, antibiotic uses, farmers' perception and health risk, Bangladesh

Prevalence and antimicrobial susceptibility of shigatoxin producing *Escherichia coli* in poultry and their products

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Shiga toxin-producing *Escherichia coli* (STEC) is an important diarrheal pathogen which may leads to watery to bloody diarrhea, hemorrhagic colitis and hemolytic uremic syndrome in humans. This study was designed to determine the shiga toxin producing genes and investigate antibiotic sensitivity or resistant patterns of the *E. coli* isolated from the diarrheic broiler, healthy broiler, indigenous birds, healthy layer, egg washing and poultry meat at Borobajar, K.R market and Jobbarer Moore of Mymensingh. A total of 60 samples comprised of 40 cloacal swabs, 10 egg washing and 10 poultry meat samples were collected and screened for the detection of *E. coli* on the basis of cultural, staining and biochemical properties followed by molecular characterization using genus specific 16SrRNA primers by Polymerase Chain Reaction. According to the study, 39 (65%) out of 60 samples, were confirmed as *E. coli*. Overall prevalence of STEC among the examined samples was 3.33%. Again, those 39 positive *E. coli* were analyzed for the presence of *Stx-1* and *Stx-2* genes by multiplex PCR. From the results, only 2 (5.12%) isolate was confirmed to be positive for the presence of the *Stx-1* gene but no isolate was found to be positive for the *Stx-2* gene. Antimicrobial sensitivity and resistant pattern of two Shiga toxin (STX) producing *E. coli* was determined by disc diffusion method against 8 antimicrobial agents. All bacteria (100%) are found sensitive to Gentamicin and Cephalexine. One of two (50%) bacterial isolates were found sensitive to Erythromycin and Ciprofloxacin. All isolates were found to be resistance against Ampicillin, Azithromycin and Cefixime. One isolate showed intermediate sensitive profile to Chloramphenicol, Erythromycin and Cefixime. Data of this study indicated that poultry harbour multidrug resistant shigatoxin producing *E. coli* which may cause public health hazard if transmitted to human through food chain.

Key words: Prevalence, STEC, poultry, antibiotic sensitivity, multiplex PCR.

Assessment of Good Hygienic Practices among food processors in small food businesses in Barisal City Corporation

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The food safety is the alarming issue for the global health. The aim of this study is to assess the awareness on GHP of food processors, working in different food businesses in Barisal City Corporation area of Bangladesh. A questionnaire was used which includes the use of cutting tool for food, use of gloves during food processing, knowledge about zoonotic diseases, work with sickness, aware during food serving, shower before work, personal hygiene, separate working dress and aware about customer health. 93 food processors were interviewed during the period from January to March 2015. In this study, we found that 89.2% food processor were used boti for cutting the food which was significantly higher than that of use knife (10.8%). 71% food processor were not used hand gloves during cutting and processing the food which was significantly higher than that of use gloves (29%). We also found out that 35.5% were processors were worked with sickness where as 54.8% worker has no knowledge about the food borne disease transmission which was significantly higher than that of knowledge about that (45.2%). 67.7% were worker not use any separate dress during their work and 28% processor did not aware about the customer health hygiene. 91.4% worker was concern about their personnel cleanliness such as cutting nail, use of shop after toilet etc. However, the food processor awareness during food processing and serving to the people is essential for public health significance. Therefore, from this study, it may be recommend that the proper training of food processors is necessary to protect consumers health.

Key words: Awareness, Barisal City Corporation, food processor, food shop, public health.

Bacteriological contamination of street food vended in Chittagong, BangladeshPlabon Paul¹, Abdul Ahad², Shamina Jahan³, A.K.M. Mostafa Anower^{1*}

