গণপ্রজাতন্ত্রী বাংলাদেশ সরকার

11th OHBC
12-14 June, 2023
One Health Bangladesh Conference

One Health Approach for Tackling Antimicrobial Resistance and Pandemics

ABSTRACT BOOK

11th One Health Bangladesh Conference 2023

12 - 14 June 2023
Radisson Blu Dhaka Water Garden

Inner Cover

Abstract Book
11th One Health Bangladesh Conference
One Health Secretariat and One Health Bangladesh
12-14 June 2023
Dhaka, Bangladesh

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Welcome Message

Majority of global, regional and national health crises of the recent past originated from animals. Beyond the pathogens of pandemic potentials, many classical zoonoses cause deaths and widespread social disruptions particularly affecting the poor population of economically disadvantaged countries. Antimicrobials were considered as a breakthrough invention saving millions of lives, but abuse of antimicrobials are pushing humanity to the post antibiotic era where people might succumb to death even with simple infections. The AMR per se is an important One Health crisis and needs strong community and multisectoral engagement with ownership and commitment. The high burden of diseases due to uncontrolled physical growth of urban centers and climate change as demonstrated by the unprecedented upsurge of vector borne diseases in recent times has caused huge sufferings, losses and woes to individuals, families, communities, and nations.

The 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 One Health approach is essential for tackling antimicrobial resistance and pandemic.

Disease emergence, food and nutrition security, many of the non-communicable diseases are linked with degrading environment and ecosystems, and restoration of the ecosystem is fundamental for humanity and the planet. The COVID-19 pandemic has demonstrated consequences of inaction of harnessing the strength of One Health to avert the chance of emergence of pandemics. The lessons learned from the COVID-19 pandemic should be translated into future planning, financing, and reassembling our health systems. One health approach at national, regional, and global scale are critical to predict, prepare and respond to future health crises.

The One Health concept evolved in Bangladesh in 2008. The government of Bangladesh institutionalized One Health within the government by establishing One Health Secretariat in 2016. One Health Bangladesh has thus far organized ten conferences. Since 2016, One Health Secretariat has taken the lead to organize the conference.

In such a context, the theme of Conference has been selected as **One Health approach for tackling antimicrobial resistance and pandemics**. There will be five plenary sessions: one health approach in pandemic preparedness; biodiversity, environment and health; one health continuing education and networking; antimicrobial resistance and food safety; and one health institutionalization; eight open oral paper sessions; and poster presentations. National and international speakers of authorities in the theme areas have been invited to speak in the five plenary sessions of the conference.

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. We welcome you to the 11th One Health Bangladesh Conference. We wish you a pleasant and fruitful time.

Prof. Dr. Nitish C Debnath
National Coordinator
One Health Bangladesh
Team Lead, Fleming Fund Country Grant to
Bangladesh, DAI Global

Prof. Dr. Tahmina Shirin
Chair, One Health Secretariate Coordination
Committee
Director, Institute of Epidemiology Disease
Control and Research (IEDCR)

Editorial

The 11th One Health Bangladesh Conference aims to bring together professionals, researchers and other stakeholders from various fields to share strategies, policies, actions, latest developments and challenges of One Health in the country or elsewhere in the world. The conference will showcase success stories of One Health in Bangladesh and beyond. The conference seeks to further solidify One Health network, sensitize policy makers and develop actionable policies and strategies to prevent, detect and respond to future pandemic as well as emerging and ongoing health threats originating at animal, human and ecosystem interface. Antimicrobial resistance is also an emerging pandemic threat. In this context, the theme of the conference is: **One Health approach for tackling antimicrobial resistance and pandemics.**

Through plenary sessions, oral and poster presentations, the conference will provide a platform for participants to share their experiences, knowledge and strengthen collaborations to promote One Health in Bangladesh and globally.

The conference received abstracts on more than eight thematic areas and huge interest was generated among the scientists, researchers and professionals. We received a large number of abstracts and selected either for oral or poster presentation after peer review. In addition to 11 keynote lectures in five plenary sessions, 39 open oral papers in eight sessions and nearly 100 posters will be presented in the conference.

The abstract book contains detailed program and abstracts of oral, poster and keynote presentations. We thank the reviewers, editing panel members and contributors for their sincere efforts. Special thanks go to the members of scientific sub-committee and souvenir publication sub-committee for their diligence for editing, compiling and publishing the abstracts in the form of a book.

Prof. Dr. Md Rafiqul Islam
Convener
Scientific Sub-committee
11th One Health Bangladesh Conference

Dr. Mohammad Mushtuq Husain
Member Secretary
Scientific Sub-committee
11th One Health Bangladesh Conference

11TH ONE HEALTH BANGLADESH CONFERENCE 2023
12-14 June 2023
Radisson Blu Dhaka Water Garden
One Health Approach for Tackling Antimicrobial Resistance and Pandemics

Conference Program Schedule

[Subject to change. Please check https://onehealthbd.org for any update]

11 June 2023	
11:00 – 17:00	Signing in and Conference Kit Distribution Venue: One Health Conference Secretariat, Institute of Epidemiology, Disease Control and Research (IEDCR), Mohakhali, Dhaka-1212 *(Please produce your registration slip for collection of the conference kit)*

Day 1: 12 June 2023	
08:00 – 09:00	Signing in and Conference Kit Distribution Venue: Radisson Blu Dhaka Water Garden (Utsab Hall, Ground Floor) *(Please produce your registration slip for collection of the conference kit)*
09:00 – 10:30	**PLENARY SESSION 1** **One Health Approach for Pandemic Prevention, Preparedness, and Response** Venue: Ball Room (1st Floor), Radisson Blu Dhaka Water Garden
	Chair: Prof. Dr. Mahmudur Rahman, Country Director, The Eastern Mediterranean Public Health Network (EMPHNET), Bangladesh
	Speakers: Dr. Gina Samaan, Unit Head, Pandemic Disease Preparedness, World Health Organization Dr. Anthony Eshofonie, Team Leader of the Health Security and Emergency Response Team, WHO Bangladesh Country Office Dr. Mahbubur Rahman, Assistant Professor, Institute of Epidemiology Disease Control and Research (IEDCR)
	Panel Discussants: Prof. Dr. Meerjady Sabrina Flora, Director, National Institute of Preventive and Social Medicine (NIPSOM) Dr. Tahmeed Ahmed, Executive Director of the International Center for Diarrheal Disease Research (icddr'b) Prof. Dr. Md. Rafiqul Islam, Bangladesh Agricultural University (BAU) Dr. Md. Giasuddin, Former Director Bangladesh Livestock Research Institute (BLRI) Dr. M. Salim Uzzaman, General Secretary, One Health Bangladesh
	Rapporteurs: Dr. Abu Sayeed Md. Abdul Hannan, Deputy Director, Department of Livestock Services (DLS) Dr. Asesha Afrin, Research Investigator, icddr,b

10:30 – 11:00	TEA BREAK AND NETWORKING
11:30 – 13:10	**INAUGURAL CEREMONY**
11:30 – 11:35	Welcome address by Prof. Dr. Nitish Debnath, National Coordinator, One Health Bangladesh and Team Lead, Fleming Fund Country Grants Bangladesh, DAI Global LLC
11:35 – 11:45	Keynote Paper by Dr. Michael Ryan, Executive Director, Health Emergencies Program, World Health Organization
11:45 – 11:50	Speech by Mr. Sheldon Yett, UNICEF Representative to Bangladesh
11:50 – 11:55	Speech by Mr. Robert D Simpson, FAO Representative to Bangladesh
11:55 – 12:00	Speech by Dr. Bardan Jung Rana, WHO Representative to Bangladesh
12:00 – 12:05	Speech by Mr. Badal Chandra Biswas, Director General of Department of Agricultural Extension
12:05 – 12:10	Speech by Mr. Kh. Mahbubul Haque, Director General, Department of Fisheries
12:10 – 12:15	Speech by Mr. Md. Amir Hosain Chowdhury, Chief Conservator of Forest, Forest Department
12:15 – 12:20	Speech by Dr. Md. Emdadul Haque Talukder, Director General, Department of Livestock Services (DLS)
12:20 – 12:25	Speech by Prof. Dr. Abul Bashar Mohammed Khurshid Alam, Director General, Directorate General of Health Services (DGHS)
12:25 – 12:35	Inaugural Speech by Mr. Md. Shahab Uddin MP, Honorable Minister, Ministry of Environment, Forest and Climate Change, Government of the People's Republic of Bangladesh
12:35 – 12:45	Inaugural Speech by Mr. S M Rezaul Karim MP, Honorable Minister, Ministry of Fisheries and Livestock, Government of the People's Republic of Bangladesh
12:45 – 12:55	Inaugural Speech by Krishibid Dr. Muhammad Abdur Razzaque MP, Honorable Minister, Ministry of Agriculture, Government of the People's Republic of Bangladesh
12:55 – 13:00	Vote of thanks by Prof. Dr. Tahmina Shirin, Chair, One Health Secretariat Coordination Committee & Director, Institute of Epidemiology, Disease Control & Research (IEDCR)
13:00 -13:10	Address by Chairperson Mr. Zahid Maleque MP, Honorable Minister, Ministry of Health and Family Welfare, Government of the People's Republic of Bangladesh
13:10 -14:30	LUNCH AND PRAYER BREAK
14:30 – 16:00	**PLENARY SESSION 2** **Biodiversity, Environment, and Health** Venue: Ball Room (1st Floor), Radisson Blu Dhaka Water Garden
	Chair: Mr. Md. Amir Hosain Chowdhury, Chief Conservator of Forest, Forest Department
	Speakers: Dr. Jonathan Epstein, Vice President for Science and Outreach, EcoHealth Alliance, NY, USA Prof. Dr. Robyn Alders, Honorary Professor, Development Policy Centre, Australian National University, Australia Dr. A. Atiq Rahman, Executive Director, Bangladesh Centre for Advance Studies
	Panel Discussants:

	Mr. Md. Jahidul Kabir, Deputy Chief Conservator of Forests, Forest Department Dr. Md. Iqbal Kabir, Coordinator, Climate change & HPU, MOHFW Dr. Md Abul Kalam, Global Health Specialist, U.S. Agency for International Development (USAID)	
	Rapporteurs: Dr. Farzana Jahan, Assistant Scientist, icddr,b Dr. Md. Nizamuddin Chowdhury, SKWC, Forest Department	
16:00 – 16:30	TEA BREAK	
16:30 -18:15	**Open Paper Session – 1(a)** **Pandemic preparedness** Venue: Antara Hall	**Open Paper Session – 1(b)** **One Health institutionalization, Workforce, Policy** Venue: Lohori Hall
	Co-chairs Prof. Dr. Md. Nazmul Islam, Director (Disease Control) and Line Director, Communicable Disease Control (CDC), DGHS Miranda Beckman, Acting Office Director, Office of Population, Health and Nutrition USAID/Bangladesh	**Co-chairs** Prof. Dr. Abul Bashar Md Jamal, Additional Director General (Medical Education), Directorate General of Medical Education (DGME) Dr. Md. Reajul Huq Director (Admin), Department of Livestock Services (DLS)
	Rapporteurs: Dr. Shaikh Shahinur Islam Deputy Chief Epidemiologist, DLS Dr. Rabeya Sultana, Assistant Professor, IEDCR	**Rapporteurs:** Dr. MA Mannan, Assistant Professor, Sher-e-Bangla Agricultural University Dr. Kazi Munisul Islam, Senior Research Investigator, icddr,b
16:30 – 16:45	11095 : One Health Event Based Surveillance (EBS) Data Visualization Dashboard, in Bangladesh	11501 : Building the Workforce Capacity in Field Epidemiology in the Region: EMPHNET's Journey in Developing the One Health Curriculum
16:45 – 17:00	11309 : Mobile laboratory capacity as a powerful tool in Nipah surveillance, outbreak prevention and response	11310 : One Health Orientation of Veterinary Education through Specially Designed Pedagogy Practices
17:00 – 17:15	11308 : The challenge of mosquito-borne diseases in Bangladesh, preliminary results and future research directions	11206 : Putting community at the center of a One Health mapping exercise in Bangladesh to strengthen animal disease surveillance by building on existing networks
17:15 – 17:30	11058 : Molecular dynamics of SARS CoV-2 circulating in Bangladesh during 2020-2021	11085 : Adapting with the new normal: Exploration of community engagement of Bangladeshi students' amidst COVID-19 pandemic
17:30 – 17:45	11119 : SARS-CoV-2 detection and serological response in the Forcibly Displaced Rohingya Myanmar Nationals in Cox's Bazar	11502 : Bridging One Health research and policy to achieve health security goals

17:45 – 18:00	11117 : Public Health Emergency Preparedness and Response Plan for Infectious Hazards in Bangladesh	11211 : Awareness and Practice on Infectious Medical Waste Management among Healthcare Workers
18:00 – 18:15	11290 : Knowledge, Attitude, and Practice (KAP) towards of COVID-19 in Bangladesh: a systematic review and meta-analysis	
Close of Day 1 ***See you tomorrow at 09:00 AM***		

Day 2: 13 June 2023		
09:00 – 10:30	**PLENARY SESSION 3** **Antimicrobial Resistance and Food Safety** Venue: Ball Room (1st Floor), Radisson Blu Dhaka Water Garden	
	Chair: Prof. Dr. Shah Monir Hossain, Former Director General, Directorate General of Health Services (DGHS), Dhaka, Bangladesh	
	A short quadripartite video on AMR – Reproduced by USAID	
	Speakers: Dr. Antonio Valcarce, Senior Advisor (Antimicrobial Resistance), Agriculture and Consumer Protection Department, Food and Agriculture Organization of the United Nations (FAO) Dr. Mohan P. Joshi, Senior Principal Technical Advisor for the USAID Medicines, Technologies, and Pharmaceutical Services (MTaPS) Program Dr. Arshnee Moodley, CGIAR Antimicrobial Resistance Hub Lead, AMR Team Leader at International Livestock Research Institute	
	Panel Discussants: Prof. Dr. Md. Nazmul Islam, Director (Disease Control) and Line Director, Communicable Disease Control (CDC), DGHS Dr. Md. Abu Sufian, Director, Department of Livestock Services, Dhaka Dr Morseda Chowdhury, Director, Health, Nutrition and Population Program, BRAC	
	Rapporteurs: Dr. Mustufa Mahmud, CDC, DGHS Dr. Mohammad Abdus Samad, Senior Scientific Officer, Bangladesh Livestock Research Institute (BLRI)	
10:30 – 11:00	TEA BREAK	
11:00 -12:30	**Open Paper Session 2(a): AMR and its mitigation (1)** Venue: Antara Hall	**Open Paper Session 2(b): Food safety and food & nutrition security** Venue: Lohori Hall
	Co-chairs Prof. Dr. Ahmedul Kabir, Additional Director General (Planning and Development), DGHS	**Co-chairs** Dr. Mohammad Mushtuq Husain, Advisor, IEDCR

	Dr. Afsana Karim, Country Project Director, Medicines Technologies and Pharmaceuticals (MTaPs)	Dr. Nathu Ram Sarker, Former Director General, BLRI
	Rapporteurs: Dr. Fahmida Khanam, Associate Professor (Virology), NIPSOM Dr. Md Abu Sayem, Senior Technical Advisor, USAID, MTaPS	**Rapporteurs:** Dr. Zakir Hassan, SSO, Bangladesh Livestock Research Institute (BLRI) Dr. Anjuman Ara Begum, SSO, National Institute of Biotechnology
11:00 – 11:15	11214 : Three Years of Fleming Fund Country Grant to Bangladesh: a review of progress in AMR surveillance	11504 : Importance of Multi-Disciplinary Interventions in One Health for Food Safety and Safe Trade
11:15 – 11:30	11267 : Molecular characterization and detection of zoonotic linkages of Methicillin-Resistant Staphylococcus aureus (MRSA) recovered from dairy farms in Sylhet	11029 : *Bacillus spp.* contamination: a novel risk originated from animal feed to human food chains in south-eastern Bangladesh
11:30 – 11:45	11403R : Prevalence of multidrug resistant Salmonella, extended spectrum beta lactamase producing Escherichia coli and methicillin resistant Staphylococcus aureus in chicken meat, eggs, beef and milk	11099 : Heavy metal contamination and antibiotic residues in poultry feed and meat in Bangladesh: A growing one health concern
11:45 – 12:00	11082 : Prevalence of multidrug resistant Salmonella, extended spectrum beta lactamase producing Escherichia coli and methicillin resistant Staphylococcus aureus in chicken meat, eggs, beef and milk	11081 : Determination of Antibiotic Residues in Animal Derived Food Commodities in Bangladesh: A Cross Sectional Study
12:00 – 12:15	11034 : Exploring multidrug resistant Salmonella carrying extended-spectrum β-lactamase from retail chicken meat and live bird market sewage in Bangladesh	11289 : Foodborne pathogens recovered from ready-to-eat foods in some selected areas of Bangladesh
12:15 – 12:30	11454R : Detection and molecular characterization of antibiotic-resistant Escherichia coli in selected commercial layer farms in Mymensingh Division of Bangladesh	11260 : Molecular detection of methicillin, vancomycin, and enterotoxin producing Staphylococcus aureus isolated from table eggs and their antibiotic susceptibility profiles
12:30 – 13:00	**Poster Viewing Session** *All poster presenters are requested to attend the visitors*	
13:00 – 14:00	LUNCH AND PRAYER BREAK	
14:00 – 15:30	**PLENARY SESSION 4** **One Health Continual Education and Networking** Venue: Ball Room (1st Floor), Radisson Blu Dhaka Water Garden	
	Chair: Prof. Dr. Md. Titu Miah, Director General, Directorate General of Medical Education	
	Speakers:	

	Dr. Mohannad Al Nsour, Executive Director, Eastern Mediterranean Public Health Network (EMPHNET) Dr. Vipat Kuruchittham, Executive Director, Southeast Asian One Health University Network (SEAOHUN) Ms. Ava Sullivan, Project Manager and Research Scientist, EcoHealth Alliance	
	Panel Discussants: Prof. Dr. Md. Sharfuddin Ahmed, Vice Chancellor, Bangabandhu Sheikh Mujib Medical University (BSMMU), Dhaka, Bangladesh Prof. Dr. Nitish Chandra Debnath, Former Vice Chancellor, Chattogram Veterinary and Animal Sciences University (CVASU) Dr. Neely Kaydos-Daniels, Country Director, US CDC Bangladesh	
	Rapporteurs: Dr. Jobaida Khanam, Upazila Livestock Officer, DLS (Deputed to OHS, IEDCR) Dr. Sohel Rahman, Assistant Professor, IEDCR (Deputed to OHS, IEDCR)	
15:30 – 16:00	TEA BREAK	
16:00 -17:45	**Open Paper Session 3(a): AMR and its mitigation (2)** Venue: Antora Hall **Co-chairs** Prof. Dr. Zakir Hossain Habib, Chief Scientific Officer, IEDCR Prof. Dr. Ahsanul Hoque, Chattogram Veterinary and Animal Sciences University **Rapporteurs:** Dr. Mst. Sonia Parvin, Associate Professor, BAU Dr. Sazeda Akter, Assistant Professor, CVASU	**Open Paper Session 3(b): Wildlife, environment & ecosystem** Venue: Lohori Hall **Co-chairs** Mr. Imran Ahmed, Conservator of Forests, Forest Department Dr. Abu Nasar Md. Aminoor Rahman, Professor, BSMARU **Rapporteurs:** Dr. Farhana Rahman, Epidemiologist, SKWC, Forest Department Dr. Mehedi Hassan, EcoHealth Alliance
16:00 – 16:15	11265 : Risk factors for colonization with extended-spectrum cephalosporin resistant and carbapenem resistant Enterobacterales among healthy adults in the community and hospitalized patients, Bangladesh: An Antibiotic Resistance in Communities and Hospitals study	11505 : Two decades of dengue outbreaks in Bangladesh (2000-2022): Climate change, environmental niche, and future planning
16:15 – 16:30	11266 : Isolation of multidrug resistant bacteria from pet birds sold at different retailer shops	11311 : *Mycobacterium orygis* associated tuberculosis in Bangladesh
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16:45 – 17:00	11503 : Containing antimicrobial resistance through multisectoral coordination in Bangladesh	11233 : Environmental surveillance for SARS-CoV-2 and enteric pathogens in humanitarian settings and municipality, Cox's Bazar
17:00 – 17:15	11282 : Driving Force of Indiscriminate Usage of Antibiotics in Small Scale Commercial Poultry Farms in Bangladesh	11234 : Environmental surveillance for SARS-CoV-2 and enteric pathogen in Megacity, Dhaka
17:15 –17:30	11295 : Effect of ABCB1, ABCC4, and GSTP1 gene polymorphisms on the response and toxicities of antiretroviral therapy in Bangladeshi AIDS patients	11112 : Diversity and Characterization of Coronaviruses in Rodents and Shrews, Bangladesh
17:30 – 17:45		11113 : Epidemiology and genetic diversity of coronaviruses in Bats, Bangladesh
Close of Day 2 **See you tomorrow at 9.00 AM**		
Day 3: 14 June 2023		
09:00 -10:30	**Open Paper Session 4(a): EID, Vaccine, & NCD (Human Health)** Venue: Antora Hall **Co-chairs:** Prof. Dr. M.A. Faiz, Former Director General, Directorate General of Health Services (DGHS), Dhaka, Bangladesh Prof. Dr. Mohammad Robed Amin. Line Director. Non-Communicable Disease Control (NCDC), DGHS **Rapporteurs:** Dr. Umme Ruman Siddique, Assistant Director, DGHS Dr. Md. Omar Qayum, Curator, IEDCR	**Open Paper Session 4(b); EID and Vaccine (Animal Health)** Venue: Antora Hall **Co-chairs** Prof. Dr. Emdadul Haque Chowdhury, Department of Pathology, Bangladesh Agricultural University (BAU), Mymensingh Dr. Amalendu Ghosh, Director, Livestock Research Institute, Department of Livestock Service (DLS) **Rapporteurs:** Dr. Shukes Chandra Badhy, Upazila Livestock Officer, CDIL Dr. Ireen Sultana Shanta, Assistant Scientist, icddr,b
09:00 – 09:15	1101 : Study Design and Operation for Evaluating Nipah Virus Vaccine Candidates Among Backyard Pigs of Indigenous Communities in Bangladesh	11013 : Diversity of Myxovirus resistance gene (Mx) and its relation with avian influenza infection in indigenous chicken
09:15 – 09:30	11109 : Understanding the zoonotic diseases risk spillover risk through wildlife hunting in Bangladesh	11007 : Occurrence, genetic diversity and zoonotic potential of *Enterocytozoon bieneusi* in children and calves in Bangladesh
09:30 – 09:45	11111 : Genetic Characterization of Dengue virus subtype diversity in Bangladesh.	11091 : Zoonotic Pathogens in Poultry Production in Bangladesh
09:45 – 10:00	11108 : Genetic diversity of Coronaviruses in humans in the pre-pandemic period at the high-risk human-animal interface in Bangladesh.	11017 : MPB83, ArfA, DnaK, GrpE, and LpqH protein to design a subunit vaccine against Bovine Tuberculosis

10:00 – 10:15	11284 : Patterns of date palm sap harvesting and trading practices and risk of Nipah virus spillover from bats to humans in Bangladesh	11100 : An integrated approach to develop an anthrax-free model area in Bangladesh
10:15 – 10:30	11063 : Chemokine Receptor-5 (CCR-5): A new hope in the immunoregulation of human-Rhinovirus exacerbated neutrophilic asthma pathogenesis	11450R : Assessment of humoral immune response in cattle immunized with an inactivated alum adjuvant Brucella abortus biovar three vaccine
10:30 – 11:00	TEA BREAK	
11: 00 – 12:30	Annual General Meeting, One Health Bangladesh (All the general members and life members are requested to join the session)	
12:30 – 13:00	**Poster Viewing Session** *All poster presenters are requested to attend the visitors and jury board during the session.*	
13:00 – 14:00	LUNCH AND PRAYER BREAK	
14:00 – 15:30	**PLENARY SESSION 5** **One Health Institutionalization** Venue: Ball Room (1st Floor), Radisson Blu Dhaka Water Garden	
	Moderator: Prof. Dr. Meerjady Sabrina Flora, Director, National Institute of Preventive and Social Medicine (NIPSOM)	
	Remarks from the Policy Makers: Dr. Md. Anwar Hossain Howlader, Secretary (Health Services Division), Ministry of Health and Family Welfare, Government of the People's Republic of Bangladesh Dr. Nahid Rashid, Secretary, Ministry of Fisheries and Livestock, Government of the People's Republic of Bangladesh Dr. Farhina Ahmed, Secretary Ministry of Environment, Forest and Climate Change, Government of the People's Republic of Bangladesh Ms. Wahida Akter, Secretary Ministry of Agriculture, Government of the People's Republic of Bangladesh	
	Rapporteurs: Dr Quazi Ahmed Zaki, Technical Advisor, (FETP,B Intermediate), Eastern Mediterranean Public Health Network Dr. Faisol Talukder, Upazila Livestock officer, Epidemiology Unit, Department of Livestock Services	
15:30 – 16:00	TEA BREAK	
16:00 -17:00	**Closing Session of the Conference**	

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ABSTRACTS

Plenary Lectures

Plenary Session 1: Pandemic Preparedness

The session will be chaired by Prof. Dr. Mahmudur Rahman, EMPHNET Country Representative and former Director of IEDCR. Dr. Anthony Eshofonie, Epidemiologist, WHO, Bangladesh will conduct an interactive session on Slido. Dr. Gina Samaan. Head, Pandemic Disease Preparedness, WHO will present the keynote lecture. Dr. Mahbubur Rahman of IEDCR will share the Bangladesh Pandemic Response Plan. This will be followed by discussion by a panel of experts representing different stakeholders including Dr. M. Salim Uzzaman (One Health Dashboard), Professor Meerjady Sabrina Flora (human health), Dr. Md. Giasuddin (animal health), Dr. Tahmeed Ahmed (Clinical nutrition), Prof. Md. Rafiqul Islam (academia).