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Street vended foods have become an integral part of urban economy in the developing world including Bangladesh. To assess the bacteriological quality of street vended foods, a total of 200 samples of ready to eat foods - Fucka, Chicken biriani, Sugarcane juice and Egg toasts were aseptically collected from five different areas of Chittagong, Bangladesh. A structured questionnaire was used in interview to determine the status of the vending sites and associated food handling practices. All bacterial isolates were identified by studying their cultural characteristics and biochemical properties. This study revealed that, 67.5% of the food samples were contaminated with one or more bacteria. The isolates found were *E. coli* 62 (30.09%), *Salmonella* spp. 10 (4.86%) and *Staphylococcus aureus* 134 (65.05%). Furthermore, it was observed that highest prevalence of *E. coli* was in Chicken biriani (40%) of other food items (Fucka 30%, Sugarcane juice 22% and Egg toast 32%). Foods from New market area were highly infected with *E. coli* (37.5%) of all other areas namely Chawkbazar (30%), GEC (22.5%), AK Khan (35%) and Agrabad (30%). The highest incidence of *Salmonella* spp. was found in Fucka (16%) of all other tested food samples namely Chicken biriani (4%), Sugarcane juice (0%) and Egg toast (0%). The highest incidence of *Staphylococcus aureus* was found in Fucka (100%) and Chicken biriani (100%) while Sugarcane juice and Egg toasts were not contaminated with *Staphylococcus aureus*. Food samples from Chawkbazar was the most affected with *Staphylococcus aureus* (70%) of the other areas namely GEC (62.5%), AK Khan (67.5%), Agrabad (67.5%) and New market (67.5%). Furthermore, the study reveals that there was significant association of *Salmonella* spp. with the vendors age ($P < 0.05$). A significant association of *Staphylococcus aureus* was observed with the vendors educational status ($P < 0.05$). There was no significant association in the occurrences of bacterial agents by protection from external environment. A significant association of *E. coli* and *Staphylococcus aureus* was observed when the vendors received informal training ($P < 0.05$). Presence of *E. coli*, *Salmonella* spp. and *Staphylococcus aureus* indicates the degree of ignorance on the part of food handlers towards proper hygienic practices.

Key words: Food-borne microbes, Public health, Street food, Vendors

Promoting Duck Farmers Consumption Patterns, Dietary Diversity and Income through Improved Duck Rearing Practices: a Field Trial in the Chittagong District, Bangladesh

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In Bangladesh, micronutrient deficiencies and stunting rates are among the highest in the world and a major part of the population is undernourished. The consumption of animal source foods, such as duck meat and eggs could provide an easily accessible household source of protein, fat, vitamins and minerals to combat malnutrition and stunting. Duck rearing is also considered a more culturally acceptable alternative to raising chickens in Bangladesh. However, interventions for duck rearing have not been developed and a demonstration of improved productivity will be necessary to convince households to invest time and resources into duck rearing. Therefore, we conducted a study between July 2016 and June 2017 in the Rangunia and Anwara upazilas (sub-district) of the Chittagong district, Bangladesh, to explore the impact of improved duck rearing on consumption, economic parameters and dietary diversity of duck owners. Six villages were purposively selected and two villagers were each classified as control, intervention-1 and intervention-2 groups. In each village a total of 25 randomly selected households participated in the research and were supplied with 15 day old ducklings. In control villages, households only received training in duck raising and a bamboo basket, while households in intervention-1 groups received in addition to the training and bamboo baskets, vaccinations of ducks. Households in intervention-2 received training, bamboo baskets, vaccination, routine deworming and supplemental feeds for a period of four months. Improved duck production (in particular in households in intervention-2) resulted in decreased mortality of supplied ducks and increased consumption and sales of eggs and ducks compared to controls. Additionally, interventions markedly improved the dietary diversity index in participating households. Overall, improved duck rearing resulted in an increased contribution of duck products to farmer's diets and income. It seems that, improved duck rearing can provide an opportunity for rural households in Bangladesh to increase the availability of ducks and eggs, which would then result in improved intake of micronutrients and protein and increased subsistence income from duck production.

Keywords: Consumption, Dietary diversity index, Duck and Intervention

One Health Approach: Improving Food Safety in Bangladesh**Dr Shah Md Mahfuzur Rahman**

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Food Safety is an important determinant of public health both in developed and developing countries including Bangladesh. Contamination of food with microbials and or chemicals which can occur at any point of food chain of the ever growing food system, not infrequently causing foodborne diseases including food safety emergencies in Bangladesh. Coordinated by the Bangladesh Food Safety Authority, some fifteen ministries and their about twenty agencies are involved across the food chain, governed by a number laws and regulations including the 'The Bangladesh Safe Food Act, 2013'. Contamination occurs as a result of lack or inadequate GAP, GHP, GMP as well as poorly enforced regulatory standards, which may be further aggravated by changing ecosystems, risky consumers' behaviour, travels, trades, globalization, population growth, interconnectedness and transboundary issues. The objective of the article is to identify the need of convergence of human, animal and environmental health to improve food safety in Bangladesh, to promote and protect public health and enhance food trades. More than two hundred fifty emerging, reemerging and persistent foodborne diseases originating from microbial, chemical or parasitic sources have been identified globally. Over the past three decades, approximately 75 percent of new human infectious diseases have been zoonotic. The human-animal-ecosystem interface is important, rapidly changing and complex. Food as a potential vehicle for disease transmission is embedded in this complex system. The scientific community, agricultural including fisheries and livestock, environment and health systems remain mostly isolated and entrenched, along with traditional thinking and habitual ways of working. Many foodborne diseases are focused on the risk to human health while the most effective control strategies are in animals, animal products, and in the environment. This type of biased and artificial severance is a critical barrier to the one health concept. So, the convergence of human, animals and the environment, with collaborative and coordinated efforts to strengthen inspection, enforcement of the regulatory standards, integrated disease surveillance and contaminants monitoring under the One Health approach-a demanding, profound and unprecedented interdisciplinary approach thus recommended for improving food safety in Bangladesh