Keynote Lecture 1

Preparedness and Resilience for Emerging Threats (PRET): An innovative approach to improving disease pandemic preparedness

Gina Samaan

Speaker's biography: *Dr. Gina Samaan is an infectious disease epidemiologist with a career focus on pandemic risk management. At the World Health Organization (WHO), she leads a global initiative to strengthen preparedness and resilience for future infectious disease threats. She also coordinates the Global Genomic Surveillance Strategy for Pathogens with Pandemic and Epidemic Potential. These portfolios encourage investment to strengthen country capacities for emerging threats. Her research interests include the management of acute respiratory infections and mass gatherings.*

Abstract:

To better prepare for the next pandemic, or even better, to prevent it, WHO recently launched “The Preparedness and Resilience for Emerging Threats initiative, or PRET for short”. PRET is to help countries ensure they have the systems and capacities in place to speed up every aspect of their management of emerging threats, from response and recovery.

PRET focuses on improving pandemic preparedness for groups of pathogens based on their mode of transmission. It recognizes that there are three tiers of systems and capacities relevant for pandemic preparedness: those that are cross-cutting for all or multi-hazards, those that are relevant for groups of pathogens (respiratory, arboviruses etc.), and those that are specific to a pathogen.

The aim is to strengthen existing systems and capacities, and to fill gaps. This approach avoids siloes, promotes coherence and efficiency, and helps streamline actions at the time of a pandemic. A One Health lens is applied in PRET recognizing that most new pathogens originate first in animals, and that preventing, preparing, and responding to emerging threats requires multi-sector action. The technical actions in PRET are mapped to the IHR core capacities and grouped under 5 subsystems namely, Collaborative Surveillance, Access to Countermeasures, Community Protection, Safe and Scalable Clinical care, and Emergency Coordination.

Based on these new guidance and experiences from recent public health events especially the COVID-19 pandemic, Bangladesh started to revise its Influenza preparedness and response plans to a Pan Respiratory plan incorporating other priority respiratory pathogen while recognizing the specificity of individual hazards.

PRET is synergistic with National Action Plan for Health Security and together should be reflected in national, regional, and global investments to strengthen preparedness.

Plenary Session 2: Biodiversity, Environment and Health

This session will be chaired by Mr. Md. Amir Hosain Chowdhury, Chief Conservator of Forest, Bangladesh. Three keynote lectures will be presented in this session by Dr. Jonathan Epstein, Vice President, EcoHealth Alliance, Prof Robyn Alders, Honorary Professor, Australian National University, and Dr Atiq Rahman, Executive Director, Bangladesh Centre for Advanced Studies. The presentations will be followed by panel discussion by Mr. Jahidul Kabir of Forest Department, Dr. Iqbal Kabir from Health Department and Dr. Md Abul Kalam from USAID.

Keynote Lectures 2.1

Using public-private partnerships and scientific research to support national One Health and pandemic prevention strategies

Jonathan Epstein

Speaker's Biography: *Dr. Jonathan Epstein is a veterinarian and epidemiologist, and currently the Vice President for Science and Outreach at EcoHealth Alliance. He has also served for WHO, OIE and FAO. He holds adjunct faculty appointments at Tufts University, Columbia University, and Mt. Sinai School of Medicine. His research focuses on the ecology of zoonotic viruses that impact animals and people, particularly those associated with bats, such as Nipah virus, Ebola, and emerging coronaviruses (SARS, MERS, and SARS-CoV-2 / COVID-19).*

For more information, visit https://www.ecohealthalliance.org/personnel/dr-jonathan-epstein

Abstract:

The COVID-19 pandemic has demonstrated the ability of zoonotic viruses to severely impact health and disrupt livelihoods and economies on a global scale. The international response to the COVID-19 emergency has primarily included investments that strengthen disease surveillance, pathogen detection, and the development of vaccines and therapeutics. However, despite substantial evidence that the majority of zoonotic pathogens originate in wildlife populations, there continues to be insufficient commitment to, or investment in, preventing pandemics at the source (e.g. preventing spillover of zoonotic pathogens from wildlife reservoirs into livestock and people). Few national health systems adequately integrate the wildlife sector into disease surveillance strategies. Environmental ministries, which may contain expertise in climate science, wildlife biology, conservation science or ecology, typically do not have a public health mandate and are frequently left out of public health strategies and activities. Fortunately, this is beginning to change as more countries (e.g., Bangladesh) adopt formalized One Health strategies to address zoonoses and antimicrobial resistance. Scientific research programs, especially those conducted in partnership with government agencies, can substantially bolster federal programs by providing additional funding and technical expertise not readily available within the country, as well as by providing data and analyses not typically obtained through routine surveillance and outbreak response programs. Research programs may also provide opportunities for infrastructure strengthening and workforce training. These aspects of collaborative research can sustainably enhance One Health systems within a country and inform national and international health and environmental policy. Here we'll discuss examples of public-private One Health research collaborations among NGOs, universities, commercial entities and government agencies that have strengthened government efforts to prevent zoonotic disease outbreaks in Liberia and Bangladesh.

Keynote Lecture 2.2

The environment underpins One Health

Robyn Alders

Speaker's Biography: *Robyn Alders AO is an Honorary Professor with the Development Policy Centre and the Institute for Climate, Energy and Disaster Solutions within the Australian National University, a Senior Consulting Fellow with the Chatham House Global Health Program, an Honorary Professor with the Department of Pathobiology and Population Sciences at the Royal Veterinary College within the University of London and an Adjunct Professor in the Veterinary Department of Infectious Disease and Global Health, Tufts University. For over 30 years, she has worked closely with smallholder farmers and producers in sub-Saharan Africa, South and SE Asia and Oceania. Robyn's current research and development interests include food and nutrition security, One Health, gender equity and Science Communication. Robyn has published over 190 publications.*

Abstract

The One Health approach recognizes that the health of humans, domestic and wild animals, plants, and ecosystems are intimately linked and inter-dependent. This holistic view of One Health aligns closely with the views of many indigenous communities whose traditional knowledge recognizes that the health of people is inseparable from the health of their environment.

The benefits of a healthy environment are immeasurable. Amongst others, ecosystems provide us with breathable air, drinkable water, productive soils and a stable climate. Ecosystems also provide us with nutritious food and medicines, both traditional and new. Healthy ecosystems provide a defense against emerging zoonotic diseases. For humans, it has been demonstrated that time spent in nature improves health outcomes, by reducing stress and hyperactivity.

Disregard for environmental health by humans over the past two hundred years is having enormous consequences for humans, animals and plants. We have changed and often degraded environments, ecosystems and human cultures in unprecedented ways. Globalized, extractive economic systems have contributed to breaking linkages between people and their environments, uneven resource consumption and changing population dynamics, including significant declines in biodiversity. Human health systems and agricultural and aquaculture practices are contributing to significant increases in environmental pollution by chemicals such as antibiotics, poisons and toxins.

Safeguarding human, animal, plant and environmental health into the 21st century necessitates the adoption of a One Health approach to: understand the environmental systems that support our health and the health of our planet; transparently monitor key indicators of environmental health; and reverse and/or mitigate negative environmental impacts associated with human activities. Integrating the One Health approach into circular bioeconomy initiatives will be key to developing and implementing the practices required to deliver a healthy world for all.

Keynote Lecture 2.3

Climate change Impacts on biodiversity and human health: health risk Management and adaptation in Bangladesh

A. Atiq Rahman

Speaker's Biography: *Dr. A. Atiq Rahman is the Executive Director of Bangladesh Centre for Advanced Studies (BCAS). He was a Lead Author of Intergovernmental Panel on Climate Change (IPCC) Fourth Assessment Report (AR4), which received Nobel Peace Prize. Dr. Rahman is a Visiting Professor of International Diplomacy and Sustainable Development at Fletcher School of Law and Diplomacy, Tufts University, Boston, USA. He is the Chairman of Climate Action Network - South Asia (CANSA). He is also the Chairperson of Coalition of Environmental NGOs in Bangladesh. For his outstanding and inspirational leadership in the field of environment, the United Nations Environment Program (UNEP) has honored Dr A. Atiq Rahman with Champion of the Earth-2008, the highest UN award on environment. During the year 2008, he has also received the Environment Award 2008 from Department of Environment, Government of Bangladesh for environment research and technological innovation. He has published over 120 papers and authored or edited fifteen books.*

Abstract:

Global climate change is affecting ecosystems, biodiversity, environment and human health very severely. The impacts of climate change on human health causing ailment, injuries and deaths are growing across the world. Bangladesh is in the forefront of climate change impacts with huge health risks, rising medical costs and vulnerability of the poor, women, children, elderly people and PwD. The loss of biodiversity can have significant direct human health impacts if ecosystem services are no longer adequate to meet societal needs. The degradation of ecosystems and loss of biodiversity are caused by many socio-economic and environmental factors including: pollution of air, soil and water, destruction of habitats, invasive species, over exploration of natural resources and climate change impacts on natural resources, wildlife and bio-diversity, The rapid changes in ecosystem services (ESS) due to climate change (salinity, drought, change in seasonal patterns and extreme events) affect livelihoods, income, food security, nutrition and human health very badly. The presentation will highlight on: (1) How climate change poses significant challenges to both human health and biodiversity, (2) The inter-relationships among climate change, biodiversity and human physical and mental of health and well-being, (3) How conservation environment, green spaces, biodiversity and ecosystem services can improve human health and well-being, and (4) Adaptation responses of the government of Bangladesh under the Health Climate Adaptation Initiative and the challenge ahead.

The GoB has prepared a Bangladesh Health-National Adaptation Plan, which is a comprehensive document designed to guide the country toward building resilience to climate change impacts on health by empowering communities and individuals through an adaptive and sustainable health system in Bangladesh.

Plenary Session 3: Antimicrobial Resistance and Food Safety

This session will be chaired by Prof. Shah Monir Hossain, former Director General, Health Services. Three distinguished speakers, Dr. Antonio Valcarce, AMR Senior Advisor to FAO, Dr. Mohan P. Joshi, Senior Principal Technical Advisor, USAID MTaPS programme, and Dr. Arshnee Moodley, CGIAR AMR Hub Lead and AMR Team Leader at ILRI will make keynote presentation. A panel of experts including Prof. Md. Nazmul Islam (human health), Dr. Abu Sufian (animal health) and Dr. Morseda Chowdhury (nutrition) will take part in discussion.

Keynote Lecture 3.1

AMR and the food chain: FAO's approach to AMR

Antonio Valcarce

Speaker's Biography: *Antonio Valcarce is the AMR Senior Advisor to FAO. He has worked for DEFRA, UK and held several different roles covering notifiable disease control, welfare, enforcement, animal by-products, and management. He became the Head of the DEFRA's EU and International relations unit to provide support to the UK's CVO. Antonio was then seconded to FAO as AMR Senior Advisor and provides high-level strategic AMR advice, leads the implementation of FAO's Fleming Fund AMR project and contributes to the Quadripartite work and Multipartners Trust Fund Projects (MPTF).*

Outline:

The whole food chain has an important role to play on AMR within the animal production sector, both directly and indirectly. FAO's approach to its work has this principle embedded and translates in all its work, including its cooperation under the One Health spectrum.

Keynote Lecture 3.2

USAID Medicines Technologies, and Pharmaceutical Services (MTaPS) Program's efforts in strengthening national antimicrobial resistance (AMR) containment

Mohan Joshi

Speaker's Biography: *Dr. Mohan Joshi currently serves as Management Sciences for Health (MSH)'s Senior Principal Technical Advisor for the USAID Medicines, Technologies, and Pharmaceutical Services (MTaPS) Program, providing technical oversight for the Global Health Security Agenda (GHSA)-supported AMR work and other pharmaceutical services-related activities. He has 20 years of experience of supporting 21 LMICs in the technical implementation of antimicrobial resistance (AMR) containment, rational medicine use, and other pharmaceutical systems strengthening activities. Before joining MSH, Dr. Joshi worked for nearly 20 years at the Tribhuvan University Institute of Medicine and Teaching Hospital in Nepal*.

Abstract

The presentation will describe a landscape analysis of the USAID Medicines Technologies, and Pharmaceutical Services (MTaPS) Program's efforts, led by Management Sciences for Health (MSH), in strengthening national antimicrobial resistance (AMR) containment capacity in 13 collaborating countries. This Global Health Security Agenda-supported work was mainly guided by two WHO tools—Joint External Evaluation (JEE) and Benchmarks for IHR Capacities—and aimed at incrementally augmenting the collaborating countries' JEE capacity levels. The presentation will briefly explain the approaches used, the results achieved, the promising practices gleaned, select challenges faced, and the lessons learned from this multi-year, multi-country collaboration experience.

Keynote Lecture 3.3

Integrating One Health principles into food systems

Arshnee Moodley

Speaker's Biography: *Arshnee Moodley is the CGIAR Antimicrobial Resistance Hub Lead and AMR Team Leader at ILRI. She is also an Associate Professor at the University of Copenhagen in the Veterinary and Animal Sciences Department. Since joining ILRI, Arshnee has focused on addressing agricultural-related AMR risks in low and middle-income countries through a One Health approach. Arshnee is a part of the CGIAR Research Initiative on One Health, which aims to integrate One Health principles into food systems to reduce zoonotic disease outbreaks, enhance food and water safety, and combat antimicrobial resistance. She contributes to the establishment of an internationally recognized Centre of Excellence for Antimicrobial Susceptibility Testing (AST) at ILRI. Arshnee is also engaged in OHRECA, a center focused on capacity building, network strengthening, and evidence-based policy advice on One Health in sub-Saharan Africa.*

Plenary Session 4: One Health Continuing Education and networking

This session will be chaired by Prof. Dr. Titu Mia, Director General, Medical Education and will include three keynote lectures to be presented by Dr. Vipat Kuruchittham, Executive Director of Southeast Asia One Health University Network (SEAOHUN), Dr. Mohannad Al-Nsour, Executive Director, Eastern Mediterranean Public Health Network (EMPHNET), and Ms. Ava Sulivan of EcoHealth Alliance. A panel of distinguished experts, Prof. Md. Sharfuddin Ahmed, the Vice Chancellor of Bangabandhu Sheikh Mujib Medical University (BSMMU), Prof. Dr. Nitish C. Debnath, former Vice Chancellor, Chattogram Veterinary and Animal Sciences University (CVASU), and Dr. Neely Kaydos-Daniels, Country Director, US CDC Bangladesh, will contribute as panel discussants.

Keynote Lecture 4.1

Strengthening health security: catalyzing One Health citizens through education

Vipat Kuruchittham

Speaker's Biography: *Dr. Vipat Kuruchittham is the Executive Director of Southeast Asia One Health University Network (SEAOHUN). He has been managing health and education programs across Southeast and South Asia for the last 15 years, working with international organizations, U.S. government agencies, ministries of health and agriculture, and international and regional NGOs. For much of this time, Vipat has led the regional drive to embed One Health knowledge and skills into the next generation of One Health professionals as the Executive Director of Southeast Asia One Health University Network (SEAOHUN). SEAOHUN is a regional network of over 102 universities in 8 Southeast Asian countries, working to develop a resilient and competent One Health workforce by leveraging education, research, and training excellence.*

Abstract

One Health (OH) workforce is fundamental to building health systems resilience. To enhance health security and minimize the impact of health threats, the Southeast Asia One Health University Network (SEAOHUN) was established in 2011 with support from U.S. Agency for International Development (USAID). We are the largest network of university-based experts in animal, human, and environmental health throughout Southeast Asia with 102 universities in eight countries (Cambodia, Indonesia, Laos, Malaysia, Myanmar, Philippines, Thailand, and Vietnam) collaborating to institutionalize OH curriculum into university offerings to build the next generation of OH professionals with the right skillset and mindset to prevent, detect and respond to increasing infectious disease threats. SEAOHUN and its country networks develop One Health competencies, introduce innovative teaching methodologies, and build research capacity providing an evidence-base for One Health policy-making and advocacy.

SEAOHUN represents academic voices often lacking at national, regional, and international forums. We are a member of Global Health Security Agenda (GHSA), an affiliate member of Southeast Asian Ministers of Education Organization (SEAMEO), and a dialogue partner of Association of Southeast Asian Nations (ASEAN) Plus Three 3 Field Epidemiology Training Network (FETN). In addition, we partner with Chevron to promote One Health education for all in Southeast Asia, and collaborate with Zoetis and Pfizer to address the silent threat of antimicrobial resistance.

SEAOHUN strongly believes in the power of networking. Our success factors form a decade journey in fostering an extensive multi-country and multi-disciplinary networks include building trust and partnership, finding OH champions, having committed OH partners, strengthening governance and operating structure, increasing visibility to advocate OH education for all, and diversifying our funding portfolio for organizational sustainability. Our model can be adapted and replicated to build networks in other regions for the development of a sustainable and competent health workforce of the future.

Keynote Lecture 4.2

One Health continual education and networking

Mohannad Al Nsour

Dr. Mohannad Al-Nsour is the Executive Director of the Eastern Mediterranean Public Health Network (EMPHNET). He has been providing strategic assistance and operational solutions, and guiding the enrichment of Field Epidemiology Training Programs (FETPs) and public health initiatives in the region. Dr. Al-Nsour serves on several regional and global initiatives, association and networks as he is a member of the Steering Committee for the Global Outbreak Alert and Response Network (GOARN), Training Programs in Epidemiology and Public Health Interventions Network (TEPHINET), International Epidemiological Association, and more. He is currently leading the establishment of the Public Health Forum and the NCD Alliance in Jordan. He also served as a consultant on several assignments with the US Centers for Disease Control and Prevention, the World Health Organization and the American University of Beirut.

Abstract:

Evolving conditions at the human-animal-environment interface, such as climate change and deforestation, are accelerating the emergence of zoonotic diseases. The One Health approach recognizes that the health of humans, animals, and the environment is interconnected.

EMPHNET is a regional public health network that works to strengthen disease surveillance and response in the countries. It is working to operationalize the One Health approach by developing training programs, conducting research, and promoting collaboration among different sectors.

In 2022/2023, EMPHNET developed Nine-month and Three-month One Health curricula. An elite of 10 experts from the region and beyond contributed to this effort. Our next steps are to Pilot these training programs and develop specialized modules, case studies, and operational research.

In Bangladesh, EMPHNET has established a Field Epidemiology Training Program for Veterinarians (FETPV), an Intermediate FETP, and an Advanced FETP. EMPHNET has also supported the Hospital Epidemiology Training program and conducted several webinars on One Health.

EMPHNET believes that the following factors are essential for the success of One Health training and education programs: (a) Ownership by the country, (b) Adoption of competency-based training with a focus on field practice, (c) Linking training to research and service provision, (d) Well-defined career paths, (e) Continuing professional development (CPD) for graduates and One Health workforce, (f) Networking among One Health partners and sectors, (g) Collaboration and smart partnerships, (h) Joint training programs with residents from different sectors can help to build a more coordinated and effective response to emerging infectious diseases, (i) One Health training programs can benefit from the experience and model of FETP.

In conclusion, EMPHNET believes investing in FETP and One Health training programs effectively improves a country's surveillance and response capacity.

Keynote Lecture 4.3

One Health curriculum development and building a One Health course

Ava Sullivan

Speaker's Biography: *Ava Sullivan is a Research Scientist and Project Coordinator based at EcoHealth Alliance, NY, USA, and a PhD candidate at Institute of Risk and Disaster Reduction, University College London. Ava has her master's degree in environmental health with a specialization in disaster management from Tulane University School of Public Health and Tropical Medicine. Ava has been a part of multiple global One Health efforts, including USAID's the viral discovery project PREDICT-2, and the capacity building project One Health Workforce-Next Generation. Ava's research interests include the complex pathways driving viral spillover, and in particular, exposure to animal hosts driven by human behavior.*

Abstract:

Given the multifaceted nature of the One Health approach, which necessitates the collaboration of stakeholders across diverse sectors, academic disciplines, and professional domains, the field of One Health education and pedagogy similarly adopts a cross-disciplinary framework. The inclusion of various areas of expertise and stakeholders is recognized both as a strength and a challenge in the implementation of the One Health approach. On one hand, this inclusivity enhances our comprehension of complex health challenges such as pathogen spillovers and pandemics. Conversely, it presents difficulties in achieving a consensus regarding the fundamental tenets of One Health and the specific knowledge, skills, and perspectives that professionals need to adopt when embracing this approach.

There exist numerous examples of One Health educational resources and assets, which encompass a wide range of scopes, scales, levels, and modes. Diligent efforts have been made to develop competency-based training in One Health, covering a comprehensive array of subjects within the fundamental, technical, functional, and integrative domains. In order to ensure the recognition of the distinctive qualities possessed by individuals trained in One Health, it becomes imperative to showcase their utility, establish mechanisms for accreditation, and provide avenues for continuous professional development.

In response to these exigencies, the concept of a One Health Workforce Academy (OHWA) was proposed as a platform dedicated to delivering competency-based training, comprehensive assessment, and the attainment of an accreditable credential in One Health, particularly targeted towards in-service professionals. Within the OHWA, the development of a Fundamentals of One Health Course was undertaken by One Health practitioners from around the globe, with the objective of codifying an emerging consensus that One Health education necessitates a combination of breadth and depth of expertise within a diverse core group of subjects. Particular attention is given to functional competencies such as effective communication, collaboration and systems thinking.

Plenary Session 5: One Health Institutionalization

This session will be moderated by Prof. Dr. Meerjady Sabrina Flora, Director, National Institute of Preventive and Social Medicine. Top policy maker, the secretaries of the relevant ministries will take part as panel discussants.

Keynote Lecture 5

One Health institutionalization from concept to practice

Meerjady Sabrina Flora

Speaker Biography: *Professor Dr Meerjady Sabrina Flora is the Director of the National Institute of Preventive and Social Medicine (NIPSOM). Before joining NIPSOM in February 2023, she was the Additional Director General of Health Services (Planning and Development), Bangladesh. As the ADG, she led the COVID-19 surveillance and containment activities and chaired the vaccine deployment core committee. Before joining as ADG in August 2020, she was the Director of Institute of Epidemiology, Disease Control and Research (IEDCR) under MoHFW. Prof Flora was the Program Director (PD) of different collaborative projects between IEDCR and US CDC, including Field Epidemiology Training Program in Bangladesh (FETP'B). She was the focal point for Global Health Security Agenda (GHSA) in Bangladesh and acted as the Chair of the Coordination Committee for Bangladesh One Health Secretariat. She is the joint coordinator (public health) of One Health Bangladesh and is the current Vice President of International Association of National Public Health Institutes (IANPHIs). She is the current President of Epidemiological Association of Bangladesh (EPAB).*

Abstract:

Since the inception of a community movement called "One Health Bangladesh" in 2008, Bangladesh's stride to institutionalize One Health began in 2012 with the formulation of National One Health Strategy and Action Plan in 2012. The decision to establish One Health Secretariat with a multi ministry oversight mechanism was the first but a solid step of One health institutionalization in Bangladesh for establishing a governance mechanism. However, internalizing One Health within the government systems requires strong political will, strategic planning, and necessary reform. The Bangladesh government clearly understands that One Health is the most efficient solution to health problems that requires joint interventions from multiple ministries. Multi Ministry framework, shared financing system, adequate workforce are foundational to one health institutionalization. Country is successful in establishing important governing structure including an Inter-Ministerial Steering Committee, Technical Advisory Committee and One Health Secretariat. But further agreement and arrangements are required on combined One Health actions such as collaborative planning, joint surveillance and combined outbreak investigation and response, and data sharing. One Health Secretariat received modest funding from the 4th sector plan of Ministry of Health and Family Welfare (MOHFW), however, a mechanism for financial contribution from other ministries is yet to be established. Ministries also need to streamline One Health capacity by increasing line ministries budget for workforce development, joint surveillance, outbreak investigation and response, risk communication and community engagement. Adequate flexibility and delegation of authority to appropriate levels also warrants attention of high-level policy makers to bring desired changes. Workforce development is at the core of One Health institutionalization. Strategy for public health workforce with One Health understanding is lacking for MOHFW, Ministry of Fisheries and Livestock (MOFL) and Ministry of Environment, Forests, Climate Change (MOEFCC). Public health workforce strategies is required for proper career planning and in-service training to improve the competencies for enabling them to quickly address any One Health issue. A critical mass of public health experts having a solid knowledge of disease epidemiology is essential for today's and future One Health solutions. MOHFW and MOFL have their field epidemiology training program but still largely depend on external funding. For sustainability, ministries need to invest adequately in these areas and need to absorb these courses within the government health education system. MOEFCC has recently been working on designing a plan for field

epidemiology training. However, Field epidemiology training is only a small part public health workforce development. Workforce for laboratory, response, certification is also equally important. Again, proper career planning is important for utilization of the limited workforce. All the ministries should work together for the development and execution of a comprehensive One Health institutionalization plan.