Characterization of *Staphylococcus aureus* Isolated from Chicken and Quail Egg Shell

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The study was attempted to determine the prevalence of *Staphylococcus aureus* in the surface of chicken and quail eggs and characterization of the bacteria taking into account their phenotypic properties, biochemical reactions, staining properties, antibiotic sensitivity pattern and PCR to test for the presence of *mecA* gene in *Staphylococcus aureus*, which is responsible for the resistance to methicillin. For this study a total 300 samples were collected from different retail shops and farms of Mymensingh district of which 220 samples were of chicken and 80 were of quails. After taking swab samples from the egg surfaces they were enriched in the nutrient broth and then the samples were streaked onto different selective media like MS agar and blood agar for *Staphylococcus aureus*. The results obtained indicate that a high percentage of the retail chicken and quail eggs tested contaminated with *Staphylococcus* spp. The prevalence of *Staphylococcus* spp. and *Staphylococcus aureus* in chicken eggs were 20.45% and 10.45% respectively. On the other hand the prevalence of *Staphylococcus* spp. and *Staphylococcus aureus* in quail eggs were 16.25 % and 5% respectively. Moreover, the molecular identifications were done by means of PCR assay using specific primers for *Staphylococcus aureus*. This was done targeting *nuc* gene and *mecA* gene where they were found to be positive showing amplification of 279 bp and 533 bp respectively. Antibiotic sensitivity test of the isolated bacteria was performed against 9 commonly used antibiotics such as amoxicillin, azithromycin, oxacillin, vancomycin, gentamycin, tetracycline, ciprofloxacin, nalidixic acid, penicillin, ampicillin and erythromycin by using disc diffusion method. It was observed that the isolates were sensitive to ciprofloxacin, gentamicin, vancomycin, erythromycin, and resistant to amoxicillin, penicillin, azithromycin, oxacillin, nalidixic acid. So the antibiotic sensitivity testing also indicates that most of the isolates to be resistant to more than one therapeutic agents tested. The present study concludes that egg surface harbor multidrug resistant bacteria which might cause public health hazards if these antibiotic resistant bacteria transfer to human.

Key words: *Staphylococcus aureus* characterization, antibiotic sensitivity, methicillin resistance, public health hazards.

A comparative study on human Health Risk due to the consumption of contaminated fish

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Fish has been known for its reputation as the established health food for most of the world's population, particularly in developing countries, as compared to meat, poultry and eggs. The protein content in fish averages from 15 to 20 percent; hence fish provides comparatively cheap and readily available protein sources in complement with long chains of n-3 fatty acids, amino acids, vitamins and minerals that further contribute to healthy nutritional options for a balance dietary intake. Although Fishes are major part of the human diet because, it has high protein content, low saturated fat and also contains omega fatty acids known to support good health, but there is a growing concern that metals accumulated in fish muscle tissues may represent a health risk, especially for populations with high fish consumption rates. Metals like Cu, Fe, Mn and Zn have normal physiological regulatory activities in organisms, but some other metals like arsenic, cadmium, mercury, nickel, and lead exhibit toxic effects on organisms. This investigation quantified spatial variability of heavy metals and followed methods of the U.S. Environmental Protection Agency (EPA) to estimate the hazard indices as well as cancer risks associated with consuming fish caught collected from Malaysia and Philippines. The calculation of metal pollution index (MPI) was carried out to classify the study area according to the level of contamination.

The level of exposure due to the consumption of each chemical in selected fish tissue was estimated in an average daily dose equation. The findings of the study showed potential health risk for both countries due to the contamination of heavy metals in fish and proper management policy is required for ensuring safe eating of fish.