ABSTRACTS

Open Papers (Oral Presentation)

Open Paper Session 1(a)
Pandemic Preparedness, Containment and Mitigation

Abstract number: 11095

One Health Event Based Surveillance (EBS) Data Visualization Dashboard, in Bangladesh

M Salim Uzzaman[1]*, ASM Alamgir[1], Nawsher Alam[1], Zakir Hossain Habib[1], Mahbubur Rahman[1], Farhana Rahman[1], TABM Muzaffar Goni Osmani[2], Tahmina Shirin[1]

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We live in the interconnected world (Global Village) with increasing risk of emerging and remerging infections. Management of emerging infections is a real challenge now a day. The evidence reported in various studies indicate that epidemic disease impacts on a country's economy through several channels, including public health, transportation, livestock, agriculture, tourism sectors and many more. Finding outbreaks and public health events faster and managing them empirically can contribute to reduce illness, death and economic loss from endemic – epidemic-pandemic. One Health recognizes that the health of humans, animals and the environment are interconnected. Climate change and other environmental factors exacerbate disease emergence and spread. Significant delays in outbreak prevention, detection and responses lead to needless morbidity, mortality and economic loss. Important delays includes (1) Weakness of disease reporting systems and inter-sectoral (& relevant sectors) sharing, (2) Lack of Digital monitoring tools to capture local Event Based Surveillance (EBS) data feeds and visualization of “multi sectoral data feeds”, (3) Lack of digital platform *integrating One Health approach* for data sharing, and (4) Lack of sharing collaboration through integrated information systems for early warning, surveillance, detection of potential outbreaks & timely response.

To mitigate the identified difficulties, One Health Secretariat (OHS) a Government agency, at IEDCR aim is to develop ‘One Health event base surveillance (EBS) enhancement and Data visualization system’, which will be an electronic, relevant, real-time event base surveillance (EBS). It is planned to use digital monitoring tools to capture “multi sectoral data feeds.” This ‘One health inter-sectoral policy’ will provide an early signal of potential out breaks and public/animal health events, an early warning sign of potential human and animal disease. One of the main objectives of this project is to “Strengthen the operational capacity of organizations, OHS to prepare, rapidly scale up, augment systems, bridge across local, national, regional, and global areas in order to more efficiently launch an integrated multi-sectoral humanitarian response to future infectious disease outbreaks and pandemics.”

Keywords: One Health, Surveillance, Dashboard, Data

Abstract number: 11309

Mobile laboratory capacity as a powerful tool in Nipah surveillance, outbreak prevention and response

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Background and Objectives: Nipah virus (NiV) is a zoonotic virus transmitted by bats, which has caused fatal encephalitis in approximately 70% of cases during nearly annual outbreaks in Bangladesh. It is recognized as a priority pathogen by the WHO and requires the urgent development of outbreak prevention and mitigation tools. There is currently no specific treatment of vaccine against the virus. Preparedness efforts are largely hampered by the lack of genetic data and real-time surveillance data. Novel molecular biology techniques can effectively provide these data with short turn around time and mobile technical background. We developed a field setup with real-time RT-PCR screening and virus genome sequencing capabilities and demonstrated its application in 2022-2023.

Method: During two field investigations between 2021 December and 2022 January and in 2023 February, in 34 days we screened 1142 pooled bat urine and feces samples for NiV RNA. Sequencing and PCR testing were performed on-site. For sequence data generation we used Oxford Nanopore technology, with an amplicon-based sequencing method, developed by our laboratory.

Results: We identified the presence of Nipah virus in 2022 January at Rajshahi city and generated sequence data on the spot within 6 hours. We diagnosed more than 1000 samples in a cumulative 34 days, demonstrating the high-throughput nature of this method. Based on the phylogenetic analysis the identified sequence grouped together with previous sequences from Bangladesh, indicating the identification of an enzootic strain from these bats.

Conclusion: As we demonstrated in the present study, active surveillance efforts with non-invasive methods can help outbreak prevention by identifying bat colonies with high virus prevalence. Also this method can provide real-time sequence data to track and better understand NiV evolution in nature. This method can also balance the uneven diagnostic and response capacity in Bangladesh by strengthening areas outside the capital.

Keywords: Pandemic preparedness, One Health, Prevention

Abstract number: 11308

The challenge of mosquito-borne diseases in Bangladesh, preliminary results and future research directions

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Background and Objectives: Mosquito-borne diseases pose significant public health challenges and require targeted interventions to reduce their impact on both veterinary and human health. Establishing a comprehensive and long-term response plan based on scientific data is crucial due to the potential devastating impact of these diseases on the country's economy and food security.

Our goal is to develop a comprehensive research plan that effectively supports the national response to mosquito-borne diseases in Bangladesh. This plan involves investigating the ecology, genetics, behavior, and vector capacity of mosquitoes.

Method: During the mosquito season in 2022 we conducted the collection of adult human host seeking mosquitoes. In addition to this we collected *Aedes aegypti* specimens outside the main season within buildings to sample the seeding population before the season. We identified these mosquitoes to species level by morphologic identification keys and used them for various genetic and disease screening efforts. Screening and genetic data generation was conducted with PCR and Sanger sequencing. Along with our research efforts we established a long-term plan for knowledge capacity building under the framework of VECTORACT EU-funded project.

Results: We analysed a comprehensive species set of mosquitoes from Chittagong and provided the first results about human host-seeking mosquito species composition and *Dirofilaria* parasite positivity. We also provided the first genetic and morphologic validation of urban-related *Aedes aegypti* infestation. These results are serving our long-term plan to build a sustainable and efficient research and knowledge basis in the country to face the growing problem of mosquito-borne diseases.

Conclusion: Our presentation aims to raise awareness about the topic and highlights how our research strategy and preliminary results could be the building blocks of an effective solution against mosquito-borne diseases in Bangladesh.

Keywords: One Health, mosquito-borne diseases, Dengue, integrated management

Abstract number: 11058

Molecular dynamics of SARS CoV-2 circulating in Bangladesh during 2020-2021

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Introduction: Genomic variations of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) have repeatedly altered the course of the ongoing pandemic. Currently, a number of variants are circulating worldwide. Bangladesh is the second-worst-affected country in South Asia by SARS CoV-2. The aim of this study is to examine genome sequences from Bangladesh in order to monitor the SARS-CoV-2 variants and the clades or lineages that are prevalent in the country.

Methods: The sequence data of SARS-CoV-2 genomes deposited in the Global Initiative on Sharing All Influenza Data (GISAID) EpiCoV database was retrieved through filtering the time period from March 2020 to November 2021. A total of 2983 complete genome sequences were considered for analysis in this study. Different web-based bioinformatic tools (Nextclade, GISAID EpiCoV, CoVsurver etc.) were used to clade assignment, lineage distribution, and diversity analysis of the circulating strains. The deduced amino acid (aa) substitutions at the receptor binding site of spike (S) protein were analyzed.

Results: Molecular analysis revealed circulation of ten GISAID clade, five major (G, GK GH, GR and GRY) and five minor (GV, L, V, O and S) or eight Nextstrain clades 20A, 20B, 20C, 20H (Beta), 20I, (Alpha), 20 J (Gamma), 21A (Delta), 21D (Eta), in the country during the study period. The GISAID clade GR that is lineage B.1.1.25 (PANGO lineage classification system) was predominant in Bangladesh and closely related to the sequences from India, USA, Canada, UK, and Italy in the 2020. In late 2020, the introduction of lineage B.1.1.7 (Alpha variant) and S_E484K mutation in lineage B.1.1.25 was noted. During the early period of 2021, Beta variant (B.1.351/ South African variant) was identified in most of the sequences. The B.1.617.2/Delta variant (Indian) surpassed Beta in May shortly after its inception in April, and it became widely visible till now. Mutations (K417N, K417T, L452R, T478K, E484K, S494P, N501Y) at the receptor binding site of spike protein are of particular importance that observed in Bangladeshi strains.

Conclusion: The current investigation on phylodynamic, distribution of variants, lineages, or clades will help in understanding the rapidly changing dynamics of SARS-CoV-2 in Bangladesh and will aid in the development of effective control strategies.

Keywords: SARS CoV-2, Bangladesh, Lineage, Clade, Variants

Abstract number: 11119

SARS-CoV-2 detection and serological response in the forcibly displaced Rohingya Myanmar nationals in Cox's Bazar

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Introduction: COVID-19 pandemic, caused by the novel coronavirus SARS-CoV-2, has posed a serious threat to human health. Bangladesh, being one of the world's most densely populated countries, is hosting nearly 1 million Forcibly Displaced Myanmar Nationals known as Rohingya who are sheltering in the world's largest refugee camp in Cox's Bazar. High population density, inadequate testing capacity, sanitation and hygiene services, practically impossible social distancing, and rising stigma are only a few of the many risk factors that make COVID-19 prevention and management especially challenging in such crisis settings. To better understand the true incidence of SARS-CoV-2 infection, more community-representative population studies are needed. The purpose of this study was to observe the SARS-CoV-2 circulation as well as the serological response against SARS-CoV-2 in the camps.

Methods: In this study 192 confirmed SARS-Cov-2 positive primary cases were enrolled along with their household members (n=152) with respective follow-up day points in compliance with the approved protocol. In brief, blood and nasopharyngeal swab specimens were collected on day-30 from 115 primary cases and 98 household members, and on day-180 from 100 primary cases only. Real-time PCR based diagnosis was employed to confirm the positivity, followed by in-house ELISA to investigate the serological responses against SARS-CoV-2.

Results: 17 of the household members were tested RT-PCR positive for SARS-CoV-2 at the time of enrollment, and 5 at the 30-day follow-up. In addition, 14 confirmed positive primary cases were tested positive again on day-30 follow-up and 3 at the day-180 follow-up. Furthermore, according to the serological testing of 300 specimens (185 confirmed cases and 115 household members), almost 57% of confirmed primary cases and 49% of household members developed IgG antibody response against SARS-CoV-2 at that time.

Conclusions: RT-PCR and seropositivity as found particularly in the household members at the time of enrollment suggest the possibility of prior exposure to SARS-CoV-2 and/or going undiagnosed. Thus, this study proposes that diagnostic measures should consider the entire population. Upon completion, this study will depict a community-specific scenario of SARS-CoV-2 circulation and seroprevalence status, which would help in better disease management in such humanitarian settings.

Keywords*:* SARS-CoV-2*,* RT-PCR, ELISA, FDMN, IgG antibody

Abstract No. 11117

Public health emergency preparedness and response plan for infectious hazards in Bangladesh

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Introduction: COVID-19 showed that if security of public health is not ensured, economy, society and politics become insecure. So it is imperative to develop plans to deal with future pandemic or public health emergency (PHE). As Bangladesh is a hot-spot for emerging infectious diseases like zoonosis, developing PHE preparedness and response plan of infectious hazards (PHE PRP-IH) within a robust public health system and universal health coverage is crucial for health security.

Objectives: To prepare for and prevent PHE caused by infectious hazards, to promptly detect and confirm, promptly response to and recover from adverse effects of PHEs caused by infectious hazards.

Methods: Since 2019, World Bank Group (WBG) has provided technical support to Government of the People's Republic of Bangladesh to IMPROVE PANDEMIC PREPAREDNESS AND RESPONSE IN BANGLADESH. As part of it the authors were responsible for leading/supporting to develop a generic PHE PRP-IH and public health risk mapping. Authors worked closely with identified sector specialists. First and second author carried out a desk review of all relevant information and consulted relevant stakeholders (through workshops, individual and group consultations) to capture primary data. During COVID-19 pandemic, consultations were conducted virtually with few exceptions. Several workshops were conducted in hybrid mode. Risk mapping was conducted for infectious hazards using WHO's Strategic Tool for Assessing Risks (STAR) with WHO support. This Plan is five-year (2023-2028) document, may be updated as needed to account for changes in assumptions, risks, or vulnerabilities.

Result (The Plan): Final document of PHE PRP-IH includes identification of infectious hazards, links with hazard specific action plans and activation of management mechanism, provision of resource deployment in real time, integrated control room, public health emergency operation centre (PHEOC), incident management system (IMS), continuation of essential health services during PHE, risk communication and community engagement (RCCE), having appropriate laws and legal instruments, providing agencies the authority to act and means to work together. A comprehensive law should be enacted for implementing PHE response. Resources which should be ready 24/7: human resources, surveillance system and laboratory for detection, continued training and exercise, framework for mobilizing funds, operational support, logistics, stockpiling, supplies; data collection, analysis and sharing. PHEOC should have a plan for activation mechanism, and clear-cut roles and responsibilities of the personnel of PHEOC. A chain of command from the highest level of the Prime Minister's Office (PMO) to PHEOC via Cabinet division, MoHFW, DGHS, and IEDCR should be operational. IMS should be led by PMO in pandemic, by MoHFW/DGHS in national PHE, by IEDCR in localized outbreaks. In every phase of PHE, IEDCR should work as technical focal institute. Political commitment, plan of action, indicators for monitoring and evaluation is conditional for implementing the Plan and to keep it rolling.

Conclusion: Keen interest was observed during workshops, group and one-to-one consultations with stakeholders. More detailed and in-depth consultations is needed from stakeholders on the document, especially on the political roles and responsibilities of stakeholders and partners, for effective implementation of the Plan and developing follow up documents.

Keywords: pandemic preparedness plan**,** pandemic response, public health emergency, incident command system, COVID-19

Abstract number: 11290

Knowledge, attitude, and practice (KAP) towards of COVID-19 in Bangladesh: a systematic review and meta-analysis

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Background and Objectives: Numerous studies on knowledge, attitude, and practice (KAP) about the prevention of COVID-19 infections are available in Bangladeshi contexts, with results that vary significantly. However, no earlier attempt has been made to analyse the available COVID-19 KAP studies in Bangladesh, which is incorporated in this meta-analysis for the first time.

Method: Following the PRISMA guidelines, articles relevant to COVID-19 KAP that were conducted among the Bangladeshi population were found in databases such as PubMed, Scopus, CINAHL, Google Scholar, and ResearchGate. Random-effects meta-analysis was used to generate a pooled prevalence of knowledge, attitude, and practice level towards the prevention of COVID-19 infection.

Results: This review included 18 articles that were published between March 2020 and November 2021. In the pooled data, there was inadequate knowledge of diarrhea as a symptom of COVID-19 infection (39.24%, 95% CI: 19.10-63.85), headache as a symptom of COVID-19 (56.23%, 95% CI: 49.80-62.46), and weakness as a symptom of COVID-19 (49.28%, 95% CI: 27.75-71.08). Overall, 89.87% (95% CI: 67.71-97.40) understood about COVID-19 symptoms, 92.09% (95% CI: 84.32-96.18) knew about how it spreads, and 79.51% (95% CI: 59.38-91.15) knew about how to treat it. The public's perception of controlling COVID-19 is mixed, with only 44.16% (95% CI: 35.74-52.93) and 60.28% (95% CI: 49.22-70.38) believing the country would win the struggle against the pandemic and the infection will be successfully controlled, respectively. Although overall COVID-19 preventative practice was good, sub-group analysis found that men had a poor practice towards controlling the infection. The practice of avoiding crowded places (70.15%) and maintaining social distance (77.17%) was found to be satisfactory in institution-based studies.

Conclusion: The findings of this study revealed that the Bangladeshi population had a good awareness of COVID-19 symptoms, treatment, attitudes, and behaviors. The subgroup analyses showed a lack of awareness among the male population. The findings of this study are likely to aid Bangladeshi governments and policymakers in putting evidence into action by identifying gaps and emphasizing the importance of educating the less informed public about COVID-19 transmission.

Keywords: COVID-19 knowledge, COVID-19 preventive behaviors KAP, Pandemic, Systematic Review and meta-analysis.

Open Paper Session 1(b)
One Health Institutionalization, Workforce and Policy

Abstract Number: 11501

Building the workforce capacity in field epidemiology in the region: EMPHNET's Journey in developing the One Health curriculum

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Background and Objectives: Countries in the Eastern Mediterranean Region (EMR) face various health and environmental threats, including emerging and re-emerging zoonoses, limited resources, weak health systems, socioeconomic and political challenges, all of which can have significant public health consequences. Since 2009, the Eastern Mediterranean Public Health Network (EMPHNET) has actively supported capacity-building activities for public health workers including epidemiologists through Field Epidemiology Training Programs (FETPs), and FETP-Vs in Bangladesh. In February 2022, EMPHNET established the Curriculum Working Group (CWG), comprising diverse experts, to develop "The Regional Curriculum Framework for One Health Professional Training Program in the EMR." The goal is to produce skilled epidemiologists and a competent health workforce, strengthen surveillance systems and respond to public health threats through competency-based training programs. A nine-month curriculum for One Health was finalized in March 2023.

Method: The CWG, consisting of international and regional experts, worked as three sub-groups within these themes: address existing One Health training programs, system readiness and training needs assessment (TNA), and One Health competencies. Extensive reviews from global experts were incorporated to ensure quality and effectiveness. The curriculum was presented at various forums: EMPHNET One Health regional meeting in Amman (March 2023), APCOVE workshop in Bangkok (April 2023), and Quadripartite Regional Meeting on One Health in Muscat (May 2023). Multiple iterations of the curriculum documents incorporated the received feedback.

Results: The curriculum includes eleven modules, covering technical and soft competencies. The eight technical modules focus on Principles of One Health, Basic Epidemiology, Ecosystem Health, Public Health Surveillance, Emergency Preparedness and Outbreak Investigation, Integrated Disease Control and Management, Joint Risk Assessment, and Scientific Writing. The remaining three modules address soft competencies, including Culture, Beliefs, Values Ethics and Social Activities, Systems Thinking and Leadership, and Management.

Conclusion: EMPHNET's involvement with FETPs has laid a foundation for capacity building in field epidemiology. The CWG and rigorous curriculum development, incorporating feedback from global and regional experts, ensured the curriculum's quality and relevance. Positive feedback received during events highlights its significance and effectiveness in strengthening workforce capacity in field epidemiology. The curriculum can be adapted for different durations and delivering modalities, as needed.

Keywords: One Health, Field Epidemiology, FETP, Curriculum, Workforce Capacity

Abstract No. 11310

One Health orientation of veterinary education through specially designed pedagogy practices

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Introduction: To satisfy the demand of the intensifying livestock industry, the number of veterinary schools soared from one to thirteen over the past two decades in Bangladesh. However, the current veterinary curriculum is based on traditional animal health and production, where the One Health orientation is missing. So, there are scopes to improve the standards of the graduates by integrating the One Health focus to meet global trends. However, changing the entire curriculum at once is challenging because of mindset and administrative hurdles. An alternative integrative approach was taken to re-orient veterinary education by adopting One Health pedagogy practices.

Methods: A curriculum review gap analysis was carried out to assess the contents of the curriculum and the One Health gaps were identified. A Teacher Training Program was developed focusing on One Health contents by adopting topics on zoonotic disease, emerging infectious diseases, and AMR to be delivered through active learning techniques, problem-based learning, and interactive teaching-learning practices with training on outcome-focused curriculum designing. Faculties were recruited under strict selection procedures and trained in different cohorts. To assess the performance of the trained faculties, teachers' evaluation guidelines, and tools were developed.

Results: About 175 faculties were trained with One Health pedagogy practices using AMR, zoonotic disease, and emerging infectious diseases as examples. The trained faculties formed Bangladesh Veterinary Pedagogy Forum to disseminate their expertise to peers and to ensure good teaching practices. The formal evaluation process of the trained faculties is being implemented.

Conclusion: Adopting the One Health content within the curriculum is sometimes time-consuming and challenging in a developing country. However, One Health pedagogy approaches could ensure the One Health orientation of veterinary education and safeguard good teaching practices and strengthen veterinary education which in turn produces quality vets to combat One Health challenges in a developing world.

Keywords: Veterinary Education, Pedagogy, Disease Control, Good Teaching Practice, Day-one-skills

Abstract number: 11206

Putting community at the center of a One Health mapping exercise in Bangladesh to strengthen animal disease surveillance by building on existing networks

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Introduction: To realize the potential of the One Health (OH) paradigm to improve the health of all species and ecosystems, the active engagement of communities is essential. To strengthen animal disease reporting, the USAID funded Livestock and Nutrition Activity aimed to identify options for involving Bangladesh livestock farmers at union and village levels in effective disease surveillance by building on existing, trusted communication channels used by OH stakeholders.

Methods: Secondary documentation was reviewed from the Ministry of Health and Family Welfare (MoHFW), Department of Livestock Services (DLS) and Ministry of Environment Forest and Climate Change (MoEFCC). During February 2023, key informant interviews were conducted with representatives of these organizations nationally and in Jashore, Barishal and Cox's Bazar; representatives and members of District Disaster Management and Relief (MoDMR) committees, livestock service providers (LPS) and farmers. Disease communication channels were analysed across all administrative levels; particular attention was given to the ease of farmer-to-local representative communication at the community level.

Results: Nationwide, MoHFW is the government organization most commonly represented by staff based within the community. In cyclone-prone areas, the Cyclone Preparedness Program (CPP) is well-represented at union and village level by over 74,000 volunteers across 13 districts. DLS representation is variable with Livestock Field Assistants and artificial insemination technicians in some, but not all, unions. MoEFCC had the least representation at union and village levels with frontline staff clustered around national parks and other strategic natural assets. Beyond public sector organizations, Livestock Service Providers (LSPs) are the most common agents supporting livestock farmers at the community level. LSPs are community members trained and supported by a range of entities including government livestock projects, non-governmental organizations and veterinary pharmaceutical companies. Existing coordination bodies involving key OH stakeholders include: monthly multi-sectoral meetings convened by district and division governments; district nutrition coordination committees; and the National OH Secretariat which meets on an ad hoc basis.

Conclusion: Collaborating with OH stakeholders, such as MoHFW and CPP personnel, will support the sharing of consistent, situation-appropriate messages in support of more timely animal disease reporting via tailored online applications.

Keywords: Animal disease reporting, Disaster management committees, Livestock Service providers, Department of Livestock Services, USAID Livestock and Nutrition Activity

Abstract number: 11085

Adapting with the new normal: Exploration of community engagement of Bangladeshi students' amidst COVID-19 pandemic

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Background and Objectives: Bangladesh has a large opportunity to work with the 'One Health' concept. From the ongoing COVID pandemic, we have learned the essence of enhancing newer ideas and working on the One Health approach more while adapting to the new normal. To make it, we aimed to create different ways to engage with various stakeholders through awareness campaigns to help them get used to the new normal, breaking the usual arrangement connecting enthusiastic students from multi-disciplines who believe in good change.

Method: During COVID 19, One Health Young Voice, Bangladesh (OHYV, B) conducted multiple online activities to encourage various stakeholders including a series of webinars with national and international experts and researchers. Facebook live talk shows and video documentaries on special days like World One Health Day, World Environment Day, World Rabies Day, World Antimicrobial Awareness week were shared on the online platform. To measure the mental health status of the gender-diverse population, an online survey was conducted. Offline activities like the school kids program and field level awareness campaign had also taken place.

Results: To accomplish the motto of "One Health" prospect with a bigger inter-connected active community, the involvement of the multisectoral students' community is the pre-requisite step. So, we arranged (n=4) webinars focusing on diverse minds of participants from veterinary medicine, human medicine, food science and technology, fisheries, social science, zoology, environmental science. According to the social media statistics, online live shows on the basic concept of One Health, conservation of biodiversity, and fake news regarding the COVID pandemic and video (n=7) documentaries that were conducted reached more than 10,000 people till now. Following the study of the survey with 33 respondents, 97% felt their mental health is being disrupted due to continuous repression by society people. Through the two offline school kids' awareness programs we had the opportunity to raise awareness among 300 students' about One Health and its importance. With (n=4) AMR campaigns, we reached 900 people successfully with the concept of the adverse effect of the antimicrobials misusage in the Chattogram district.

Conclusion: One health can be the start for all to think out of the box and create momentum for a revolution in the field of inter-sectoral collaboration while engaging general people to adapt to the changing world.

Keywords: One Health, Activities, Campaign, Collaboration, Online

Abstract number: 11502

Bridging One Health research and policy to achieve health security goals

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A growing number of national and sub-national governments have attempted to implement One Health policies and platforms whereby animal, human, and environmental sectors work collaboratively toward shared health security goals. This multisectoral approach represents a progressive step forward towards addressing complex global health challenges such as epidemics, climate change and antimicrobial resistance. However, gaps remain in operationalizing One Health governance across the realms of pandemic prevention, workforce development, resource allocation, and information availability and exchange among stakeholders in the public and private sector. While research programs have been used to effectively support under resourced disease surveillance and outbreak response activities, and to inform One Health policies, in general, there remains a gap between current One Health research programs and government- implemented health and environmental programs. Public private partnerships allow two disparate pathways towards One Health change (that is, research and governance) to inform each other, maximize efficiencies, and build towards shared health security.

Here we review three examples of public-private partnerships that illustrate how research activities can support disease surveillance, outbreak response and inform health and conservation (e.g., One Health) policies.

Research partnerships between EcoHealth Alliance, a science-based nonprofit, and government institutions in Bangladesh, Liberia, India, and Brazil are highlighted as successful engagements where scientific research around zoonotic disease in partnership with health and wildlife agencies strengthen the science-policy connection. Examples include providing developing a One Health strategy in India, understanding patterns of Nipah virus circulation and spillover in Bangladesh, and informing land-use policy to improve health in Brazil.

Barriers to solving complex One Health challenges include the refusal of coordination or cooperation, lack of capacity building, and poorly allocated resources, including information. A stronger connection between the research and policy sectors provides a low-cost, bilateral benefit which fills gaps and leverages existing strengths.

Keywords: One Health, Policy, epidemics, Research, Public-private Partnerships

Abstract number: 11211

Awareness and practice on infectious medical waste management among healthcare workers

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Introduction: Among all healthcare workers, those who handle infectious medical waste and patient secretions run a higher risk of developing major health problems. Improper handling of infectious medical waste can lead to serious health hazard as well as environmental problems.

Methods: This cross-sectional study was carried out at Dhaka Medical College Hospital to find out the level of awareness and practice on infectious medical waste management among healthcare workers by using a pre-tested semi-structured questionnaire through face-to-face interview. Practice on infectious medical waste management was carried out by an observational checklist.

Results: The mean age of the healthcare workers was 33.46±9.725 years and 67.7% were female and 64.6% of respondents were nurses. Most of them 42.8% had diploma education. 47.4% of the respondents had work experience less than five years. Most of the respondents were from medicine, surgery, gynae & obstetrics 49.8%, 21.8% and 12.0% respectively. Majority of respondents 72.3% attended training on infectious medical waste. Out of 325 respondents, 207 (63.7%) had adequate awareness, 91 (28.0%) had moderate awareness and 27 (8.3%) of the respondents had inadequate awareness. Regarding practice on infectious medical waste management, the clinical departments had shown more compliance, but still improvement is required. Awareness level was statistically significant with educational status, years of experience, place of work and training attended on infectious medical waste management.

Conclusion: The findings of the study provide some information for the development of strategies for the policymakers to take effective measures to find out the level of awareness and practice on infectious medical waste management among healthcare workers of Bangladesh.

Keywords: Infectious medical waste management, Practice regarding infectious medical waste management, Healthcare workers

Open Paper Session 2(a)
Antimicrobial Resistance and its Mitigation (Part 1)

Abstract number: 11214

Three years of Fleming Fund country grant to Bangladesh: a review of progress in AMR surveillance

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The 'Fleming Fund Country Grant to Bangladesh' (FFCGB) is funded by the UK Department of Health and Social Care (DHSC), under its Fleming Fund Grants Program. It focuses on establishing AMR surveillance systems in human, animal, and aquatic sectors including surveillance of antimicrobial consumption and use, facilitating multisectoral governance of AMR containment with One Health approach. FFCGB activity is being implemented by a consortium led by DAI Global, and participated by icddr,b, Chattogram Veterinary and Animal Sciences University (CVASU) and Liverpool School of Tropical Medicine (LSTM) FFCGB functions are centered around Fleming Fund's "Theory of Change" for maximizing country ownership and value for money.

During last three years FFCGB has acted as catalyst to build a strong system of AMR governance and stewardship through revitalizing important governance and technical bodies like National Technical Committee, Core Working Group, Sectoral Working Groups. It has refurbished 12 laboratories - three national reference laboratories and nine sentinel laboratories in human health, animal health and aquaculture sectors, supplied modern equipment, provided necessary trainings to the concerned staff. It has built infrastructure for data management system involving relevant sectors to generate quality AMR data for use by practitioners to promote rational use of antibiotics. It is also promoting development of communication materials targeting general public for awareness building, and for policy makers for prudent evidence backed decision making. FFCGB has promoted development of AMC and AMU surveillance strategies - "Political Economy Analysis of AMR", Study on antimicrobial use with a One-Health approach, and Point Prevalence Survey (PPS) on AMU in selected hospitals. Presently, a farm-level AMU study sponsored by FFCGB is currently underway in selected poultry and dairy farms which aims to quantify the per capita AMU.

Last but not the least, FFCGB has initiated concept of public private partnership in AMR by inclusion of leading private sector laboratories in AMR surveillance to ensure clearer picture of AMR prevalence and trends in the country with more representative data. It has initiated "Clinical Engagement" to promote diagnostic and AMR Stewardship for both promoting AMR data generation and prudent use of antimicrobials based on the generated data.

Keywords: AMR Surveillance, Antimicrobial Stewardship, AMU/ AMC study, PPS, PEA, Public Private Partnership, Clinical engagement

Abstract number: 11267

Molecular characterization and detection of zoonotic linkages of Methicillin-Resistant *Staphylococcus aureus* (MRSA) recovered from dairy farms in Sylhet

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Introduction: Nowadays, Methicillin Resistant *Staphylococcus aureus* (MRSA) has become a major threat towards the public health due to ubiquitous characteristics within human, animal and environmental interfaces. The MRSA produce different super-antigenic heat-stable toxins in foods that cause toxicity and other illness to human. Due to the increasing patterns of resistance against commonly used antibiotics; here we intended to isolate the MRSA in cows' milk to reveal any potential genetic lineages within the dairy cows-environment-human interfaces.

Methods: A total number of 636 samples were collected from raw milk, environment, and nasal swabs of both the dairy cows and farm workers, and environment from different dairy farms in Sylhet. Following standard microbial culturing, biochemical tests, staining, and PCR of targeted *nuc* and fem*A* genes, we differentiated the *Staphylococcus aureus* isolates. Based on CLSI 2020 guidelines, we isolated the MRSA through the disc-diffusion method followed by the reconfirmation of mec*A* gene by PCR. Moreover, we also applied the mPCR method to screen the super-antigenic and heat-stable SE toxin genes, Panton-Valentine Leukocidins, Toxic Shock Syndrom Toxin, and those of Exfoliative toxic genes. Finally, we have sequenced mec*A* positive isolates from each source to find the linkage between dairy cows-environment-human lineages.

Results and Conclusion: The overall prevalence of MRSA is 13.4% (n=271/636), with the highest in environment as 19.3% (n=11/57), while lowest prevalence found in cows' milk as 11.8% (n=31/263) following 13.3% (n=35/263) in cow and 15.1% (n=8/53) in human. All MRSA isolates revealed totally resistance to Oxacillin (100%), Ampicillin (100%), Penicillin (100%), and various degree of resistance to Meropenem (93.3%), Aztreonam (85.1%), Cefatazidime (71.6%), Cefotaxime (74.3%); while highest sensitivity was found to Vancomycin (94.3%). The mPCR revealed with heat-stable toxic genes *sea* (47.4%), *seb* (33.3%), *sed* (25%), and eta/etb (25%), though none of MRSA were *pvl* and *tsst-1* positive. Phylogenetic analysis of *mecA* gene from MRSA showed close relation (>90%) among the MRSA isolated from all origins that is a great concern for food safety and public health issues. Therefore, our study discloses the prevalence of super-antigenic MRSA in dairy animals-environment-human lineages.

Keywords: Super-antigenic MRSA, dairy cows, environment, human

Abstract number: 11403R

Prevalence of multidrug resistant *Salmonella*, extended spectrum beta lactamase producing *Escherichia coli* and methicillin resistant *Staphylococcus aureus* in chicken meat, eggs, beef and milk

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Introduction: Emergence of antimicrobial resistance (AMR) in food borne bacteria is a growing public health concern. In order to tackle the AMR it is important to know the role of animal originated foods in the transmission of AMR bacteria to the human. The present study was undertaken to determine antimicrobial susceptibility patterns of food borne bacteria in animal originated foods.

Methods: Poultry meat (n=100), beef (n=100), milk (n=100) and egg (n=100) samples were collected. Routine bacteriological and molecular methods were performed for isolation and identification of food borne bacteria: *E. coli*, *Salmonella* spp. and *Staphylococcus aureus.* The antibiotic susceptibility test of food borne bacteria was performed by disc diffusion method against 17 different classes of antibiotics. Extended spectrum beta lactamase (ESBL) producing *E. coli* were determined by double disc synergy test (DDST) and methicillin resistant *Staphylococcus aureus* (MRSA) was detected by cefoxitin disc diffusion test.

Results: The prevalence of *E. coli*, *Salmonella* spp. and *Staphylococcus* spp. in chicken meat was 75%, 38% and 48% respectively. In beef prevalence of *E. coli*, *Salmonella* spp and *Staphylococcus* spp. in chicken meat was 55%, 25% and 28% respectively. In eggs prevalence of *E. coli*, *Salmonella* spp and *Staphylococcus* spp. was 60%, 15% and 36% respectively. In milk prevalence of *E. coli*, *Salmonella* spp and *Staphylococcus* spp. was 68%, 28% and 65% respectively. *E. coli* isolates (100%) were found to be resistant to Ceftazidime, Ampicillin and Mecillinam.. *E. coli* isolates 26 of 51 (50.98%) were found to be multidrug resistant (MDR). *Salmonella* spp. showed highest resistant profile against tetracycline (96.67%) followed by azithromycin (90.70%), colistin (69.76%) and ciprofloxacin (60.47%). Eight of 43 (18.28%) Salmonella isolates exhibited MDR profiles. *Staphylococcus aureus* were found highly resistant to benzyl penicillin (66%) followed by amoxicillin (62%), ciprofloxacin (56%). Eighteen of 50 *Staphylococcus aureus* isolates (36%) were found MDR since they were resistant to at least three different classes of antibiotics. The prevalence of ESBL producing *E. coli* was 27.45% and MRSA was 16%.

Conclusion: Data of this study indicate that animal originated foods were contaminated with MDR bacteria which might cause public health problem.

Keywords: Food borne bacteria, Animal originated foods, antibiotic susceptibility patterns, ESBL, MRSA

Abstract number:11082

Virulence and antimicrobial resistance profile of *Salmonella enterica* serovars recovered from poultry processing environments at wet markets in Dhaka, Bangladesh

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The rapid emergence of virulent and multidrug-resistant (MDR) *Salmonella enterica* serovars are a growing public health concern globally. The present study focused on the assessment of the pathogenicity and antimicrobial resistance (AMR) profiling of NTS *enterica* serovars isolated from chicken processing environments at wet markets in Dhaka, Bangladesh. A total number of 870 samples consisting of carcass dressing water (CDW), chopping board swabs (CBS), and knife swabs (KS) were collected from 29 wet markets of Dhaka city. The prevalence of *Salmonella* was found to be 20% in CDW, 19.31% in CBS and 17.58% in KS, respectively. Meanwhile, the MDR *Salmonella* was found to be 72.41%, 73.21% and 68.62% in CDW, CBS, and KS, respectively. All isolates were screened by polymerase chain reaction (PCR) for eight virulence genes, namely *inv*A, *agf*A, *Ipf*A, *hil*A, *siv*H, *sef*A, *sop*E, and *spv*C. The *S*. Enteritidis and untyped *Salmonella* isolate harbored all virulence genes while *S*. Typhimurium isolates carried six virulence genes except *sef*A and *spv*C. Phenotypic resistance revealed decreased susceptibility to ciprofloxacin, streptomycin, ampicillin, tetracycline, gentamycin, sulfamethoxazole-trimethoprim, amoxicillin-clavulanic acid and azithromycin. Genotypic resistance showed higher prevalence of plasmid mediated *bla*TEM followed by *tet*A, *sul*1, *sul*2, *sul*3, and *str*A/B genes. Harmonic and symmetrical trend was observed among the phenotypic and genotypic resistance patterns of the isolates. The research findings anticipate that MDR and virulent *Salmonella enterica* serovars are prevailing in the wet market environments which can easily enter into the human food chain. There was a resilient and significant correlation existent among the phenotypic and genotypic resistance patterns and virulence genes of *Salmonella* isolate recovered from carcass dressing water, chopping board swabs, and knife swabs ($p < 0.05$), respectively.

Keywords: Antimicrobial resistance; multidrug resistant; *Salmonella*; virulence; wet markets

Abstract number: 11034

Exploring multidrug resistant Salmonella carrying extended-spectrum β-lactamase from retail chicken meat and live bird market sewage in Bangladesh

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Introduction: Extended-spectrum β-lactamase (ESBL) producing *Salmonella* is a global public health threat. Contamination of retail chicken meat with ESBL-*Salmonella* is a matter of concern to the consumers because of the risk to human health. Therefore, a cross sectional live bird market (LBM) survey was conducted to determine the prevalence and antibiotic resistance pattern of ESBL-*Salmonella* in retail chicken meat and LBM sewage in Bangladesh.

Methods: The LBM survey was carried out on 64 LBMs of 32 upazilas of 16 districts in eight divisions of Bangladesh during August 2018 to July 2019. A total of 320 retail chicken meat and 64 sewage water samples were subjected to cultural, biochemical and PCR assay for the detection of *Salmonella*. The antimicrobial susceptibility test was done with 31 antimicrobial agents belong to 15 antimicrobial classes. ESBL-*Salmonella* were screened by double-disk diffusion test, and resistance genes were identified by multiplex PCR and sequencing.

Results: The results showed that 55.9% and 32.8% of *Salmonella* spp. were recovered from retail chicken meat and LBM sewage, respectively, of which 77.7% and 85.7% were ESBL producers. The prevalence of multidrug resistant (MDR) *Salmonella* was 99.4% in retail chicken meat and 100% in sewage samples. Notably, three isolates from retail chicken meat were identified as possible extensively drug-resistant (pXDR). The results of broad-spectrum β-lactamase (BSBL) genes showed that all the isolates of *Salmonella* spp. isolated from retail chicken meat and LBM sewage samples were positive for *bla*TEM gene. None of the *Salmonella* spp. isolates had *bla*SHV gene. In case of ESBL-encoding genes, five (2.8%) isolates of *Salmonella* spp. from retail chicken meat were positive for *bla*CTX-M-1 gene. However, no *bla*CTX-M-2 gene was detected in any *Salmonella* spp. isolates from both types of samples. Among plasmid-mediated quinolone resistance (PMQR)-genes, the *qnrA* gene was detected in 11.2% isolates of *Salmonella* spp. from retail chicken meat. Moreover, 4 (2.2%) isolates of *Salmonella* spp. from retail chicken meat harbored *qnrB* gene. None of the *Salmonella* spp. isolates from LBM sewage samples carried *qnrA* and *qnrB* genes. The *qnrS* gene was simultaneously detected in 19% and 38.1% of *Salmonella* spp. isolates from retail chicken meat and LBM sewage samples, respectively.

Conclusions: This study indicates that ESBL–*Salmonella*, most of them MDR, are highly prevalent in retail chicken meat and LBM sewage in Bangladesh. Therefore, it is important to ensure the good hygienic practices during slaughtering and processing of chicken in the retail market and to monitor the resistance continuously.

Keywords: ESBL-*Salmonella*, MDR, resistance gene, retail chicken meat, LBM sewage

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Detection and molecular characterization of antibiotic resistant *Escherichia coli* in selected commercial layer farms in Mymensingh Division of Bangladesh

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Poultry is a potential source for the transmission of antibiotic resistant *E. coli* that may result in treatment failure, leading to economic losses and also be a source of resistant bacteria/genes that may represent a risk to human health. The present study was undertaken to isolate and identify *E. coli* from apparently healthy commercial layer birds of selected poultry farms in Mymensingh division of Bangladesh for a certain period of time with phenotypic and genotypic characterization of antibiotic resistant pattern. Initially a questionnaire was prepared and survey was done to check the status of antibiotic use by the owners of the selected layer farms. A total of 27 layer farms were selected for the present study. First sampling was done from day old chick and then once a month from each of 27 selected farms up to six months. We collected 567 fresh feces or cloacal swabs from layer birds for the isolation of *E. coli*. It was found that most of the farmers used more than five different antibiotics (Amoxycillin, colistinsulphate, ciprofloxacin, tetracycline, neomycin, levofloxacin or doxycycline etc.) randomly in their farms. Among 567 samples, 407 were suspected for *E. coli* on the basis of culture and staining characteristics followed by confirmation of species using species specific *mal*B primers. Antibiotic resistant pattern against 12 commonly used antibiotics were studied by disc diffusion method. All the *E. coli* isolates showed high phenotypic resistance to erythromycin (100%), ampicillin (97%), amoxicillin (97%), doxycycline (93%), tetracycline (87%) and ciprofloxacin (71%). All isolates were found to contain tetracyclines encoding *tet*A, *tet*B*,* beta-lactams encoding *bla*$_{\text{TEM}}$ and floroquinolones encoding *qnr*S genes. It can be concluded that multidrug resistant *E. coli* prevailing in the layer farms can be a potential threat not only for the poultry population but also for public health.

Keywords: Antibiotics, commercial layer, E. coli, multidrug resistant, Bangladesh

Open Paper Session 2(b)
Food Safety, Food and Nutrition Security

Abstract number:11504

Importance of multi-disciplinary interventions in One Health for food safety and safe trade

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One Health was not clearly conceptualized when it was adopted and was at the time narrowly focused on human health, domestic animal health, and food systems without embracing the ecological, socioeconomic, cultural, and political contexts within which the agenda was framed. At present, no formally recognized objectives or standards for the implementation of One Health exist, nor rigorously derived and validated metrics to assess performance or added value, trade-offs, and either positive or negative effects. A global analysis of One Health Networks (OHNs) revealed deficits in geographical distribution and partnership structures, with potential effects on the effectiveness and sustainability of One Health efforts to address urgent threats to global health. There are still self-identified OHNs that have little involvement with environment or ecosystems stakeholders, which restricts the extent to which a multisectoral One Health approach is done in reality; OHNs are engaging fewer community stakeholders in the design and agenda-setting phases of implementation than other types of stakeholders (eg, academic institutions and government bodies). The One Health movement and those involved should stop high-income hegemony and a global health framework that is based on colonial structures to establish more egalitarian networks that genuinely attempt to overcome One Health issues and help communities most affected by emerging and endemic threats. This and other similar analyses should be used as a baseline to establish databases and repositories of OHNs worldwide, help identify deficits in their mandates and activities, and improve directions of investment.

The objective of the talk is to highlight the critical need on bringing the multi sectoral agencies that works on plant, human and animal diseases and their interface with the environment together to act on the one health approach. The importance of awareness generation, policies, networking and partnership for research, development and innovation among different stakeholders in One Health approach will be highlighted based on a case study of management of aflatoxins being conceived under the STDF/WTO project by APAARI by engaging global team of experts.

Keywords: One Health, food safety, safe trade

Abstract number: 11029

Bacillus spp. contamination: a novel risk originated from animal feed to human food chains in south-eastern Bangladesh

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Introduction*:* *Bacillus* spp. are gram-positive, rod-shaped, motile (flagellated), aerobic or facultative anaerobic, spore and biofilm forming bacteria that have been widely used as probiotics in humans, plants and animal production. Although some countries are developing guidelines to ensure the safety of probiotic products, lack of legal inspection or requirement to demonstrate efficacy, may pose threat of getting *B. cereus* contamination in animal-used probiotics. Our hypothesis for this study is to explore the key information on contamination levels and toxigenic profiles of isolated *Bacillus* spp. in animal feeds, animal-derived products and human stool that will help us better understand the pathogen's current status and pathogenic potential in Bangladesh.

Methods: A cross sectional study was conducted on total of 180 collected samples from various sources including layer (n=20), broiler (n=20), duck (n=13), fish (n=15) and cattle (n=20) feed, table egg (n=20), milk (n=20) and human stool (50) in different locations across the Noakhali district. All the collected samples were evaluated by culture, biochemical, and molecular assays. Data on the various types of farms, the age and populations of birds, the type of housing, feeds, egg production, feed additives and antibiotics, feed source and clinical history were collected using a questionnaire survey. A structured data collection schedule was also used to obtain information on diarrheal patients and types of food consumed.

Results: Out of 180 different samples, 218 *Bacillus* spp. were isolated and identified where *B. cereus*, *B. subtilis*, *B. amylolequefaciens, B. licheniformis, B. thuringiensis, B. megaterium* and *B. coagulans* accounted for 51%, 22%, 9.1%, 5.9%, 5%, 3.6% and, 2.2% respectively. Regarding the enumeration of Total Viable Count (TVC) and Total Bacillus Count (TBC), correspondingly 67% and 39% samples were found to be contaminated with above 10,000 CFU/g, while highest contamination was 85% and 75% in broiler feed, respectively. Detection rate of enterotoxin genes (*nheA, nheB, nheC, cytK, hblA, hblC, hblD,* and *entFM*) showed that 55% isolates carried *nheABC* genes, 80% *entFM*, 71% *cytK*, whereas only 33% of the isolates contained *hblACD* gene clusters. These virulence genes were posing a threat to human health due to spread across the food and feed chain. The hospital-based survey showed that food-borne Bacillus spp. contributed to 4.5% human diarrhea cases and 25% food contamination associated with vegetables, rice, RTE food, milk and egg, accounting for 46%, 34%, 14%, 4% and 2%, respectively.

Conclusion: This is the first study in Bangladesh to investigate the quantity of *Bacillus* spp. contamination and toxigenic potentials persistent in animal feed, animal-derived food and human stool. The findings revealed that this feed-borne *Bacillus* spp. group collection has significant toxigenic potentials, contaminating animal feed, animal products and daily food.

Key words: Food-borne pathogen, *Bacillus* spp., Toxin gene, Food chain risk, Diarrhea

Abstract number: 11099

Heavy metal contamination and antibiotic residues in poultry feed and meat in Bangladesh: A growing one health concern

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Presence of harmful contaminants and residues in poultry feed and meat might cause serious public health consequences. This study was carried out to identify and quantify antibiotic residues, heavy metals and toxins in poultry feed and meat in the two selected poultry production belts of Bangladesh. A total of 94 broiler feed samples and 60 broiler meat samples were collected and tested utilizing Thin Layer Chromatography (TLC), High Performance Liquid Chromatography (HPLC) and Enzyme-linked Immunosorbent Assay (ELISA) for identification and quantification of the parameters. Antibiotic residues were detected in 18.89% of the feed samples, whereas, no toxin (Aflatoxin) positive sample was identified. Among the antibiotic positive samples, Oxytetracycline (OTC) was found predominant and detected in 12.22 % cases. The mean concentrations of Cadmium (Cd), Lead (Pb), Chromium (Cr) were found as 0.04 mg/kg, 1.28 mg/kg and 2.55 mg/kg respectively in feed samples. In the case of meat samples, the mean concentration of OTC, Ciprofloxacin (CIP), and Tetracycline (TCL) residues were found 8.67 ppb, 7.18 ppb and 0.81 ppb accordingly. The highest mean concentration of Oxytetracycline (OTC) (10.15 ppb) was found in samples collected from local poultry sellers, whereas, the highest mean concentration of Tetracycline (TCL) (1.35 ppb) and Ciprofloxacin (CIP) (10.62 ppb) were observed in the samples obtained from local farm. The highest percentage of TCL and CIP (64% and 48% respectively) were found in samples collected from local farms. Chlor-tetracycline (CTC) was found predominant (70%) in samples collected from Contract Farms (CF). On the other hand, out of 60 meat samples, Cd and Cr were detected in only one meat sample with concentration of 56.41 mg/kg and 14.44 mg/kg respectively. Lead was not detected in any of the meat samples. To manage severe public health implications derived from antibiotic resistance and heavy metal contamination all the relevant agencies should act under One Health approach, and need to be sincere, proactive and vigilant for ensuring adequate supply of safe food for the wellbeing of animal and human health.

Key words: antibiotic residue; heavy metal; food safety; public health; one health

Abstract number: 11081

Determination of antibiotic residues in animal derived food commodities in Bangladesh: a cross sectional study

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Antibiotic residues in foods of animal origin have received great attention in recent years due to growing concerns about food safety and public health. A cross-sectional study was conducted to investigate the antibiotic residues in animal-derived food commodities in Bangladesh. A number of 159 samples were analyzed consisting of meat (broiler, cattle and goat), milk (cattle, goat and buffalo) and eggs (chicken and duck) of diverse animal origin. Thin Layer Chromatography (TLC) method was used for the qualitative screening of seven antibiotics which revealed overall the prevalence of antibiotic residue 30.81% (49/159; 95%CI: 23.75-38-62). TLC positive samples were further analyzed by Ultra High-Performance Liquid Chromatography (UHPLC) method and found different concentration of antibiotic residues. The amoxicillin (AMC) residue was found above the maximum residue limits (MRL) in 7.14% meat and 2.5% milk samples while ampicillin (AMP) residue was found above MRL in 4.76% meat and 5% milk samples respectively regardless of origin. Among the overall samples, the residue of AMC, AMP and oxytetracycline (OTC) has increased linearly and steady with greater concentrations in meat samples. This study anticipates that due to irrational use of antibiotics in animal production along with without following the withdrawal periods prior harvesting and marketing can cause unexpected residue in animal-derived food products lead to the emergence of antimicrobial resistance (AMR).

Keywords: Antibiotic residue; antibiotic resistance, animal derived food; MRL; public health

Abstract number: 11289

Foodborne pathogens recovered from ready-to-eat foods in some selected areas of Bangladesh

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Introduction: Ready to eat foods are widely used at home, restaurants and festivals. Hence, it is very important to investigate the total microbial load in ready to eat foods. The present study was undertaken to determine the microbial load, isolate, identify and characterize the bacteria obtained from ready to eat foods.

Methods: A total of 100 ready to eat foods were collected from different super markets of Mymensingh, city. Microbial quality of ready to eat foods were assessed by total viable count (TVC), total coliform count (TCC), total staphylococcal count (TSC) and total listeria count (TLC). Isolation of the bacteria were performed by inoculating the samples onto selected media and incubated at 37°C for 24-48 hours. Identification of the bacteria was done by colony morphology, Gram's staining and biochemical test. Characterization of the bacteria was performed by polymerase chain reaction (PCR).