Seroprevalence of West Nile virus in wild birds in Bangladesh

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West Nile virus (WNV) is the most widespread arbovirus in the world capable of causing epidemics in both humans and animals. It is transmitted by a wide range of mosquitoes and multiple species of birds can act as amplifying hosts. Migratory birds are considered to be the main vehicle for introducing WNV into new regions. In humans, the pathogenicity of WNV varies from mild, self limiting, non-fatal, febrile illness to severe encephalitis. The status of WNV in Bangladesh is currently unknown. We conducted this study to assess the prevalence of WNV among resident and migratory wild birds of Bangladesh. During the period of 2010 to 2012 birds were captured using mist nets and noose traps, and blood samples were taken from wild birds landing on the coastal sandbars of Cox's Bazar, Hakaluki *haor* (seasonal wetlands) of Sylhet and Moulvibazar, Tanguar *haor* of Sunamgonj and the rice paddy fields of Patuakhali, Netrokona and Guibandha. Recovered serum was tested at 50% dilution for detection of WNV antibodies using a commercially available competitive ELISA following the manufacturer's instructions (ID Screen[®] West Nile Competition, IDVet, Montpellier, France). Blood samples were obtained from a total of 888 birds comprising 21 families and 80 species; 250 (28%) of them were resident and 638 (72%) were migratory. Forty eight birds (5.4%, CI 0.04-0.07) tested positive for WNV antibody. The positive birds consisted of 45 common coots (*Fulica atra*), one ferruginous pochard (*Aythya nyroca*), one fulvous whistling duck (*Dendrocygna bicolor*) and one great crested grebe (*Podiceps cristatus*). Among those birds, two common coots, one fulvous whistling duck and one great crested grebe were from the Hakaluki haor, and 43 common coots and one ferruginous pochard were from Tanguar haor. Only one positive bird, a fulvous whistling duck, was a resident species. Both resident and migratory wild birds of Bangladesh demonstrated exposure to WNV infection. Most of the WNV positive birds were migratory common coots, which is similar to previous reports from India and Iran. Future isolation and molecular characterization of the virus will allow us to better understand the epidemiology of this virus in Bangladesh.

Key words: West Nile virus, wild birds, sero-prevalence, Bangladesh.

Assessing the Risk of Disease Emergence from Indian Flying Fox (*Pteropus Medius*) Hunting at High-Risk Interfaces in Bangladesh.

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Understanding hunting, trading, and consumption of wildlife at the community level in Bangladesh is limited. This qualitative study purposes to understand hunting behavior, wildlife consumption patterns, and the wildlife value chain assessing the risk of zoonotic disease transmission in Faridpur communities. Participant observation and 15 targeted ethnographic interviews were conducted between October-December 2015. Participants included wildlife hunters, collectors, transporters, vendors, and consumers. “Sharder” communities hunt wild animals as traditional practice and key protein source. This community is dependent on various sources of income, including: day labor, potter, barber, and cobbler. Hunting provides an additional source of income in the community. Hunters are mostly illiterate and unaware of zoonotic disease risk, such as Nipah from bats (*Pteropus medius*). All hunters were male, whereas women were primarily involved in butchering. The wild animal value chain is centered in Sharder communities, though some neighboring Muslim communities reported hunting wild animals as a free protein source. Participants were observed using bat bone to remedy joint pain and asthma. Hunters reported declining local bat populations due to over-hunting and ecological changes. A shared human and animal dependence on limited natural resources amplified biodiversity declines, however to be successful communities need sustainable alternative livelihoods solutions and protein sources. Unprotected hunting practices and limited or no hygiene measures can yield greater risk of zoonotic disease spillover. Hunting flying foxes in Bangladesh may represent a previously unrecognized pathway for Nipah emergence. The dearth of disease transmission knowledge posed by wildlife may facilitate zoonotic spillover.

Key Words: Bat, Hunting, Interface, Zoonotic diseases, Spillover, Conservation,

Comparing seasonality of bats' feeding behavior to seasonality of Nipah virus transmission to humans in Bangladesh