Results: The highest level of TVC found in pizza, salad vegetables and milk shake and they are 6.50±0.30, 5.85±0.48 and 5.84±0.25 mean log CFU±SD/ml respectively. The highest level of TCC and TLC found in Burger and pizza samples, that were 3.69±.08 and 4.54±0.10 mean log CFU±SD/ml respectively**.** The mixed vegetable salad samples (40%) showed higher positives results for *E. coli.* Whereas, prevalence of Staphylococcus in Chicken meat loaf was 50%. Pizza and yogurt show higher positive results for *Listeria* sp (30%). Multi-drug resistant *E. coli*, Salmonella, Staphylococcus and Listeria were detected by disc diffusion test using 12 commonly used antibiotics. All the 21 isolates were subjected to antibiotic susceptibility test against 12 different antibiotics and it was observed 46.1% were susceptible, 16.6 % were intermediate, 46.1 % were resistant and 47.6% were multi drug resistant among 7 different antibiotic classes. Antibiogram study showed that the isolates from ready to eat food samples were resistant to Cephalexin, Ceftazidime, Oxytetracycline and Ampicillin and sensitive to Gentamycin followed by Kanamycin, Ceftriaxone, Colistin, and Enrofloxacin.

Conclusion: The study revealed that unhygienic food handling platforms are becoming a serious issue on public health point of view and in order to achieve a somewhat safe level in RTE foods for human consumption. Moreover, presence of multi-drug resistant bacteria in these foods might pose serious public health threats.

Keywords: Prevalence, microbial load, Ready-to-eat foods, Antibiogram profile

Abstract Number: 11260

Molecular detection of methicillin, vancomycin, and enterotoxin producing *Staphylococcus aureus* isolated from table eggs and their antibiotic susceptibility profiles

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Introduction: *Staphycoccus aureus* are major food poisoning bacteria. The study was conducted to identify the prevalence as well as molecular detection of methicillin resistance (MRSA), enterotoxin producing (*seb*), vancomycin resistance (VRSA) and assessment of antibiotic susceptibility profiles of *S. aureus* isolated from table eggs.

Methods: A total of 200 eggs (egg shell=100) and (egg content=100) were collected from various retail shops (n=50), super shops (n=50), farms outlet (n=50) and wholesale markets (n=50) located at Mymensingh city corporation. Swab samples were taken from the eggshell surface, and egg content samples were taken from the inner membrane, egg white and yolk. Both samples were enriched into Trypticase soy broth (TSB) at 37℃ overnight, cultured on Mannitol salt agar (MSA) and incubated at 37℃ for 24hrs for isolation of Staphylococcus spp. The identification of Staphylococcus *aureus* was performed by the conventional culture method. Molecular detection (PCR) was performed for confirmatory identification of the bacterial species targeting the nuc gene, followed by confirmation of methicillin-resistant, enterotoxin producing and vancomycin resistance S. aureus by targeting the mecA, seb and vanC genes. The sensitivity of S. aureus was performed against 13 different antibiotics (Azithromycin, Erythromycin, Cefoxitin, Oxacillin, Penicillin, Ciprofloxacin, Levofloxacin, Norfloxacin, Tetracycline, Doxycycline, Clindamycin, Gentamycin and Vancomycin) by disc diffusion test.

Results: The prevalence of S. aureus in the table eggshell surface was 40%, and egg content was 32%. All 72 table eggshell and content coagulase-positive isolates were tested, where 29 (40.27%) were positive for the nuc gene. On the other hand, the mecA, seb and vanC genes could be detected in 12 (41.37%), 5 (17.24%) and 5 (17.24%) from all S. aureus isolates from egg shells and their content. The antibiogram study indicated that most of the isolates were resistant to the antibiotics under β-lactam [penicillin (100%), cefoxitin (100%) and oxacillin (96.55%)] and Glycopeptides [vancomycin (44.82%)] group. 100% S. aureus showed Multidrug resistant profile.

Conclusion: Multidrug-resistant (MDR) S. aureus, methicillin-resistant S. aureus (MRSA), enterotoxin-producing (seb) and vancomycin-resistant S. aureus (VRSA) were found in the table eggs sold at retail markets which might pose a public health risk if these MDR bacteria enter into the food chain.

Keywords: Table eggs, MRSA, *mec*A, Antibiogram, VRSA, MDR, Public health.

Open Paper Session 3(a)
Antimicrobial Resistance and its Mitigation (Part 2)

Abstract number: 11265

Risk factors for colonization with extended-spectrum cephalosporin resistant and carbapenem resistant Enterobacterales among healthy adults in community and hospitalized patients, Bangladesh: An Antibiotic Resistance in Communities and Hospitals study

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Background: Antimicrobial resistant (AMR) organisms are an increasing global health threat that are spreading within hospitals and even in communities. Understanding the risk factors for colonization with AMR organisms is critical to inform prevention and control strategies. We identified associated factors for colonization of two clinically important phenotype: Enterobacterales with extended-spectrum cephalosporin resistance (ESCrE), and carbapenem resistance (CRE).

Methods: During April- October 2019, we conducted a cross-sectional study and collected stool specimens from adult patients in three hospitals and healthy community dwellers within the hospitals' catchment area in urban Dhaka. Specimens were tested for ESCrE and CRE using selective media followed by VITEK-2 confirmation. Community participants completed demographic surveys assessing food consumption, animal contact, sanitation, water sources, and healthcare exposure, whereas; we recorded information on patient characteristics, admission wards, antibiotic use, duration of hospitalization and healthcare exposures. We used multivariate logistic regression models adjusting for potential confounders to identify the risk factors for colonization.

Results: Of 714 enrolled community individuals, 557 (78%) were colonized with ESCrE and 66 (9%) with CRE. In multivariable analysis, factors associated with ESCrE colonization was fresh fruit consumption in the past week (aOR 2.0, 95%CI 1.3-3.2) and factor that was significant for CRE colonization was hospitalization in the last 3 months (aOR 3.0, 1.0-8.7). No association was detected with antibiotic usage in past three months, animal exposure, or other food consumption patterns for both outcomes.

Among 743 enrolled patients, 592 (82%) were colonized with ESCrE and 267 (37%) with CRE. In multivariable analysis, patients transferred from other hospital/clinic (aOR 3.1, 1.5-6.4); staying in surgical wards (aOR 1.7, 1.1-2.5); hospitalization for 3-7 days (aOR 1.6, 1.1-2.3) and >=7 days (aOR 2.7, 1.7-4.3); invasive procedures (aOR 2.4, 1.3-4.4); urinary catheter (aOR 2.1, 1.1-4.2), and antibiotic received in last 14 days (aOR 2.9, 2.0-4.0) were identified as risk factors for CRE colonization.

Conclusion: ESCrE and CRE colonization is common in communities and hospitals, whereas; hospital exposure is associated with CRE colonization which may be contributing to community spread of CRE as well. Targeted infection control interventions may be needed to mitigate the transmission of AMR organisms.

Keywords: ESCrE, CRE, colonization, AMR, Bangladesh

Abstract number: 11266

Isolation of multidrug resistant bacteria from pet birds sold at different retailer shops

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Introduction: Pet birds can act as reservoirs of multidrug-resistant bacteria for human who are involved in pet bird rearing directly.

Objective: This research was conducted to detect multidrug resistant bacteria isolated from pet birds and their antibiotic sensitivity patterns.

Methodology: A total of 77 feces and hand washing samples were collected from retail pet shops located at Mymensingh, Dhaka and Gazipur of Bangladesh for the isolation of *E. coli*, *Staphylococcus* spp., *Salmonella* spp., and *Shigella* spp. Samples were inoculated in selective media after primary enrichment. Colonies were selected, purified, chromosomal DNA was extracted, and PCR was done to detect the isolates. Finally, the antibiotic susceptibility pattern was studied against 12 antibiotics.

Results: Out of 77 samples, 37 suspected *E. coli* were confirmed by PCR using the fliC gene. The *stx*1 and *stx*2 genes were not detected in the isolates. Similarly, 32 were detected as *Staphylococcus* spp. using 16sRNA and no nuc gene was detected in any of the isolates. No isolate was detected as *Salmonella* and only one isolate was detected as *Shigella* sp. The isolation rate of *E. coli* was higher (57%) compared to *Staphylococcus* spp. (44%) and *Shigella* sp. (2%) from the pet birds. Antibiotic susceptibility revealed that most of the selected isolates of *E. coli* and *Staphylococcus* spp. were 100% resistant to amoxicillin, cefixime, and cefuroxime. Tetracycline resistant genes (*tet*A & *tet*B) were also detected in 18 species of *E. coli* and 19 species of *Staphylococcus* spp.

Conclusion: It can be concluded that pet birds may harbor bacteria that are resistant to most of the antibiotics, and the presence of such bacteria in pet birds might be life-threatening to humans who are involved in their caring.

Keywords: Pet bird, antibiotic, resistance, tetracycline, MDR

Abstract number: 11040

Screening of antibiotic residue in transported live fish and water collected from different fish markets of Mymensingh district

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Introduction: The present experiment was conducted to evaluate the persistence of oxytetracycline residue in common fish species such as Catla (*Catla catla*), Rui (*Labeo rohita*), Mrigal (*Cirhinus cirrhosus*), Pangas (*Pangasius pangasius*) available in local fish markets and corresponding transporting water of Mymensingh region.

Methods: Fish and water samples were analyzed by using Thin Layer Chromatography (TLC) and High Performance Liquid Chromatography (HPLC) for qualitative and quantitative detection of oxytetracycline residue, respectively. 240 fish samples (in total) and 60 water samples (in total) were randomly collected from three local fish markets under the study area from May to July 2019 (as Summer Season) and November to January 2019-20 (as Winter Season).

Results: Detectable oxytetracycline residues were observed in eighteen (18) samples (13 fish and 05 water samples) in summer season and eight (08) samples (08 fish and 00 water samples) in winter season. The overall percentage of antibiotic residue positive in fish sample was 8.75% and water samples was 8.33%. Oxytetracycline concentrations of positive samples in fish were 34.7-56.85 ppb in Catla, 23.45-35.37 in Rui, 11.02-26.80 in Mrigal, 10.80-77.55 in Pangas during summer and positive samples in fish were 18.5 ppb in Catla, 15-16.09 in Rui, 10-14.63 in Mrigal, 21.02-40.11 in Pangas during winter season. Besides, the range of detected oxytetracycline concentrations of positive samples in water were 12.9-59.18 ppb during summer and below detection level during winter. The comparison between summer season and winter season shown that the percentage of positive antibiotic residue in summer season (10.38% for fish and 16.67 for water) is higher than the winter season (6.67% for fish and 0% for water). This variation indicates that fish transporters use more antibiotics during summer season compared to winter season. The means concentration of oxytetracycline in fish and water samples were not exceeded the maximum residue limits.

Conclusion: Although the concentrations of antibiotic residues in fish edible tissues are below MRL values, however, along with edible tissues, presence of antibiotic residues in transported water would lead to develop the antimicrobial resistance bacteria which are detrimental both for human, animal and aquatic culture.

Keywords: Oxytetracycline residue, UHPLC, TLC, fish and water samples

Abstract number: 11503

Containing antimicrobial resistance through multisectoral coordination in Bangladesh

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Antimicrobial resistance (AMR) is a major public health concern in Bangladesh, and globally. It caused 1.27 million deaths in 2019. There is also high AMR prevalence in Bangladesh making some first-line antibiotics ineffective and leading to higher healthcare expenditure. To mitigate AMR, the World Health Organization (WHO) has recommended multisectoral coordination (MSC) as one component of an effective AMR containment strategy. Since 2019, the USAID Medicines, Technologies, and Pharmaceutical Services Program (MTaPS) has been collaborating with the Communicable Disease Control (CDC) department of the Directorate General of Health Services (DGHS) under the Ministry of Health and Family Welfare to improve the country's Joint External Evaluation (JEE) capacity level on MSC to contain AMR.

MTaPS supported the CDC to complete 25% actions at developed capacity (level 3), 75% at demonstrated capacity (level 4) and 20% at the sustainable capacity (level 5), bringing the country to overall 29% achievement on MSC-AMR based on the WHO benchmarks for International Health Regulation (IHR) Capacities. The National Technical Committee, a high-level technical body on AMR, has restarted regular meetings to coordinate with all the sectors to mitigate AMR in the country through review interventions and guideline, policy documents, taking corrective measures and decision making. Further, with MTaPS support, the CDC program of DGHS has updated the National Strategic Plan and the National Action Plan on AMR (NAP-AMR) (2021–2026) and developed a monitoring and evaluation framework and costed operational plan for the NAP-AMR in collaboration with the animal and environmental sectors. The new iteration of the NAP-AMR has further consolidated the One Health spirit and multisectoral plans. MTaPS continues to support joint stakeholder meetings to accelerate operationalization of the NAP-AMR, including developing an inventory of AMR interventions in the country, updating the NAP-AMR implementation roadmap, and establishing an in-country agenda for the annual World Antibiotic Awareness Week events.

Additional coordinated initiatives, partnerships, funding, and capacities are needed to further institutionalize and sustain these gains.

Keywords: Multisectoral Coordination, Antimicrobial Resistance, Joint External Evaluation, National Technical Committee, WHO Benchmark

Abstract No. 11282

Driving force of indiscriminate usage of antibiotics in small scale commercial poultry farms in Bangladesh

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Introduction: The ascent of antibiotic resistance is an emerging public health concern, propelled by an array of factors, including widespread use of antibiotics in livestock production. The reported overuse of antibiotics in poultry farming is leading to concerns about the potential for antibiotic resistance to emerge in humans. Hence, we conducted this study to explore driving forces of antibiotic usage in commercial poultry along with the farmer's perception of antibiotics.

Methods: We conducted a qualitative study in three districts (Dhaka, Manikganj, Narayanganj) of Bangladesh between September and December 2021. We collected data from 60 poultry farmers using in-depth interviews and participant observation to understand the pattern of antibiotic use and perceptions of farmers on antibiotics and its effects. Recorded interviews were transcribed in Bangla and developed thematic codes from the transcribed data for analysis based on the grounded theory approach.

Results: The farmers use antibiotics for any kind of sickness of their birds without diagnosis of diseases. They believe that antibiotics do not have any side effects or transfer to humans. Farmers purchase chicks, poultry feeds, and antibiotics from poultry dealers on credit, they repay the debt by selling their poultry to these dealers. However, farmers are obligated to sell their poultry exclusively to these dealers. Dealers offer a reduced price and sometimes may refuse to purchase their poultry. The dealers wield significant influence over farmers regarding antibiotic usage, as they decide which antibiotics to use and how frequently they should be administered. Occasionally, veterinary professionals from various pharmaceutical companies visit the farms to provide treatment to poultry. Farmers reported that if they do not use antibiotics recommended by these veterinarians, who often represent a specific company, then the veterinarians do not provide further advice.

Conclusion: Poultry farmers are often forced to use antibiotics by poultry dealers and veterinary professionals from pharmaceutical companies. To create successful interventions that offer economic benefits and increase farmers' awareness of antibiotics and their usage, it is important to address this influence. Moreover, it is crucial to impose stringent regulations on the use of antibiotics in poultry farming to prevent the emergence of antibiotic resistance.

Keywords: Misuse, antimicrobial resistance, poultry farmers, influencing factors

Abstract No. 11295

Effect of ABCB1, ABCC4, and GSTP1 gene polymorphisms on the response and toxicities of antiretroviral therapy in Bangladeshi AIDS patients

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Background: Antiretroviral therapy was reported to show varying degree of responses and toxicities. The inter-individual variation of the therapy outcomes is due to different factors including biological factors. Genetic factors are one of the leading causes of this variation. Therefore, it is warranted to investigate the influence of genetic factors that leads to variation of the therapy outcomes.

Objective: Our objectives were to evaluate the role of genetic polymorphisms in ABCB1, ABCC4 and GSTP1 on the drug response and toxicities of antiretroviral therapy in AIDS patients and to identify molecular (genetic) marker for selecting better treatment regimen and reducing toxicities

Methodology: A total 414 AIDS patients were recruited from Infectious Diseases Hospital (IDH: 208) & (BSMMU: 206) of Bangladesh receiving Lamivudine-300 mg+ Tenofovir-300mg + Efavirenz-400mg (for 6 months). PCR-RFLP had been applied to determine the genetic polymorphisms. Viral load and regimen change and drug induced toxicities have been evaluated from recorded hospital data of the patients as well as it was matched with the data obtained from interview of the patients with the help of structured questionnaire.

Result: ABCB1 gene was associated with the high viral load such as for CT (p= 0.0095, OR=0.49), TT (p= 0. 0.0068, OR=0.40), and for CT+TT (p= 0.0018, OR=0.45) as well as regimen change (drug resistance) like for CT (p= 0.0091, OR=0.50), TT (p= 0. 0.0017, OR=0.36), and for CT+TT (p= 0.0009, OR=0.45). On the other hand, GSTP1 gene was linked with drug induced toxicities like drug allergy (hypersensitivity) such as for AG (p= 0.048, OR=1.99), GG (p= 0.04, OR= 2.39), and for AG+GG (p= 0.016, OR=2.2), nausea and vomiting: for GG (p= 0.017, OR= 2.96), and for AG+GG (p= 0.025, OR=1.9), hyperacidity: for GG (p= 0.023, OR= 2.96), and for AG+GG (p= 0.026, OR=2.16) , diarrhea: GG (p= 0.031, OR= 2.98), and for AG+GG (p= 0.03, OR=2.22) and insomnia: for AG+GG (p= 0.039, OR=2.1). No other significant association was observed for ABCB1, ABCC4 and GSTP1.

Conclusion: ABCB1 gene was associated with viral load and drug resistance. On the other hand, GSTP1 gene was related with drug induced toxicity in AIDS patients.

Keywords: Antiretroviral therapy, drug resistance, drug toxicity, gene polymorphism

Open Paper Session 3(b)
Wildlife, Environment and Ecosystem

Abstract number: 11505

Two decades of dengue outbreaks in Bangladesh (2000-2022): Climate change, environmental niche, and future planning

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After 1964, the dengue virus reappeared in Bangladesh in 2000, and then the virus is detected every year with all four serotypes (DENV:1-4) being detected in the country over time. The aim of this study is to summarize the two decades of dengue outbreaks in Bangladesh with a light on the impact of climate change, seasonality, meteorological parameters, and future control plan.

We collected monthly reported dengue cases and deaths data from the Ministry of Health website for the period of 2000-2022. We collected meteorological data from Bangladesh Meteorological Department for the same period. We performed statistical (Generalized Linear Mixed Model [GLMM] and Autoregressive integrated moving average (ARIMA) model) and mathematical modeling to understand the biological transmission parameters (biting rate, mosquito survival rate, Extrinsic Incubation Period [EIP]) of the dengue virus and the effect of meteorological parameters on the transmission cycle.

Compared to the first decade (2000-2010) the annual temperature has increased by 0.29°C and rainfall decreased by 33.1 mm, respectively in the recent decade (2011-2022). During this time dengue cases have increased 8.3 times and dengue-related deaths have increased by 9.6 times. In the time series model, we detect an increasing trend of dengue cases in Bangladesh with a much stiffer rise after 2018. We detected July-September as Bangladesh's peak season of dengue cases whereas the monthly growth factor remains above one between June and August. Mathematical modeling using the temperature of Dhaka city showed that an Aedes mosquito would bite an individual at minimum 3 days (maximum 9 days) intervals after taking a blood meal and the EIP would complete as minimum as 4 days (Maximum: 23 days) indicating a rapid transmission potential of the virus in the country. Monthly mean temperature (Odds ratio [OR]: 1.07 (95% CI: 0.90-1.28)), first-lagged rainfall (OR: 30.31 (95% CI: 29.33-31.33) and second-lagged rainfall (OR: 12.91 (95% CI: 12.52-13.33) were associated with monthly dengue incidence in Bangladesh.

Over two decades, Bangladesh has experimented with a significant burden of dengue cases with an increasing trend of dengue cases and deaths. Climate change, unusual rainfall, urbanization, and population growth might have contributed to this increased incidence of dengue cases in Bangladesh. Community engagement and regular monitoring and destruction of Aedes mosquitoes' habitats should be prioritized to control dengue virus outbreaks in Bangladesh.

Keywords: Dengue, climate change, environmental niche

Abstract No. 11311

Mycobacterium orygis-associated tuberculosis in Bangladesh

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Introduction: The cause of animal tuberculosis (TB) is primary *Mycobacterium bovis*. However, in Bangladesh, *Mycobacterium orygis (M. orygis)*, a new sub-species of *M. tuberculosis* complex (MTBC) had been reported as causal agent of TB in dairy cattle and captive wild animals. The present study was designed to confirm the presence of *M. orygis* in cattle-human-captive wildlife interface in Bangladesh.

Methods: Active surveillance was conducted to collect post-mortem samples (lung, liver, kidney, intestine and lymph nodes) from suspected TB infected cattle (n=9) of dairy farms and different animals(n=11) of zoo. Lung tissue with nodules from suspect cattle (n=973) at slaughterhouse/ meat-shops, and sputum samples were collected from cattle and captive wildlife handlers and butchers (n=113). The samples were processed following standard procedures including smear-microscopy, and culture on Lowenstein-Jensen (L-J) slants for 8 weeks at 37°C. Cultures were observed weekly for the formation of mycobacterial colonies. DNA of culture-isolates were initially analyzed using the Line Probe Assay (LPA) for genotyping, followed by whole genome sequencing (WGS) and phylogenetic tree construction.

Results: A total of 11 isolates from animals (including five cattle and six captive wildlife) and two human isolates were positive in culture media for MTBC. Genotyping results confirmed that all of animal 11 isolates (six cattle from four dairy farms and one slaughterhouse as well as six captive wildlife) were *M. orygis.* However, both human isolates were confirmed as *M. tuberculosis.* Of 11 isolates, seven were analyzed using WGS as significant amount of DNA materials present; among them, six were found to be fit for phylogeny. The strains of *M. orygis* were clustered in the same location of the phylogenetic tree in two sub-branches. All isolates were reported susceptible to first-line of anti-TB drugs.

Conclusion: Humans are potentially at risk due to the close contact with infected cattle and captive wildlife. The circulation of *M. orygis* in diverse cattle and captive wildlife animal species indicates that this new species may be a zoonotic tuberculosis risk in Bangladesh, and that larger-scale prevalence studies are needed. Therefore, a One Health approach is best equipped to further assess risks for the control and elimination of zoonotic tuberculosis in Bangladesh.

Keywords: *Mycobacterium orygis,* zoonotic tuberculosis, cattle-human-captive wildlife interface, Bangladesh

Abstract No. 11302R

Detection and management of tuberculosis at wildlife-public health interfaces in Bangladesh - A One Health approach to combat zoonoses

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Introduction: Zoonotic Tuberculosis (zTB) caused by *Mycobacterium Tuberculosis Complex* (MTC) is one of the emerging challenges for wildlife conservation and public health in South Asia including Bangladesh. Although Bangladesh is one of the high Tuberculosis burden countries, wildlife Tuberculosis and its consequences remain largely unknown. In light of the current situation, the Bangladesh Forest Department (BFD) has launched a research project for the detection and management of Tuberculosis at wildlife-human interfaces, with the primary goal of investigating the diversity of MTC strains of zTB circulating in wildlife and their impact on public health.

Method: A two-year longitudinal study was designed to investigate zTB in wild animals-human interfaces in Bangladesh. Both invasive and non-invasive samples were collected from eighteen major wildlife settlement areas. Invasive samples were initially screened by Z-N testing and positive samples were confirmed by PCR. DNA was extracted from non-invasive samples using the Monarch genomic DNA purification kit and finally, PCR was followed. To identify Mycobacterium species, at first multiplex PCR was performed based on the amplification of the 16S rRNA gene of *Mycobacterium tuberculosis complex.* Later on, uniplex PCR was performed based on the amplification of H37Rv and MPB83 genes of *M. tuberculosis* and *M. bovis* respectively. Furthermore, data were collected from all study sites and to identify potential risk factors multivariate regression analysis is going on.

Results: A total of 17 cases were confirmed by PCR out of 737 collected (both invasive and non-invasive) wild animal samples tested that include *Mycobacterium Tuberculosis complex, M. tuberculosis and M. bovis*. The 17 infected wildlife species included were Spotted Deer (n=03), Samber Deer (n=01), Goyal (n=02), Asiatic Elephant (n=03), Asiatic Black Bear (n=03) and Rhesus Monkey (n=05). Further laboratory analysis particularly bacterial isolation and sequencing of targeted genes are in progress.

Conclusion: This is for the first time Bangladesh Forest Department took initiative to detect wildlife tuberculosis in collaboration with the Department of Pathology, Bangladesh Agricultural University. This study identifies zoonotic tuberculosis and tries to formulate feasible solutions to prevent its spreading among the wildlife population in Bangladesh and protect public health.

Keywords: Wildlife, Tuberculosis, Public health, Conservation.

Abstract number: 11233

Environmental surveillance for SARS-CoV-2 and enteric pathogens in humanitarian settings and municipality, Cox's Bazar

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The influx of nearly one million Rohingya refugees from Myanmar in Cox's Bazar since 2017, had a huge social and environmental impact. Living conditions in the camps are overpopulated and threats of enteric diseases and the SARS-COV2 prevail in the camp. Cox's Bazar municipality sanitation network is similar to other major cities of Bangladesh. The study on environmental surveillance is first ever in humanitarian settings and municipality area. The study is designed to develop a systematic sample site selection strategy for city-wide environmental surveillance and to monitor temporal and spatial trends in vaccine-preventable enteric pathogens (Group A Rotavirus, Salmonella typhi, and Vibrio cholerae) and SARS-CoV2.

The research team conducted stakeholders' meetings, scoping visits and transect walks in different camps and used GIS tools to predict the movement of wastewater. The team modelled micro-watersheds and estimate catchment areas and populations to identify strategic sampling points. Concentration, detection, and quantification of SARS-CoV-2, *Vibrio cholerae*, *Salmonella Typhi* and Group A rotavirus performed in Multiplex qPCR assays.

We conducted environmental surveillance from 16 October 2022 to 8 February 2023 on three refugee camps in Ukhiya, Cox's Bazar, and the Cox's Bazar municipality to explore the spatial and temporal trend of four vaccine-preventable diseases causing pathogen- SARS-CoV-2, Group A Rotavirus, *Salmonella typhi,* and *Vibrio cholerae.* A total of 192 wastewater samples (153 from refugee camps and 39 from the municipality) were collected from well mapped selected locations of drain, canals that represents specific geographical area and or community and analyzed through RT-PCR. All pathogens were successfully detected from wastewater. Rotavirus was highly positive in both camps (97%) and municipality (100%), and *Salmonella typhi* was less positive in both camps (5%) and municipality (18%). SARS-CoV-2 is more positive in the camps (68%) than in the municipality (31%), whereas *Vibrio cholerae* is more positive in the municipality (51%) than in the camps (29%). SARS-CoV-2 (96% to 36%) and Vibrio cholerae (57% to 20%) showed a decreasing pattern in positivity from October 2022 to February 2023, but the other two pathogens didn't follow any monthly pattern. Environmental surveillance could be a useful tool for tracking SARS-CoV-2, enteric pathogens.

Keywords: Environment, surveillance, humanitarian, sanitation, pathogen

Abstract number: 11234

Environmental surveillance for SARS-CoV-2 and enteric pathogen in megacity Dhaka

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The megacity Dhaka, faces considerable challenges with sanitation management. 80% of neighborhoods in Dhaka are without sewerage network coverage and 97% of the fecal waste of the city enters the environment that discharge directly or indirectly into open drains. Environmental surveillance to monitor trends in enteric pathogens and SARS-CoV-2 has not been tested at scale in Dhaka. The study is designed to develop a systematic sample site selection strategy for city-wide environmental surveillance and to monitor temporal and spatial trends in vaccine-preventable enteric pathogens (Group A Rotavirus, *Salmonella typhi,* and *Vibrio cholerae)* and SARS-CoV2 through analyses of environmental samples.

The research team conducted stakeholder's meetings, scoping visits and transect walks in different wards and used GIS tools to predict the movement of wastewater. The team modelled micro-watersheds and estimate catchment areas and populations to identify strategic sampling Points. Concentration, detection, and quantification of selected pathogens were performed by Multiplex qPCR assays. We collected samples from 16 October 2022 to 8 February 2023 on 7 sampling points from Dhaka North City Corporation (DNCC) and 4 points from secondary pumping stations under Dhaka Water and Sewerage Authority (DWASA).

A total of 180 wastewater samples (119 from Dhaka North City Corporation and 61 from pumping stations) were collected. All pathogens were successfully detected from wastewater. 96% of rotavirus samples were found positive in all sampling points in Dhaka. The sample positivity rate in Dhaka for *V. Cholerae* (56%), SARS-CoV-2 (54%), and *Salmonella typhi* (43%). Rotavirus was highly positive in both DNCC (98%) and pumping stations (90%), and *Salmonella typhi* was less positive 58% and 13% in both areas. SARS-CoV-2 and *V. cholerae* are more positive in the DNCC (61% and 69%) than in the pumping stations (41% and 31%). SARS-CoV-2 (96% to 36%) and Vibrio cholerae (57% to 20%) showed a decreasing pattern in positivity from October 2022 to February 2023, but the other two pathogens didn't follow any monthly pattern. Environmental surveillance could be a useful tool for tracking SARS-CoV-2, enteric pathogens and other emerging diseases and may possibly provide temporal and spatial trends to support rapid response for public health measures.

Keywords: Environment, surveillance, monitor, sanitation, pathogen

Abstract number: 11112

Diversity and characterization of coronaviruses in rodents and shrews, Bangladesh

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Background: Rodents are the most diverse mammalian order, along with shrews, have frequent direct and indirect contact with humans. These species are important hosts of many viruses affecting both human and animals. The current pandemic COVID-19 have sparked to explore the coronaviruses (CoVs) circulating in wildlife. Hence, the study sought to detect and characterize the known and unknown CoVs in rodents and shrews in Bangladesh.

Methods: We collected and tested oral and rectal samples from rodents and shrews twice a year, winter and summer, from 5 sites in Bangladesh from 2015-2018, using consensus PCR for CoVs and confirmed by sequencing of positive samples. We performed DNA barcoding to confirm host species.

Results: Twenty-three rodents (2.13%; n=1075) and seven shrews (3.09%; n=226) were positive for CoVs. Three CoV strains where one strain of *Alphacoronavirus* and two strains of genus *Betacoronavirus,* were identified. Wencheng Sm shrew coronavirus (WSSC; AlphaCoV) was detected in *Suncus murinus* (n=6). Longquan Aa mouse coronavirus (LAMV; BetaCoV) was detected in *Bandicota bengalensis* (n=2) and *Suncus murinus* (n=1). Murine coronavirus (MC; BetaCoV) was detected in *Bandicota bengalensis* (n=1), *Bandicota cf. indica* (n=1), *Bandicota sp*. (n=1), *Mus musculus* (n=2), *Rattus rattus* (n=14), *Rattus tanezumi* (n=1) and *Rattus cf. tanezumi* (n=1). Overall, highest CoV prevalence was found in rats belonging to the species *Rattus rattus* (3.9%) and in samples collected in the dry season (2.6%) and from Dinaipur district (4%). We did not detect any novel CoVs including SARS CoV-2 related virus in our study samples.

Conclusions: The study findings advance our fundamental understanding of CoVs in rodents and shrews and suggest that rodents and shrews may carry additional unrecognized CoVs in Bangladesh.

Keywords: Coronavirus, Rodents, Shrews, Bangladesh

Abstract number: 11113

Epidemiology and genetic diversity of coronaviruses in Bats, Bangladesh

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Background: Bats are considered the natural progenitors for mammalian coronaviruses. Both severe acute respiratory syndrome (SARS) and the Middle East respiratory syndrome (MERS) CoV have been associated with bat hosts and cause human morbidity and mortality. The WHO includes SARS and related coronaviruses among its top threats to global health. Here we report on coronaviruses (CoV) detected in bats in Bangladesh in the pre-pandemic period of COVID-19.

Methods: We collected oral and rectal samples and blood from fruit (n=1056) and insectivorous bats (n=493) twice a year (winter and summer) from eight districts in Bangladesh from 2016 to 2019. We tested swab samples using consensus PCR targeting the RdRp gene to screen a total of 3098 samples from 18 different species of the bat. Bat species were confirmed with both morphometric measurements and genetic barcoding.

Results: Overall, 4.6% (n=69; 95% CI: 3.6-5.8) bats were positive for CoV, among which 1.7% were fruit bats (n=17) and 10.7% (n=52) were insectivorous bats. *Tylonycteris pachypus* (20.7%) and *Megaderma lyra* (15.8%) were most frequently positive for CoV. The presence of CoVs was associated with the season, body conditions, bat type, feeding habit, landscape, and interfaces ($p<0.001$). Insectivorous bats were 4.6 (95% CI: 2.7-7.8) times more likely to harbor CoVs than fruit bats. We identified 10 CoV strains from 96 samples of eight bat species. Of these, five were alpha (α)-CoVs, and five were beta (β)-CoVs. Four α-CoVs and three β-CoVs were novel in nature. Both known alpha and beta coronavirus are closely related to bat coronaviruses from southeast Asia and Africa, suggesting that co-circulation of coronaviruses is common in multiple bat species with overlapping geographical distributions. Phylogenetic analysis revealed that novel β-CoVs, detected in *Tylonycteris pachypus*, are genetically related to a known human pathogen-MERS CoVs and therefore warrant further investigation.

Conclusion: This study demonstrates that diverse coronaviruses, including MERS-related β-CoVs, are present in various bat species in Bangladesh. We recommend One Health surveillance at human-animal interfaces to detect novel coronaviruses before emerging to humans and to prevent future epidemics and pandemics by Disease X.

Keywords: Surveillance, bat coronavirus, Novel, Diversity, interface

Open Paper Session 4(a)
EID, Vaccines and NCD (human health)

Abstract number: 11016

Study design and operation for evaluating Nipah virus vaccine candidates among backyard pigs of indigenous communities in Bangladesh

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Background: Nipah virus (NiV) causes a severe and often fatal neurological disease in humans. Although only bats were identified to cause NiV outbreaks in Bangladesh, direct pig-to-human transmission of NiV was responsible for outbreaks in Malaysia and Singapore during 1998-99. Despite the threat, both in animals and humans, no licensed vaccines are currently available. To address this gap, we aim to evaluate the immunogenicity of three NiV vaccine candidates in pigs under field conditions in Bangladesh.

Methods: From January-August 2021, we enrolled 7 indigenous communities/villages and carried out community mobilization and engagement activities through interactive discussions. Subsequently, we sampled blood from 60 randomly selected pigs and examined the presence of NiV G and F specific antibodies by ELISA. The NiV antibody-negative 45 pigs were immunized with three NiV vaccine candidates: (1) an adjuvanted NiV sG protein; (2) NiV G protein delivered by a replication-deficient simian adenoviral vector (ChAdOx1 NiV G); and (3) an adjuvanted, molecular clamp stabilized NiV F (mcsF) protein. We followed up the pigs for any adverse effects and collected blood samples on day 14, day 28 and day 42 to test both humoral and cellular immunogenicity.

Results: We identified that 63% (143/238) households raised pigs as free scavenging livestock in the selected villages. Among the 60 pigs that selected for NiV antibody testing, the mean and median age was 6 months; 16 were female. To analyze the ELISA test positivity for NiV antibodies, we used a standard arbitrary threshold of 4 x the OD of the negative sera. We did not detect any NiV G or F reactive responses in the enrolled pigs. No adverse effects were observed among immunized pigs. Collected blood samples in different time points were stored at icddr,b biorepository for future laboratory investigation to determine T cell IFN-γ responses, NiV-neutralizing antibody (nAb) titers, and NiV antigen-specific Ab ELISA titers.

Conclusion: The absence of antibodies against NiV G/F in pigs should be interpreted cautiously due to the relatively small sample size and single-location investigation. The impending findings of this study will provide a platform and strategy for developing NiV vaccine(s) not only for animals but also for humans.

Key words: Nipah virus vaccines, antibodies, pigs, Bangladesh

Abstract number: 11109

Understanding the zoonotic diseases risk spillover risk through wildlife hunting in Bangladesh

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Introduction: Emerging infectious diseases (EIDs) are a significant burden on global public health. Approximately 75% of emerging and reemerging diseases in humans are caused by zoonotic pathogens. Human behaviors and practices are key risk components for pathogen spillover, amplification, and the spread of zoonotic diseases. We conducted a qualitative study to understand the hunting behavior, wildlife consumption patterns, and the wildlife value chain structures and to assess the risk of zoonotic disease transmission in different communities of Bangladesh.

Methods: Participant observation (26 hours) and in-depth ethnographic interviews (50) were conducted from July 2018 to March 2019 in three districts - Rajbari, Faridpur, and Dinajpur in Bangladesh. Interview data were coded using computational data analysis software (MAXQDA), and emergent themes were identified using a grounded theory approach.

Results: Hunting wild animals are found as a traditional practice, key protein source, ethnomedicine, alternative livelihood, and pest control in studied areas. Most hunters are male, where women were primarily involved in butchering. Sometimes children handled and played with hunted animals. Hunters are mostly illiterate and unaware of maintaining hygiene and have limited knowledge of zoonotic disease risk. Prepare the bushmeat in the yard or beside the kitchen, and improper waste disposal poses a greater health risk. Hunters primarily sell bushmeat within the neighboring indigenous communities. Moreover, communities with religious prohibitions against hunting were reported to be involved in hunting and consumption of wild animals as well. Additionally, several people said that bat meat and bones cure asthma and joint pain, consistent with their traditional beliefs. Hunters reported declining local wild animal populations due to over-hunting and ecological changes. A shared human and animal dependence on limited natural resources amplified biodiversity declines; however, thriving communities need sustainable alternative livelihoods solutions and protein sources.

Conclusion: Unprotected hunting practices and limited hygienic measures can yield a greater risk of zoonotic disease spillover. The scarcity of disease transmission knowledge posed by wildlife may facilitate zoonotic spillover. Targeted one health education, training, and behavior change interventions should be developed to reduce zoonotic spillover by mitigating the risks associated with human-animal interactions at high-risk interfaces in Bangladesh.

Keywords: Wildlife, Hunting, Interface, Spillover, Conservation

Abstract number: 11111

Genetic characterization of dengue virus subtype diversity in Bangladesh

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Introduction: Dengue fever is a mosquito-borne viral disease that has been one of the major causes of morbidity and mortality in tropical and subtropical regions in the last few decades. Bangladesh has been suffering from dengue outbreaks nearly annually since 2000. Understanding the spread and virulence patterns of the dengue virus (DENV) and identifying the strains responsible for epidemic outbreaks requires the accurate identification of genetic variations. DENV genotypes in Bangladesh were demonstrated in this study, focusing on molecular epidemiology.

Methods: We tested oral, rectal swabs, and blood samples from 862 individuals from three communities and one tertiary hospital from October 2017 to January 2019 using consensus PCR targeting NS5 gene for DENV. Positive PCR products were confirmed by sequencing. To understand the genomic characteristics and diversity of DENV, we analyzed 228 DENV sequences, and their metadata from July 2000 to October 2019 of Bangladesh extracted from NCBI Dengue Virus Database. Phylogenetic analysis has been employed using the maximum likelihood tree method to understand the genetic evolution and diversity of DENV subtypes.

Results: In DENV diversity, we found prevalence of serotype 1, 2, and 3 were 10.09%, 57.46%, 32.46% respectively. DENV serotype 1 occurrence was more common in summer (66.67%) and serotype 2 in monsoon (56.57%) and winter season (70.37%). The highest prevalence of DENV was found in Dhaka (94%). DENV 3 was commonly a circulating strain over the time period, although serotype 1 and 2 have a high rise pf prevalence in 2017-2019. Phylogenetic analysis suggests that Bangladeshi DENV type 2 have a close evolutionary relatedness with one another and a more distant genetic relationship with any of the three clades of DENV2 circulating in other Asian countries. In the context of DENV3, strains from Bangladesh cluster with China, Singapore, and Sri Lanka, but not with DENV3 strains from the rest of South Asia.

Conclusion: Findings from this study provide fresh insights into the genetic evolution of DENV subtypes and emphasize the importance of continuous DENV case management and vector control surveillance to prevent DENV epidemics in Bangladesh.

Keywords: Epidemiology, Molecular characterization, Dengue virus, Bangladesh

Abstract number: 11108

Genetic diversity of Coronaviruses in Human in pre-pandemic period at the high-risk human-animal interface in Bangladesh

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Introduction: Coronavirus (CoV) has caused three epidemics and pandemics in the past decades, resulting in a substantial impact on human and animal health and the global economy. This study aimed to screen pre-pandemic human samples to detect and molecularly characterize known and novel coronaviruses in humans at high-risk animal-human interfaces in Bangladesh.

Methods: The study was conducted as a part of One Health biological-behavioral surveillance prior to the COVID-19 pandemic period. We interviewed 862 participants from three district communities and one tertiary hospital from 2017 to 2019. Participants having symptoms with Influenza-like illness (ILI), Severe Acute Respiratory Illness (SARI), or fever of unknown origin (FUO), and participants having exposure with domestic and wild animals, were included. Survey data were used to characterize behavioral risk factors associated with virus spillover and collected biological specimens twice (dry and wet season). We tested samples using consensus PCR targeting RNA-Dependent RNA Polymerase (RDRP) gene. Positive PCR products were confirmed by sequencing.

Results: Overall CoV were positive in 13 (95% CI: 0.8-2.5) participants; 7 CoV-OC43, 4 CoV-HKU1, and 1 CoV-222E were detected. We detected 3 CoV in respondents having influenza-like illness (n=372), 4 in fever of unknown origin (n=103), and 6 in apparently healthy participants (n=295). Detecting CoVs was not associated with the age or gender of the participants; however, virus detection was associated with samples collected in the dry season (p= <0.001). The study revealed that HCoV-OC43 was circulated in diverse locations, whereas HCoV-229E and HCoV-HKU1 were detected in Madaripur and Dhaka, respectively. Phylogenetic analysis demonstrated that HCoV-229E was closely similar to CoV strains detected in China, HCoV-HKU1 in the USA and Thailand, and HCoV-OC43 in France and China. However, we did not find any novel coronavirus, including the SARS-CoV-related virus, in the pre-pandemic studied samples.

Conclusion: This study demonstrates the diverse strains of CoVs are circulating in pre-pandemic studied samples. Our research reports the molecular characterization of human CoV strains in Bangladesh. Moreover, a One Health approach coronavirus surveillance is recommended to better understand the CoV viral diversity and serological assays to determine the spillover events at human-animal interfaces in Bangladesh.

Keywords: Epidemiology, Molecular characterization, Coronavirus, Interface, Diversity

Abstract number: 11284

Patterns of date palm sap harvesting and trading practices and risk of Nipah virus spillover from bats to humans in Bangladesh

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Introduction: Bangladesh has been experiencing a nearly annual Nipah virus (NiV) outbreak through drinking contaminated raw or fermented date palm sap (RDPS) with bat excreta since 2001. RDPS harvesting practices and trading patterns have not been explored extensively. Hence, we conducted a study to understand RDPS collection, consumption, and selling practices and the risk of NiV spillover at the community level.

Methods: We performed an explorative qualitative study in two NiV outbreak districts, Rajbari and Naogaon, between 2021 and 2022. We recorded participant observations (n=14) and conducted ethnographic interviews (n=31) with RDPS collectors (Gacchi) on collecting and selling practices and using the diversity of protective apparatus. The interview data were analysed using coding and thematic analysis based on the grounded theory approach.

Results: Gachi prefers selling RDPS more than making molasses due to time consumption, fuel costs of preparing it, and the high demand for consuming RDPS. They informed RDPS that selling is not limited to their local community, and sale distends the location of non-harvesting areas based on customer demand through a middleman, which increases the transmission risk of NiV and other bat-borne diseases in more expansive geographical areas. We observed, and participants reported that Pteropus and non-Pteropus bats and rodents visited the trees and drank RDPS. They are replacing clay pots with discarded plastic pots, due to the free cost. They also prefer to use non-conventional protective apparatuses like jute bags, plastic bags, and nylon nets due to the time and resources to prepare bamboo skirts. Moreover, they reported that bats scratched out bamboo skirts and trunks to lick sap.

Conclusion: We recommend adopting a culture-sensitive intervention, including efficacy tests of bat access protection on several apparatuses with economic outcomes of the date palm sap harvesting practices to prevent spillover of NiV and other bat-borne emerging viruses in Bangladesh.

Key words: date palm sap harvesting, date palm sap trading, protective apparatus, Nipah virus, Bangladesh

Abstract number: 11063

Chemokine Receptor-5 (CCR5): A new hope in the immunoregulation of human-Rhinovirus exacerbated neutrophilic asthma pathogenesis

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Introduction: Human Rhinovirus (hRV) is the most common cause (nearly 80%) of virus induced asthma exacerbation characterized by clinical and pathophysiological heterogeneity, bronchoconstriction, goblet cells metaplasia, influx of neutrophils and ultimate poor prognosis. Steroid-sensitive, Th2 type-eosinophilic asthma has been somewhat studied, but the non-classical hRV-induced neutrophilic asthma exacerbation is poorly understood.

Methods: We have used a chicken ovalbumin-based model of wild-type (C57BL6) and CCR5 knock-down mice to develop canonical asthma immune response (Th2). Then the pathogenesis was exacerbated through i/n infection with human rhinovirus (hRV-1B) to develop the human neutrophilic prototype (non-Th2) in mice airways.

Results: The CCR5 knock-down mice represented a more exacerbated neutrophilic asthmatic response following hRV-1B exposure than wild-type. CCR5-deficient mice showed enhanced mucus expression and altered expression of tight junction proteins with the influx of CD45+CD11b+Siglec-F+Gr-1+ neutrophils and enhanced production of IL-17A, IFN-γ, IL-6, IL-1β cytokines in inflamed airway parenchyma. More interestingly, the lack of CCR5 altered the equilibrium of CD4+FoxP3+ Tregs and IL-17+CD4+ Th17 in inflamed tissues. CCR5-deficient mice showed increased frequency and the absolute number of IL-17-producing CD4+ Th17 cells in lung tissues compared to wild-type mice, whereas the reduced infiltration of CD4+FoxP3+ Treg cells was observed. Compared to BL/6 mice, CCR5 deficiency resulted in the skewed production of Th17 and Th1 cytokines in lymph nodes and lungs upon OVA stimulation. Likewise, CCR5-deficient mice showed enhanced expression of Th17-inducing cytokines (IL-1β, IL-6, and TNF-α) in lung tissues.

Conclusion: These results imply that CCR5 regulates neutrophilic (Th17) airway inflammation with the characteristic transition to Th2 responses during asthma exacerbation. Our results suggest that CCR5 attenuates neutrophilic airway inflammation and convert to eosinophilic response through conserving the equilibrium of CD4+Foxp3+ Treg cells and IL-17+CD4+ Th17 cells in hRV-induced asthma exacerbation. This is the first-time report to ensure the underlying mechanism of transition of Th17 to Th2 asthmatic response to the best of our knowledge. And thus, our findings will be a new hope in treating most deadly non-Th2 asthmatic patients.

Keywords: Human rhinovirus, exacerbated asthma, Th2/Th17 immune response, CCR5

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EID and Vaccines (animal health)

Abstract number: 11013

Diversity of Myxovirus resistance gene (Mx) and its relation with avian influenza infection in indigenous chicken

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Introduction: Highly pathogenic avian influenza virus (HPAIV) is a serious threat for animal and human health. Since first outbreak in 2007, limited number of HPAI outbreak was reported from indigenous chicken and duck. It is hypothesized that there might some host factors contributing in the lower occurrences of HPAI. Presence of Myxovirus resistant gene (Mx) may be one of the host factors. It is reported that Mx gene codes for Mx protein confers resistant activity to Orthomyxovirus infection. Therefore, the study was designed to investigate the diversity of Mx gene and its relation with AIV infection.

Methods: A total of 1536 samples (blood, sera and cloacal swabs, each 512) were examined from different types of non-vaccinated indigenous and vaccinated commercial chickens. Mx gene and its diversity were determined by PCR-RFLP, anti-AIV antibody was detected by indirect ELISA and AIV was tested by isolation in chicken embryo followed by haemagglutination and RT-PCR. Relationship was indirectly determined by General linear model (GLM) procedure of SAS 9.1.0 software (SAS Institute Inc., Cary, NC).

Results: Three genotypes of Mx gene viz., AA (resistant), GG (sensitive) and AG (heterozygous) were detected. AA genotype (0.48) was found to dominate over GG (0.19) and AG (0.33) genotypes. Largely, AA genotype was found higher in indigenous chicken than in commercial chicken. Anti-AIV antibody was detected in 44.92% samples. However, it varies 27.37-67.65% in indigenous chicken and 26.00-87.50% in commercial chicken. On the other hand, a total of 17 haemagglutinating viruses were isolated and only 0.39% (2/512) was AIV subtyped as H1N1. Others were confirmed as NDV. Anti-AIV antibody was detected in 40.16, 65.98 and 39.77% of chicken having resistant, sensitive and heterozygous genotype, respectively and associated significantly ($p<0.001$). Although AIV isolation rate was low but antibody prevalence was found high indicate exposure to virus with resultant sero-conversion. Detection of anti-AIV antibody in chicken with resistant type Mx genotype might indicate that the resistant genotype could not stop virus infection.

Conclusion: Resistant genotype of Mx gene may not protect chickens from AIV infection. However, challenge experiment is essential to ascertain the role of Mx gene.

Keywords: Myxovirus resistance gene (Mx), Mx gene diversity, avian influenza virus, indigenous chicken

Abstract number: 11007

Occurrence, genetic diversity and zoonotic potential of *Enterocytozoon bieneusi* in children and calves in Bangladesh

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Introduction: *Enterocytozoon bieneusi* is a widespread microsporidian species that causes gastrointestinal disorders in humans and domestic animals, including cattle, and poses a public health risk. The purpose of this study was to determine the prevalence, genotypic diversity, and zoonotic potential of *E. bieneusi* in children and calves in Bangladesh.

Methods: A total of 998 fecal samples were collected from children (n=299) and calves (n=699) and examined by nested PCR and sequencing of the ribosomal internal transcribed spacer (ITS).