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Nipah outbreaks occur during the winter in Bangladesh and have been linked with the consumption of either fresh or fermented date palm sap presumed to be contaminated with bat (*Pteropus giganteus*) urine or saliva. A few communities collect date palm sap throughout the year to ferment and consume. This study's objective was to characterize *Pteropus* bats' sap feeding behavior round the year to identify potential for sap contamination with bat excreta. We used infrared cameras to observe bats' feeding behavior for 28 tree-nights per month for 22 months from March 2013 to December 2014. We placed the cameras at 4 sap producing date palm trees focused at the sap producing surface and collection pot from 5:00 PM to 6:00 AM for seven consecutive nights. We extracted the number and duration of bat visits (flying and/or landing on and around the tree) and duration of contact (landing, licking, or urinating either on shaved surface or collection pot) with date palm sap from the images. We described the frequency of bat visits during four seasons: winter (December-February), spring (March-May), monsoon (June-September), and post-monsoon (October-November). We recorded a total of 26,870 bat visits (5% *Pteropus*, 90% non-*Pteropus* and 5% unidentified) from 616 observation tree-nights. Median duration of each visit was higher for *Pteropus* bats than non-*Pteropus* bats (8 versus 0.03 minutes, $P < 0.001$). Median duration of contact with date palm sap was higher for *Pteropus* bats (0.67 versus 0.03 minutes, $P < 0.001$) for each visit. The average number of *Pteropus* bat visits per night was the highest during spring (17) followed by winter (14), post monsoon (6) and monsoon (3). Even when date palm sap is harvested year-round, *Pteropus* bats visit the date palm trees more frequently during the spring and winter, perhaps due to lack of other available food. Feeding behavior could be one reason why the risk of Nipah infection to people has been concentrated in the winter season, even when fermented sap is consumed year-round. Sap harvesters should regularly use skirts to prevent bats from contaminating the date palm sap to prevent Nipah virus and other bat associated zoonoses.

Key words: Nipah, bats, infra red camera, feeding behavior

Feeding Ecology and Conservation of the Endangered Hoolock Gibbon (*Hoolock hoolock*) in a Semi-evergreen Forest of Bangladesh

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Determining the diet composition and identifying factors that influence the food selection are important in understanding habitat requirements of primates and designing conservation plans. We studied the feeding ecology and conservation of hoolock gibbon (*Hoolock hoolock*) at Satchari National Park (24°7'25.65"N 91°27'5.43"E) in Sylhet, Bangladesh from April 2016 to March 2017. Data were collected using scan sampling method from dawn to dusk observation on all visible members of the group at every 5-min interval. The time of feeding on different food species, food items, feeding heights and substrate utilization were recorded. Hoolock gibbon in Satchari National Park spent 34.6% of their active time in feeding, followed by 26.1% resting, 22.4% travelling, 12.0% foraging and 4.9% social activities. Fruits were the main dietary items (57.5%) followed by leaves (20.1%), flowers (8.7%), barks (4.7%), shoots (3.7%) and animal matters (5.4%). A total of 76 plant food species under 33 families consumed by hoolock gibbon during study period. The largest number of plants (n=16) were species of Moraceae family, and gibbons spent more feeding time (27.4%) on them alone. Hoolock gibbon ate highest proportion of food items from *Ficus gibbosa* (8.2%) providing fruits and leaves throughout the year. They spent 63.4% of their feeding time in upper canopies and most frequently used substrate was twigs or terminal branches (37.8%). The main threats facing by gibbon in the study area are habitat fragmentation, illegal timber extraction, introduction of exotic tree species and lack of environmental awareness and education. The essential key elements of suitable gibbon habitats are a closed canopy structure, suitable combination of food tree plantation and raising awareness through conservation education programs.

Keywords: Hoolock gibbon, Feeding ecology, Conservation, Semi-evergreen forest, Bangladesh.

Human and rhesus macaque (*Macaca mulatta*) interactions at thriving ecosystem interfaces and risk of disease spillover in Bangladesh

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Though human-macaque interactions may trigger public health concerns, there is insufficient research on effects of environmental changes and rhesus macaque (*Macaca mulatta*) interactions with humans. This qualitative study aims to understand context, risk practices, and patterns of human-macaque interactions and potential risk of spillover in Bangladesh. Participant observations, Ethnographic Interviews (58), and Focus Group Discussions (3) were conducted between August, 2015-January, 2016 in Old Dhaka, Madaripur, and Chandpur. Respondents reported changes in the physical environment from natural disasters or manmade causes. All three areas reported significant anthropomorphic landscape transformation. As natural water sources diminish macaques increasingly depend on human water sources, allowing possible water source contamination. Macaques have expanded their foraging range, invading new areas without a history of close contact with monkeys. Causing violent interactions and increased incidents of bites/scratches. People accepted the presence of monkeys in homes and communities because monkeys aren't considered a threat for disease transmission. As a result, they do not mind sharing food or water with macaques. Monkey bites/scratches are not always taken seriously, in some cases victims are not taken to the hospital. Medicinal beliefs reported stated, food touched by macaque is a remedy for respiratory problems or bones relief joint pain. Ascertaining mechanisms for disease transmission it is important to identify direct and indirect interactions between humans and macaques caused by environmental change. The lack of awareness surrounding zoonotic diseases transmission and potential spread to wider populations needs to be addressed.

Key words: Rhesus macaque, Interactions, zoonotic Disease, Environmental changes

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