Results and Conclusion: The overall prevalence of *E. bieneusi* infection was 6.4% in children and 7.9% in calves. ITS sequence analysis of 74 isolates revealed ten genotypes, including eight known genotypes (A, D, Type IV, PigEBITS7, I, J, BEB4 and BEB6) and two new genotypes (BANEB1 and BANEB3). Specifically, genotypes A, D, Type IV, PigEBITS7, BANEB1 and BANEB3, and genotypes D, PigEBITS7, I, J, BEB4 and BEB6 were detected in children and calves, respectively. Among them, genotypes D and I were dominant genotypes in children and calves, respectively. The genotypes D and PigEBITS7 were found in both children and calves, with PigEBITS7 being observed for the first time in calves. In phylogenetic analysis, six genotypes (A, D, Type IV, PigEBITS7, BANEB1 and BANEB3), detected in 39.2% of the isolates belonged to zoonotic Group 1. The remaining four genotypes I, J, BEB4, and BEB6 were clustered in Group 2 and are common members of the group with zoonotic potential. To the best of our knowledge, this study provides the first report of *E. bieneusi* infection in calves in Bangladesh and also the first molecular characterization of the parasite in children and calves in this country. Two new genotypes in children have been found, which is noteworthy. Furthermore, the presence of zoonotic genotypes indicates that cattle may serve as reservoirs for *E. bieneusi*, which can be a source of human microsporidiosis.

Keywords: *Enterocytozoon bieneusi*, molecular characterization, prevalence, genetic composition, zoonotic potential

Abstract number: 11091

Zoonotic Pathogens in Poultry Production in Bangladesh

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Background and objectives: Zoonotic diseases pose a significant threat to human and animal health. Pathogens such as Avian influenza Virus (AIV), *Campylobacter* species, *Escherichia coli* and non-typhoidal *Salmonella* (NTS) can be common in poultry populations and challenge human as well as poultry health. The objective of this cross-sectional study is to assess the occurrence of these pathogens in at the source of origin, i.e., the farm, and at the terminal source of major trading, i.e. the live bird market (LBM) levels as a prelude to genetics-led studies of pathogen flow and human exposure.

Methods: Chickens were sampled from selected farms and LBMs in Dhaka, Chattogram, Cumilla, Bogura, Jessore, and Joypurhat from September to November 2021. LBMs were selected randomly, and for each LBM, two credit-dependent farms raising Exotic broiler and Sonali (a cross bred of Fayoumi (Hen) and Rhode Island Red (RIR) (Cock) and located in the LBM's catchment area were selected based on link tracing. Oropharyngeal and cloacal swabs were collected into viral transport medium for AIV detection by real-time reverse-transcription polymerase chain reaction (rRT-PCR) targeting the M-gene. Caecal and rectal swabs were collected into Preston and brain-heart infusion broths for subsequent selective culture of *Campylobacter* species and *E. coli*, respectively. Feaces and litter materials were collected as pooled environmental samples for selective culture of NTS. Standard virological and bacteriological techniques was applied to detect and confirm pathogen identity.

Results: Fifty LBMs are planned to be sampled for exotic broiler, Sonali and Deshi chickens, accompanied by 50 exotic broiler and 50 Sonali farms. In total 525 of 2610 birds were found to be rRT-PCR positive for the AIV M-gene, 521 of which derived from LBMs (99.23%). A total of 150 caecal samples were found to contain *Campylobacter* species from a sample set of 755 (19.86) among which 114 were *C. coli*. Only two *C. jejuni* was detected. Additionally, we cultured extended spectrum beta-lactamase (ESBL) producing *E. coli* from 224 caecal samples. *Escherichia coli* and NTS were cultured from 157 rectal and 20 environmental samples from 172 sampled locations, revealing a prevalence of 91.2% and 11.63% respectively.

Conclusion: Preliminary results of pathogen detection are presented here from the GCRF program of the UKRI, One Health Poultry Hub, shows that poultry-borne pathogens AIV, *Campylobacter* and *Salmonella* could enter the food-chain if the sources are not identified and proper control strategy is designed based on research-based evidence to nullify them at the source of origin and dissemination. It is a prelude to more detailed genetic analysis of pathogen occurrence and flow through poultry production and distribution networks (PDNs).

Keywords: Avian influenza, Campylobacter, E. coli, Non-typhoidal salmonella, Zoonosis

Abstract number: 11017

MPB83, ArfA, DnaK, GrpE, and LpqH protein to design a subunit vaccine against bovine tuberculosis

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Introduction: Tuberculosis is a persistent contagious zoonotic illness that imposes significant economic losses in the livestock sector annually. Worries about the spread of disease and the subsequent economic slump have increased in recent years due to many outbreaks of animal diseases. Combating TB requires developing a vaccine that specifically targets the disease-causing proteins. Therefore, the present research's goal was to anticipate a new vaccine against *Mycobacterium bovis* concurrently targeting five crucial proteins of the organism by Reverse vaccinology.

Methods: Several immunoinformatic tools were used in this study to develop an effective vaccine candidate against bovine tuberculosis. The proteins were utilized to generate a large number of immunostimulatory epitopes (T and B cells), from which the best epitopes for vaccine production were selected based on their antigenicity, allergenicity, conservancy, and toxicity. Three vaccine candidates (MBV1, MBV2, and MBV3) were designed utilizing top epitopes and boosted with an adjuvant, PADRE, and linkers. Numerous characteristics of the vaccines were examined to determine which one was the greatest match for the research. The best vaccine construction was selected for further research based on the validation score of the three originally produced vaccines' 3D structures.

Results: The best candidate, MBV3, had 88.7% of amino acids in the most Favorable regions of the Ramachandran plot, indicating the better quality of the vaccine. In disulfide engineering, MBV3 had the capability of forming 9 pairs of disulfide bonds. Docking study of MBV3 with BoLA-A11 showed lower global energy. According to the molecular dynamic simulation, the complex had a relatively high eigenvalue 2.318704e-06, indicating a lower chance of deformability. The *in silico* immune simulation study confirmed the immune cell response against antigen clearance rate. Following vaccination, high levels of IgM production indicated a primary response. In the codon adaptation study, the relative adaptiveness and GC content were quite high.

Conclusion: Since the results of the studies were quite promising, we may assume that it can be used to prevent tuberculosis. However, wet-lab experiments employing model animals to validate the proposed vaccine molecule may be accomplished (in vivo and in vitro).

Keywords: Zoonotic illness, Tuberculosis, Reverse vaccinology

Abstract number: 11100

An integrated approach to develop anthrax-free model area in Bangladesh

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Introduction: Repeated anthrax outbreaks occur in some areas of Bangladesh. The objective of this study was to establish an anthrax-free model area where there would be no anthrax in an anthrax-prone area of Bangladesh.

Methods: The location of the work was Jamtoil village in Kamarkhanda Upazila of Sirajganj District, located between 24°18' and 24°27' north latitudes and between 89°35' and 89°42' east longitudes. Numerous interventions that included both social and laboratory work were implemented from 2017 to 2020. The integrated approach included regular vaccination, increased public awareness, rapid confirmation, and prompt disposal of carcasses, setting up an effective surveillance system, developing an emergency prevention system, enforcement of regulations, and enhancing collaboration between animal and human health departments.

Results: After rigorously implementing the study work, it showed that most community members (97.5%) were aware of the nature, occurrence, public health importance, and management of the disease. The risky habits and attitudes of the farmers toward the slaughtering of sick cattle were significantly reduced (<85%; $P < 0.001$). The vaccination coverage expanded from 40 to 85% (95% CI: 0.06-0.22), and the percentage of farmers who can presumptively diagnose anthrax by its notable clinical findings has increased from 30% to 85% (95% CI: 0.16-1.41). A PCR-based confirmation protocol was applied. Soil samples were collected to examine the pathogenic spores of Bacillus anthracis, and we developed a map so that the farmers in the area would be more cautious about grazing their cattle. A steering committee was formed with the administration, law enforcement agency, local government, livestock, health department, and political elites. This committee periodically reviewed the progress of research work. At the beginning of the investigation, the score of situations was 18, but after implementing research interventions, it increased to 100 out of 120. A slaughterhouse was set up in the region, and people slaughtered their animals after having them examined by qualified veterinarians. As a result of all these efforts, the model area has been free of anthrax infection for the last four years.

Conclusion: The integrated approach is an efficient, effective, and suitable method to establish an anthrax-free model area where there will be no anthrax outbreak

Keywords: One Health, Awareness, Integrated Extension Model, Community.

Abstract number: 11450R

Assessment of humoral immune response in cattle immunized with an inactivated alum adjuvant *Brucella abortus* biovar 3 vaccine

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Background: Brucellosis is a bacterial zoonotic disease caused by *Brucella abortus*. Globally more than 50,000 brucellosis cases have been reported in human. It causes a huge economic loss in cattle mainly due to abortion and infertility. There is a need to develop an effective brucella vaccine to control brucellosis. The present study was undertaken to determine humoral immune response in cattle vaccinated with alum adjuvant *Brucella abortus* biovar 3 vaccine.

Methodology: *Brucella abortus* biovar 3 (BAU21/S4023) was inactivated by 1% formalin. Alum (4%) was added in it as an adjuvant. A total of 80 cattle from on farms and house hold at Dhaka and Gazipur districts were vaccinated with experimentally developed inactivated *Brucella abortus* biovar 3 vaccine subcutaneously with 2 ml (3×10^8 CFU *Brucella abortus* biovar 3) per cattle. Booster vaccination was administered at 60 days after first vaccination. Sera from vaccinated cattle were collected at 0, 15, 30, 60, 90, 120, 150 and 180 days of post vaccination (dpv). *B. abortus* specific antibody titer was measured by rose Bengal plate test (RBPT) and Indirect ELISA.

Result: Seroconversion rate of vaccinated cattle was 0%, 100%, 100%, 83%, 100%, 100% 92% and 83% at 0, 15, 30, 60, 90, 120, 150 and 180 dpv respectively ($p<0.05$). The reciprocal RBPT antibody titer of sera of vaccinated cattle at 15 dpv were 15±2.21, at 30 dpv were 15±2.21, at 60 dpv were 10±3.77, at 90 dpv were 14±2.91, at 120 dpv were 15±2.21, at 150 dpv were 12±4.41 and at 180 dpv were 7±3.031($p<0.05$). The i-ELISA OD value of sera of vaccinated cattle were 0.235±0.002, 1.930±0.031, 1.968±0.263, 1.579±0.012, 2.955±0.374, 2.855±0.374, 2.555±0.374 and 1.755±0.374, at 0, 15, 30, 60, 90, 120, 150 and 180 dpv, respectively ($p<0.05$).

Conclusion: Data of this study suggested that inactivated alum adjuvant *B. abortus* vaccine induced a strong humoral antibody in vaccinated cattle and could be used for controlling bovine brucellosis in Bangladesh. if brucellosis is controlled in cattle human brucellosis could also be prevented under one health approach.

Keywords: Humoral immune response, Bovine brucellosis, Inactivated alum adjuvant Brucella abortus vaccine, Human brucellosis

ABSTRACTS

Open Papers (Poster Presentation)

Pandemic Preparedness, Containment and Mitigation

Poster No. 01 (Abstract No. 11116)

Perceptions of buffalo micro-entrepreneurs on health and environmental risk and safety measures

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Introduction: Health (human and animal) awareness is considered an important factor concerning creating pro-environmental awareness. Ensuring the safety, health, and overall well-being of animals raised for food is both an ethical obligation and a critical component of providing safe food products. Therefore, the survey was aimed to deepen the understanding of the perceptions of and their potential adaptation responses to existing constraints in terms of health, environment and safety situation etc.

Methods: The questionnaire-based survey was conducted during August-October, 2020, in which variables were collected from 103 micro-entrepreneurs engaged in buffalo rearing, production and marketing of buffalo's products in three Upazillas of Bhola districts. Micro-entrepreneurs (ME)'s perceptions of the effects Covid-19 as was considered as case study to manifest ME's performances in a sudden challenging situation. Chi-square (χ^2) test was performed to observe a significant difference in respondents' groups.

Results: Results show that an average of 39.21% and 50.22% of MEs focused on approaches regarding human health and animal health concerns, respectively. A small percentage of MEs reported that they provided emergency health care kits for workers (18.45%) and training to the workers about primary health care (20.39%). Average 53.01% MEs knew about the risks originated from the farm among which (35.92%) of MEs were concerned about antimicrobial resistance and farm environment affecting the living conditions of inhabitants. A few MEs knew to develop a biosecurity plan for the herd (22.33%). During the Covid-19 pandemic, though 98.06% of MEs were concerned about this pandemic, 31.07% of them provided safety materials to their workers. MEs had been facing difficulties like increased farm cost (61.17%), unable to sell milk (19.42%) and changing milk price (77.67%). Furthermore, 49.51% of MEs focused on possible remedial measures to be taken to address those problems and challenges in future to manage milk, such as preparation of milk products (ghee, butter, yoghurt) (27.45%, $P<0.01$), storage of milk (25.49%, $P<0.01$), awareness and pre-planning about risk (19.61%) and online marketing (5.88%).

Conclusion: MEs' unawareness of health and environmental management is a growing component of production risk within farming and understanding of farmers' concerns to these factors will help to design effective policies for supporting successful adaptation at the microenterprise level.

Keywords: Buffalo, Microenterprise, health and environmental risk

Poster No. 2 (Abstract No. 11120)

Factors that influence COVID-19 preventive behaviors in Bangladesh

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Introduction: USAID's Breakthrough Action project being implemented by Johns Hopkins CCP conducted a phone-based survey with the objectives: (1) Assess knowledge, perceptions, and practices related to COVID-19, (2) Assess recall of messages/programmatic content among intended audiences. The survey was implemented during February and March 2021.

Methods: Administered computer assisted telephone interviewing (CATI) survey in partnership with Geopoll. Sampling method was Random-Digit Dialing (RDD); supplemented by Geopoll phone number database to reach division, gender, and age quotas based on national demographics.

Results and conclusion: Perceived susceptibility to COVID-19 – 64% among the survey population. Factors that influence COVID-19 preventive behaviors includes: (1) Knowledge about COVID-19, (2) Think they might get infected, (3) Belief in effectiveness of the behaviors, (4) (Many) Neighbors do so, (5) Exposed to helpful, trusted sources of information.

Television is the most trusted source – 53.4%, 27.7 % through family and health workers as well as miking, 9.7% social media 8.2 % through print media and 31.1 % through other medias. Sources of information, trusted information sources, and self-report of key preventive behaviors varied by socio-demographic characteristics. Beyond socio-demographics, key factors associated with doing key COVID-19 preventive behaviors included - Perceived effectiveness of the behavior, social norms and exposure to information on COVID-19 (for specific behaviors such as mask wearing and social distancing).

Recommendations: Need to design audiences specific messaging for the better and effective Social and Behavior Change outcome. Besides, Social and Behavior change activities should focus on behavioral determinants to influence specific preventive behaviors.

Keywords: COVID-19, Preventive behavior, Behavioral change

Poster No. 3 (Abstract No. 11216)

Protozoal food vacuoles induce bacterial SOS response that controls integron-intergase and gene cassette recombination in Vibrio cholerae: A novel way of DNA movement

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Vibrio cholerae, the bacterial pathogen responsible for the diarrheal disease cholera, resides in the aquatic environment between outbreaks. For bacteria, genetic variation by lateral gene transfer (LGT) is important for survival, adaptation and resistance to diverse stresses. In the aquatic environment, *V. cholerae* is predominantly found in biofilms associated with chitinous organisms or with chitin “rain”. Chitin induces competency in *V. cholerae*, which can lead to LGT. In the environment, *V. cholerae* is also subjected to predation pressure by protist. Here we investigated whether protozoal predation affected LGT using the integron as a model. Integrons facilitate the integration of mobile DNA (gene cassettes) into the bacterial chromosome. We report that protozoal predation enhances transformation of a gene cassette by as much as 405-fold. We show that oxidative radicals produced in the protozoal phagosome induces the universal SOS response, which in turn upregulates the integron-integrase, the recombinase that facilitates cassette integration. Additionally, we show that during predation, *V. cholerae* requires the type VI secretion system to acquire the gene cassette from *Escherichia coli*. These results show that protozoal predation enhances LGT thus producing genetic variants that may have increased capacity to survive against stresses in the environment. Additionally, the conditions in the food vacuole may make it a “hot spot” for LGT by accumulating diverse bacteria and inducing the SOS response helping drive genetic diversification and evolution.

Keywords: *V. cholerae*, Integron, LGT, Evolution and Adaptation

Poster No. 4 (Abstract No. 11231)

Attitude and interest of dental patients towards teledentistry services for oral healthcare management in COVID-19 pandemic

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Background and Objective: Oral and dental health are considered as the integral part of general health but it is regularly ignored in healthcare delivery system. Due to Covid-19 pandemic the condition is more critical as there is chance of spreading corona virus by dental procedures. Many countries of the world are practicing Teledentistry (smart phone based digital platform) services which could be play an important role for oral healthcare management in Bangladesh. So the main aim of this study was to assess attitude & interest of dental patients towards Teledentistry services for oral healthcare management in COVID-19 Pandemic.

Methodology: This cross-sectional study was conducted from May 2020 to October 2020 using a pretested semi structured questionnaire for the dental patients. An online questionnaire was sent to 300 participants of both rural and urban people of Bangladesh and 206 responded. The response rate was 68%. The analysis was done by using IBM SPSS-20 and was presented by frequencies, percentages, charts & diagrams.

Results: Findings of this study showed that, 92.7% dental patients were highly interested about Teledentistry for using in future if available in our country. Majority of them were worried (79.60%) of visiting dentist due to COVID-19 pandemic and more than 90% of the participants felt need of Teledentistry like platform during COVID-19 pandemic. In this study, about 55% dental patients previously consulted with dentist by mobile conversation, video call, facebook/ whatsApp/ messenger and 94.2% of them found the conversation beneficial. Our study findings showed that 81.6% participants were agreed that Teledentistry will improve the access to oral health care services in Bangladesh. All socio-demographic groups in respect of their gender, age, education, residence and occupation were interested to Teledentistry for oral health care management purposes ($p>0.05$).

Conclusion: The findings of this study will help in future development of smart phone based Teledentistry platform in Bangladesh which will be highly beneficial for any kind of COVID-19 Pandemic situation

Keywords: Teledentistry, smart tools, oral healthcare management, attitude & interest, dentist, dental patient

Poster No. 5 (Abstract No. 11263)

Knowledge, perception and practices of teledentistry among the dentists during COVID-19 pandemic

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Background: Virtual dentistry practices, when implemented correctly, reduce the burden on healthcare systems by preventing COVID-19 and asymptomatic carriers from infecting healthcare professionals and high-risk employees.

Methods: A descriptive cross-sectional study was conducted among 218 dentists through a semi-structured questionnaire to evaluate the state of teledentistry practices among 6 dental college and hospitals in Dhaka City.

Results: Most of the dentists (87.2%) mentioned that teledentistry practice increased during COVID-19 pandemic and it can reduce spread of infection. Majorities recommended teledentistry is a good tool for oral hygiene instruction (72.5%) but couldn’t provide accurate diagnosis (73.9%). One fourth of the respondents (26.1%) prescribed medicine virtually and others prefer providing health education and counseling only. There are some barriers during practicing teledentistry such as poor audio or audio-video quality, expensive set-up, accurate diagnosis provision and difficulty to use software.

Conclusion: Teledentistry isn't intended to replace traditional methods of treatment that involve patient examination, but rather to provide a new way to practice healthcare. Dentists should be encouraged to practice virtual health education tool which may lower the cost burden, overcrowding and spread of COVID-19.

Keywords: Teledentistry, Practice, Effectiveness, Perception, COVID-19

Poster No. 6 (Abstract No. 11264)

Economic losses in small and medium-scale commercial poultry farming during COVID-19 pandemic in Bangladesh

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Background: The COVID-19 pandemic and the subsequent lockdown measures have had a substantial impact on numerous economic sectors including poultry production and trading in Bangladesh. The poultry farmers had to face difficulties to sell their birds due to transportation restrictions, sharp decline of demand and suffered significant losses due to reduction of price. Therefore, we intended to estimate the total economic losses in small and medium-scale commercial poultry farms during COVID-19 lockdown in Bangladesh.

Methods: We conducted a cross-sectional study in six districts surrounding the capital Dhaka from September to December 2021. We conducted interviews using a semi-structured questionnaire in 220 commercial broiler (78), Sonali (85) and layer (57) farms. We used stepwise regression to select the best model that can predict the average loss per farm due to COVID-19. We used average of reduced egg price, reduced bird price, and increased feed price of each farm to form a regression model and used average reduced egg price, reduced bird price, and increased feed price to predict average loss of a farm from the model. Then total number of the poultry farms is multiplied to get total national loss.

Results: We estimated the national loss in small and medium scale poultry sector during Covid-19 lockdown was 101.35 million USD whereas the model predicts the average economic loss for each commercial farm was found $1,447.8. Majority (90%) of the farmers suffered loss during lockdown period that they had to reduce the 25% of batches during COVID-19 pandemic period in comparison to pre-pandemic. Furthermore, 22.7% of farmers reported about change in their supply chair and trading practice while only 34.5% of them believe that they could overcome the loss.

Conclusion: The marginal and small-scale poultry sectors in Bangladesh was severely impacted by the COVID-19 pandemic and the subsequent lockdown, and many are still facing challenges in recuperating their financial losses. It is imperative that government should provide assistance to farmers so they can contribute protein supply and poverty alleviation to the community.

Keywords: Small and medium scale poultry farm, Covid-19 pandemic, Economic loss

Poster No. 7 (Abstract No. 11003)

Improvement of hand hygiene practices among the healthcare workers in a Neonatal Intensive Care Unit

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Background: Health-care workers' hands become progressively colonized by potential pathogens during their patient care and act as vehicle for transmission of microorganisms to the patients. Hand hygiene is undisputedly one of the most effective infection control measures.

Objective: The objective of this study was to measure the hand hygiene (HH) compliance among the doctors and nurses in a neonatal intensive care unit of a tertiary care setup before and after intervention.

Methodology: This quasi-experimental (before after intervention) study was conducted from July 2019 to July 2020 in the Department of Neonatology of Bangabandhu Sheikh Mujib Medical University (BSMMU). All the doctors and nurses working for more than three months in NICU (n=33) were enrolled in the study. They were observed for their compliance to HH over first six months. Then education sessions were conducted on WHO recommended HH practice over one month, reminders were attached at work stations regarding the practice and subsequently observed over next six months to measure the effect of the intervention over HH compliance.

Result: A total of 312 pre and 339 post intervention patient contacts were analyzed. The hand washing (HW), hand rubbing (HR) and missed HH opportunities were 27.9%, 36.2%, 35.9% and 17.4%, 74.6%, 8% in pre and post intervention period respectively. There was significant decrease in missing HH (p= .000) after the intervention. Compliance was significantly increased in both the case of high and low risk contacts by 42.9-84.9% (p=<.0001) and 43.1-81.8% (p=<.0001) respectively following intervention. A significant reduction in frequency of inadequate HH, 20.2-9.7% (p= .0001) HH was documented. A statistically significant improvement in compliance was observed in both the moment of before (from 42.9 to 83.8%, p= <.0001) and after (28.5 to 95.9%, p= <.0001) patient contact following the intervention among both the doctors and nurses separately. In logistic regression analysis, HCWs were found significantly more compliant to HH after intervention (aOR= 13.315, 95% CI: 7.248-24.458). Similarly, being physician (aOR= .012, 95% CI: .005-.030) and moments after patient contact (aOR= .114, 95% CI: .049-.261) were found significant positive predictors for compliance to HH.

Conclusion: Significant improvements in HH compliance was achieved through a systemic, multidimensional intervention approach among the doctors and nurses in an intensive newborn care setting.

Keywords: Healthcare associated Infection, Hand hygiene, Healthcare workers, Hand washing, Hand rubbing

One Health Institutionalization, Workforce and Policy

Poster No. 8 (Abstract No. 11069)

A stakeholder analysis of the poultry sector in Bangladesh

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Background and objectives: Given the size of its contribution to the national economy and the consistently high rates of growth, the poultry sector has become a leading industry in Bangladesh. However, many aspects of its functioning are still opaque. The sector is characterized by a high degree of organization and specialization involving a large number of actors at different stages of the production and distribution processes. We present preliminary findings from the first systematic attempt to map these actors and characterize them according to their institutional interest and influence.

Method: We used a multi-stage approach which included the analysis of policy literature to develop a long list of actors who might influence the poultry sector dynamics in Bangladesh. We refined the list of actors by conducting descriptive analysis to find blind spots in our coverage and interviewing senior poultry and public health scientists and policymakers to fill in the identified gaps. We used a semi-quantitative scoring method to assess levels of interest and influence for shortlisted actors and categorized them based on ownership, roles, sectors, and regulatory functions.

Results: We shortlisted 67 actors whose distribution would be indicative of the landscape of the poultry sector in Bangladesh. A majority (39%) of included actors belonged to the public and represented the private sector (30%). The rest were found as being affiliated with international agencies, NGOs, UN organizations, and the informal sector. According to the role and position, most of them had management position (43.3%) followed by financiers (22.4%), producers (11.9%), and others (4.5-7.5%). According to power/matrix analysis, the public sector scored the highest on being influential. And the private and non-govt sectors including some informal actors as well showed the maximum interest. But they were overlooked as they lack in terms of having legislative power and the ability to get involved with policy action. The inclusion of these less dominant actors in a single frame is much needed for the development of the poultry sector as they bear the interest thus are capable of contributing the most.

Conclusion: This study suggests that a balanced multisectoral collaboration is needed at the local level where those with the highest level of interest and willingness to work for the welfare of the poultry production cycle in Bangladesh should be brought together on board.

Keywords: Actors, policy, sector, interest, influence

Poster No. 9 (Abstract No. 11075)

The One Health Poultry Hub: A research platform for sustainable poultry production and, distribution with emphasis on reducing disease risks for humans and animals

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Background and objectives: The One Health Poultry Hub (OHPH) is a five-year research and impact-driven program funded by the UK Research and Innovation through the Global Challenges Research Fund. Launched in 2019, it comprises leading experts in zoonoses from 30 institutions across Asia, Australia, Europe and the UK. Taking a One Health approach, it explores how rapid expansion of poultry production creates conditions for zoonotic disease emergence and spill-over. OHPH works closely with stakeholders at all levels, from farmers and traders to those from government departments and the private sector, as it seeks to achieve sustainable poultry production and distribution with the aim of reducing disease risks for both animals and people.

Method: OHPH's work is organized into four programs: I) configurations of chicken production and distribution networks; ii) transmission and evolutionary dynamics of zoonotic health hazards along these networks; iii) flexible funding; and iv) maximizing impact.

Results: Despite COVID-19-associated interruptions, research activities have progressed well. Impact activities focus on: I) Influence policy; and ii) capacity building:

(i) The Impact, Communication and Engagement Strategy allows for six-monthly meetings of an intersectoral National Advisory Group comprising high-level experts representing animal and human health policy-makers and poultry producers. This facilitates: a) discussion of ongoing and future activities, and b) advice on planning, sustaining and expanding stakeholder engagement. Such ongoing high-level discussions and relationship-building set the pathway for evidence to inform policy. The team is currently contributing to the development of Bangladesh's 3rd National Avian and Pandemic Influenza Preparedness and Response Plan.

(ii) To date 26 online trainings live streamed to the OHPH Bangladesh Facebook page involving over 10k participants have been conducted for farmers, feed dealers, veterinarians, and veterinary students. They have covered poultry health (including principles of disease management and biosecurity), production and trading, with a focus on zoonotic diseases, antimicrobial use and resistance, and their public health relevance. Feedback about the sessions and provided material (handouts, manuals) is encouraging.

Conclusion: The impact-oriented evidence generated by OHPH is contributing to inclusive policy development and the promotion of enhanced management practices for safer, more sustainable and diverse poultry value chains in Bangladesh.

Keywords: One Health, poultry production, zoonoses, antimicrobial resistance, policy.

Poster No. 10 (Abstract No. 11103)

National bulletin of public health provides an opportunity for One Health Hub to disseminate the learnings and a larger communication framework

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One of the nine objectives of the strategic framework for the One Health approach to infectious diseases is to build networks and partnerships to foster collaboration among stakeholders at all levels of the health system. A second objective is to share information to enable health workers and communities to take action to protect their health. A national public health bulletin is the government's communication channel that provides a strategic foundation to successfully achieve both objectives of the One Health approach.

The *National Bulletin of Public Health, Bangladesh* (NBPH,B) is the first, open access, national, peer-reviewed public health bulletin published by the Government of Bangladesh. It is produced and disseminated by the Institute of Epidemiology, Disease Control and Research (IEDCR) with funding from Bloomberg Philanthropies Data for Health Initiative and technical support from the US Centers for Disease Control and Prevention and the-CDC Foundation USA. The goal of the NBPH,B is to transform knowledge from research to practice by disseminating widely important new findings rapidly to inform policy, update health professionals on best practices, and displace misinformation to enable the public to take action to protect their health. The NBPH,B is available in print and online at IEDCR webpage.

Since 2018, the NBPH,B produced and disseminated eight issues, including articles relevant to One Health. As it is written in plain language both in English and Bangla, it can reach to larger audience. Thus it serves as a "content provider." Journalists, health bloggers, teachers, and opinion leaders can adapt its reports for their audiences. It has also sponsored workshops to strengthen skills of young health professionals in scientific writing and communicating with the media. NBPH provides opportunities for new authors, recognition for public health workers at the peripheral, as well as the national levels, by publishing their work. The poster presentation will describe the governance structure, trainings, and standard operating procedures used to produce and disseminate quality scientific articles that are relevant and timely and support the One Health strategic framework.

Key Words: Public-Health, Bulletin, Communication, Collaboration, Data-Sharing.

Poster No. 11 (Abstract No. 11257)

Strengthening rabies diagnosis at the Field Disease Investigation Laboratories: A promising opportunity for rabies surveillance and control in Bangladesh

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Rabies is a fatal but preventable disease that remains neglected worldwide. Bangladesh has committed to eliminating rabies by 2030 through a comprehensive control program that includes mass dog vaccinations, dog birth control, and surveillance. Despite ongoing surveillance efforts in limited sub-districts through the Veterinary Public Health Service Strengthening and Protection Project, rabies samples are only being sent to and diagnosed at the Central Disease Investigation laboratory (CDIL). However, a significant challenge remains in the lack of rabies diagnostic capacity at Field Disease Investigation Laboratories (FDILs) across Bangladesh.

To address this challenge, the FDILs could develop competencies in rabies diagnosis by following the World Organization for Animal Health (WOAH) reference laboratory protocol. The protocol includes collecting brain samples using the occipital foramen approach and testing the samples using a lateral flow assay (LFA) test, direct fluorescent antibody (DFA) or rapid immunohistochemistry (dRIT) tests.

To strengthen rabies diagnosis at the local level, it is essential to provide necessary equipment, such as microscopes for the DFA technique or reagents for the dRIT technique. DFA and dRIT are costly and time consuming techniques. However, the LFA technique, with its low cost and high sensitivity (96%) and specificity (99%), presents a promising opportunity to be established in FDILs for rabies diagnosis. By using this technique, positive samples can be sent to the CDIL for confirmatory diagnosis, thus reducing their diagnostic burden after adopting the sample collection method. Bangladesh has 9 FDILs in different parts of Bangladesh, which can act as sentinel sites for diagnosis of rabies in animals.

The establishment of rabies diagnostic competencies at the local level is crucial for effective rabies surveillance and control in Bangladesh. By providing necessary equipment and training programs for veterinarians, the FDILs can adopt the WOAH reference laboratory protocol and establish LFA technique for rabies diagnosis. This will not only improve diagnostic capacity at the local level but also reduce the burden on the CDIL. With continued efforts towards mass dog vaccinations and birth control, as well as ongoing rabies surveillance and control programs, FDIL based surveillance might help Bangladesh achieving its goal of eliminating rabies by 2030.

Keywords: Rabies, FDILs, diagnostic techniques, surveillance, control

Poster No. 12 (Abstract No. 11018)

Assessment of genetic diversity and population structure of *Tenualosa ilisha* Bangladesh based on partial sequence of mitochondrial DNA Cytochrome b gene

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Introduction: *Tenualosa ilisha* is an important fish in the Indian Ocean regions and the most profitable fishery in Bangladesh. Hilsa is an anadromous fish showed the migration pattern for many factors like spawning, feeding, nursing and five major spawning grounds have been identified in Bay of Bengal. Genetic diversity parameters like selection effects, effective population size are associated with mtDNA studies. Mitochondrial DNA (mtDNA) is verified in resolving population structure of marine fishes.

Methods: Samples of *T. ilisha* were collected from Chandpur, Noakhali, Patuakhali and Cox's Bazar and *Hilsha kelee* (outgroup) from Bagerhat region of Bangladesh. Cytochrome b region of mtDNA were sequenced to investigate their genetic structures.

Results: A total of 270 polymorphic sites were found with 18 haplotypes. A network of these haplotypes was constructed along with molecular differentiation of *T. ilisha* and *H. kelee* by phylogenetic analysis. High genetic variability (0.902) and low nucleotide diversity (0.193) were found among the four populations. Analysis of molecular variance (AMOVA) showed significantly different population structure (Fst 0.031, $p<0.001$). Our study revealed a high genetic variability and distinct population structure in the *T. ilisha* populations. Moreover, the non-significant negative value of Tajima's D for all population and negative Fu (*FS*) value for Chandpur population suggested a recent population expansion of hilsa.

Conclusion: Our assessment on genetic structure of hilsa provides the information on high haplotype diversity of different populations of riverine (Chandpur), estuarine (Noakhali) and marine (Patuakhali and Cox's Bazar) sources. Hilsa populations have the trans boundary migration among different countries hence further research is also needed to investigate the level of population discrimination including samples from hilsa occurring countries or territories.

Keywords: Haplotype diversity, Genetic structure, Phylogenetic analysis

Poster No. 13 (Abstract No. 11023)

The origin and genetic diversity of Bangladeshi indigenous sheep: an updated perspective based on mitochondrial cytochrome oxidase subunit I Sequences

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Sheep is an important indigenous genetic resource in Bangladesh that have higher adaptability to fluctuating climate, poor nutrition and management system, resistance to local diseases and parasites and suitable for subsistence farming. The country possesses two types of sheep breed known as Native sheep and Garole. The history of domestication, genetic background and variability of the local sheep (Ovis aries) populations in Bangladesh remains largely unknown. Therefore, the aim of this study was to provide a characterization, possible origin and genetic relations within the Bangladeshi sheep breeds and to study their genetic connections with the global sheep breeds. A 632-bp fragment of mitochondrial COI region was sequenced in 54 sheep representing two populations; native sheep and garole. The 51 reference sequences representing different domestic sheep clades in Asia, Africa, America, Australia, Europe and Eurasian regions were included. Sequence polymorphism and maternal origin of two Bangladeshi populations were analyzed. Sequence analysis revealed 72 variable sites that defined 20 haplotypes. The haplotype and nucleotide diversity were 0.766 ± 0.040 and 0.013 ± 0.0025, respectively. Furthermore, ANOVA analysis revealed 94.12 % of the total genetic diversity was accounted for within population variation. The median network and phylogenetic analysis indicated that individuals from all Bangladeshi sheep populations were represented in the clade A, those maternal origins are presumed to be from Asian, more particularly India and China, European and Australian countries. These results inferred that Bangladeshi indigenous sheep still have abundant genetic diversity and have originated from multiple maternal lineages, and further conservation efforts are warranted to maintain the diversity.

Key words: Sheep, genetic sequence, Bangladesh

Poster No. 14 (Abstract No. 11059)

Poultry waste management practices in poultry farms in Bangladesh and environmental concern

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Introduction: In Bangladesh, the current condition of poultry waste production and management procedures in poultry breeder farms and trading is suboptimal, with numerous challenges. Effective waste management and utilization are essential to reduce environmental contamination and provide economic benefits from the poultry wastes.

Methods: Commercial and Breeder farms as well as live bird markets (LBM) were visited and observed their waste management practices and problems were notified. Different literature was searched regarding the waste management systems in respective countries and compare with commonly used practices in Bangladesh.

Results: Collection of poultry waste into bag and subsequent direct uses as fertilizer in nearby agricultural fields and aquaculture are widely practiced in small and medium size poultry farms in Bangladesh. In some breeder and commercial chicken farms, alternative and more structured disposal methods such as composting or vermicomposting, followed by use on agricultural land and biogas plant generation, are currently being implemented. During slaughtering and processing at LBM, retailers keep the offal and leftover chicken parts, except the feathers, and sell these as fish feeds either for African catfish or other farmed fishes while chicken feces, feathers, and other solid chicken wastes are disposed into municipal waste disposal bin. However, a lack of awareness and capital with a large requirement for free land for composting, proper recycling and rendering of poultry waste are major constraints. Moreover, the direct use of poultry waste and disposal at waste bin contributes to poor air and soil quality and environmental degradation due to high levels of atmospheric ammonia, as well as the production of significant amounts of greenhouse gases, which contribute to global climate change. These make farm areas and LBM most vulnerable place to spread pathogen to the environment and eventually act as hub for the community transmission of zoonotic and avian pathogens.

Conclusion: As a result, an effective and recommended standard poultry waste management and related future research on precise waste characterization, improved understanding of poultry waste management, and increased efforts on developed waste disposal for safe environment are suggested.

Keywords: Poultry, Bangladesh, Waste composition, Management & utilization, Environmental impact

Poster No. 15 (Abstract No. 11121)

The ameliorative effect of selenium on inorganic arsenic-induced estrous cycle disturbance, pregnancy complications, defective fetal and post-natal growth in mice

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Background and Objectives: Sodium arsenite ($NaAsO_2$) as an endocrine disruptor interrupts reproduction and poses a risk for offspring's health outcomes later in life. Sodium selenite (Na_2SeO_3) as a potential antioxidant plays a significant role in the amelioration of $NaAsO_2$ induced toxicity. The present study investigated the ameliorative effect of Na_2SeO_3 on $NaAsO_2$ induced estrous cycle disturbance, pregnancy complications, defective fetal and post-natal (birth to weaning) growth in mice.

Methods: Four different treatment groups namely control, sodium arsenite ($NaAsO_2$), sodium arsenite ($NaAsO_2$) plus sodium selenite (Na_2SeO_3), and sodium selenite (Na_2SeO_3) were commenced. Each estrous cycle was considered 5 days and a total of 6 estrous cycles were observed and evaluated. Then E12.5 mice were evaluated for placenta formation and embryo development. Different organs were collected and evaluated. The post-natal growth of mice was evaluated based on the growth of offspring until weaning (4 weeks of age).

Results: Na_2SeO_3 could minimize estrous cyclicity interruption induced by $NaAsO_2$. Mice at E12.5 showed that Na_2SeO_3 could rescue the $NaAsO_2$ induced pregnancy loss. The placenta and embryos showed morphologically normal features except for Na_2SeO_3 treated mice where a rare phenomenon monochorionic-diamniotic twins were observed. Results showed that liver and lungs were severely affected in $NaAsO_2$ exposed mice, which was minimized by Na_2SeO_3. The litter size and litter weight were improved after Na_2SeO_3 treatment, although the differences were not at a significant level. The study evaluates post-natal (birth to weaning) growth of offspring and observed that the final body weight, total body weight gain, and rate of body weight gain were significantly ($p=<0.01$) hampered in offspring obtained from $NaAsO_2$ treated mice than offspring of non-treated control mice, and Na_2SeO_3 could not minimize the effects of $NaAsO_2$. Data revealed that in offspring obtained from both control and NaAsO2 treated groups, the rate of body weight gain was significantly ($p=<0.005$, $p=<0.02$ respectively) higher in males than females.

Conclusion: Overall, these results suggest that Na_2SeO_3 can be potential against $NaAsO_2$ induced reproductive toxicity, and further experimentation is needed to clarify the effect of $NaAsO_2$ in the later life of offspring as well as their amelioration strategy using Na_2SeO_3.

Keywords: *Sodium arsenite, Sodium selenite, Estrous cycle, Pregnancy, Placenta*

Poster No. 16 (Abstract No. 11217)

Climate-smart livestock practices in Bangladesh: adaptation and mitigation to reduce the methane emissions

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Introduction: Bangladesh ranks 7th vulnerable country to climate change as per the Global Climate Risk Index. The agriculture sectors are highly sensitive to climate change risks including sea-level rise and saline water intrusion, mean temperature rise, rainfall variability, and high-incidence and severity of acute weather episodes in Bangladesh. The emission of greenhouse gases (GHGs) namely methane (CH_4), nitrous oxide (N_2O), and carbon dioxide (CO_2) directly from fermentation in ruminant animals and manure management; and indirectly from feed production and processing activities are connected with the climate change. The objective of this study was to understand the existing climate-smart livestock (CSL) practices and methods at national and sub-national levels and to validate the pertinent CSL practices as climate adaptation and mitigation measures of GHGs to combat the future climate challenges associated with the livestock sectors.

Methods: The study has utilized the data primarily through a review of literature from secondary sources of peer-revived journals, and reports of different national and international organizations. Additionally, the data on best practices were collected virtually from stakeholder interviews (n=21) at selected districts of Bangladesh. Further, data from both sources (primary and secondary) were utilized through an expert opinion elicitation process (n=10) which included livestock-sectoral experts, extension officers, and researchers at the national and sub-national levels to substantiate the best practices and way forwards.

Results: In this study, we identified the different types of CSL practices as adaptation and mitigation of GHGs to combat climate challenges. So additional support and investment are required at the field–level trials for the demonstration to validate and prioritize the CSL best practices in climate-vulnerable areas against key climatic-risks.

Conclusions: Integration and mainstreaming of climate change issues in the existing policies of the government to internalize CSL practices in Bangladesh is very much necessitated.

Keywords: Climate-smart livestock, Climate change, greenhouse gases, mainstreaming, policy

Poster No. 17 (Abstract No. 11227)

The possible pathway of water-borne species invasion in Malaysia: where danger overthrows beauty

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Introduction: Biologist and philosopher Herbert Spencer, once said on social Darwinism, "survival of the fittest", but this term is not only implacable on “Invasion” but also, dangerous for the endangered native species. The state-of-the-art water-borne invasive species in Malaysia is scrutinized and assembled in this research work to assess the different pathways of water-borne species invasion in Malaysia.

Methods: The data were collected from different sources including, published literatures, which are cross checked and validated with Global Invasive Species Database, CABI, IUCN Invasive Species Specialist Group, IUCN Red List, Malaysian government websites and WoRMS database.

Results: There are 59 water-borne invasive species available in Malaysia (where 10 native species are invasive to the other regions) and classified into plants, fishes, algae, amphibians, mollusks, reptiles, microorganisms, crustaceans, seastar, coral, and sponge; among them 47 are freshwater species and 12 species are from marine habitat. The four invasion stages are proposed for the Malaysian invasive species, for instance arrival, establishment, localized and widespread. This review found a major number of the species are already established and since a long time, they have been spreading around the country’s local habitat. It is also revealed that most species are introduced in Malaysia due to the intentional, purpose of aquaculture and aquarium trade from the different regions especially the South American Continent; where some of the species came accidentally, through international maritime trade using 13 commercial seaports around the country. The local dispersion of these invaders, occurred in many ways, including, local transport, natural dispersal, agriculture, and aquaculture. The long-run consequence of different invasions and invasive species is performing irreparable damage such as, impact on local habitat, niche, and ecosystem; competition with local species, hybridization and the transmission of disease.

Conclusions: The most alarming phenomenon occurring right now; some illegal ornamental species importations from around the globe towards Malaysia, without concerning the invasion possibilities. That might lead to the permanent collapse of the food chain, ecosystems, and ecological balance. Which demands urgent investigation into different aspects of ecosystem degradation including their extensive taxonomy, ecological and economic impact.

Keywords: Biological invasion, international route of invasion, local dispersal, biodiversity, Sundaland

Poster No. 18 (Abstract No. 11235)

Environmental surveillance for SARS-CoV-2 and enteric pathogen: initial learning to the future direction

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Environmental surveillance data have been recognized as a valuable supplement to epidemiological case data, especially in understanding the burden associated with enteric diseases. In low-resource nations like Bangladesh, environmental surveillance can identify the selected pathogens and quantification of pathogens in wastewater can be a valuable low-cost, noninvasive public health tool where limited epidemiological data are available. Institute of Epidemiology Disease Control and Research (IEDCR), with technical support from icddr,b is implementing environmental surveillance in Dhaka and Cox's Bazar (Rohingya camps and the Cox's Bazar municipality). Wastewater samples were collected from well-mapped selected locations of drain, canals and pumping station that represents specific geographical area and community from both Dhaka and Cox's Bazar.

The study developed an environmental surveillance strategy and identified sampling points based on a comparative analysis of all possible sampling sites. The sampling point represented the population with a specific catchment area. Sampling techniques for collecting wastewater samples were established. The weekly sample collection from specific sampling points provided the temporal and spatial trends of the pathogens in a geographic area. The standard developed for sample collection and processing maintained adequate biosafety and biosecurity measures. Laboratory method optimization is completed with the development of the Standard Operating Procedure (SOP) of RT-qPCR for the detection of the Rotavirus, Salmonella Typhi, Vibrio Cholera and SARS CoV-2 in wastewater. The project plans to share the environmental surveillance results in near real-time with health authorities to enable a more targeted public health response to current outbreaks and endemic diseases. Multisectoral collaboration of the research team (icddr,b) and implementors were established. The project will explore the impact of climate variability (rainfall, humidity and temperature) and the correlation of clinical cases with environmental data.

Environmental surveillance initiatives can be a priority to One Health strategies of Bangladesh. Based on the existing evidence and result, integrated surveillance can benefit clinical practice and mitigate the spread of endemic diseases. Standardized methods, reporting, and data-sharing platform development with actionable wastewater data can be an effective tool for monitoring diseases with epidemic potential. The approach can be effectively expanded to explore antimicrobial resistance containment in the environment.

Keywords: Environment, surveillance, epidemic, standard, policy

Poster No. 19 (Abstract No. 11402R)

Carcass disposal practices of small-scale livestock farmers in anthrax outbreak and non-outbreak areas in Bangladesh

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Introduction: Anthrax is a global zoonotic disease caused by the spore-forming bacterium *Bacillus anthracis.* In Bangladesh, outbreaks are periodically reported among people and livestock, with approximately 4,000 reported suspected human cutaneous anthrax between 2009-2020. Suspected animal anthrax outbreaks were reported from 58 of the 64 districts in the country between 2008 and 2009. Improper disposal of anthrax infected carcasses can contaminate grazing land with spores that may survive for years and infect healthy animals. Understanding carcass disposal practices of small-scale livestock farmers in rural Bangladesh can guide anthrax control and prevention strategies.

Methods: We enrolled 1,620 households, 800 from outbreak and 820 from non-outbreak areas. We conducted a cross-sectional survey from October 2017 to March 2018 in four districts with the highest number of suspected human cases and four districts having never reported cases. We randomly selected 10-11 villages per district; totaling 81 villages. From each village, 20 households with at least one domestic animal (cattle/buffalo/goat/sheep) were randomly enrolled and the primary raiser was interviewed to understand the practices of carcass disposal.

Results: Among 1,382 households with cattle/buffalo, 85 reported unexpected animal deaths within the last 12 months. Among them, 78% of households reported burying carcass (non-specific depth), 11% disposed in open field, 8% disposed in a water body, 2% gave the carcass to cobbler, and 1% disposed in the jungle. Among 1,007 households with goat/sheep, 336 reported unexpected deaths of animals within the past 12 months. Among them, 62% reported burying carcass, 21% disposed in open field, 12% disposed in a water body, and 6% disposed in jungle. The burial practice was found higher in cattle/buffalo than goat/sheep (p=006). However, there were no significant ($p>0.05$) differences in carcass disposal practices among outbreak and non-outbreak areas.

Conclusion: Most of the households reported the burial of livestock carcasses. However, educational intervention about deep burial (minimally 6 feet), its feasibility in flooded areas, and potential alternatives for carcass disposal in the region should be assessed.

Keyword: Anthrax, Carcass disposal, small-scale livestock farms

Poster No. 20 (Abstract No. 11453R)

Isolation and identification of multidrug resistant pathogens from shellfishes

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Introduction: Mud crabs (*Scylla serrata*) and mussels are commercially important aqua species in the coastal regions and are good sources of food with higher protein and lower harmful cholesterol value. This study was undertaken to detect pathogenic strains of *E. coli*, *Salmonella* spp. and *Vibrio* spp. from both mud crabs and marine mussels.

Methods: A total of 108 mussel samples were collected from coastal area of Cox's Bazar and 62 samples from 31 mud crabs were collected from crab farms of Satkhira and Khulna. All samples were processed, enriched and cultured on EMB, SS and TCBS agar media for the growth of *E. coli*, *Salmonella* spp. and *Vibrio* spp., respectively. Colonies were selected, purified, chromosomal DNA was extracted and PCR (uniplex and multiplex) was done to detect and differentiate different species. Antibiotic resistance of selected isolates were also studied against commonly used antibiotics and presence of *tet*A, *tet*B, *aadA1* and *aac(3)-IV* genes were determined in phenotypically positive isolates by PCR.

Results: Among the isolates from mud crab and mussels, one and 20 *E. coli* isolates were confirmed as pathogenic strains containing *stx*-2 and *rfb* genes. Similarly, 20 isolates were detected as *S.enterica*, 16 as *S.* Enteritidis, 7 as *S.* Typhimurium, 8 as *S.* Dublin,16 as *V. cholera*, 16 as *Vibrioalginolyticus* 6 as *Vibriovulnificus* and 30 as *V. parahaemolyticus*. Variations in antibiotic resistance were observed for the isolates. The isolates resistance to tetracycline, gentamycin and streptomycin were also found to contain *tet*A, *tet*B, *aadA1* and *aac(3)-IV* genes.

Conclusion: It can be concluded that captive mud crab and mussels harbor and transmit multidrug resistant pathogenic bacteria to human which are life threatening.

Keywords: Mud crab, mussel, pathogenic strain, antibiotic resistance, marine

Emerging Infectious Diseases and Vaccine (human health)

Poster No. 21 (Abstract No. 11004)

Anosmia and/or Ageusia as a presenting symptom in COVID-19 positive patients, a single center study at Dhaka, Bangladesh

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Background: As the COVID-19 pandemic progresses, the understanding of respiratory and non-respiratory symptoms expand. The loss of smell and taste in COVID-19 patients is now acknowledged as one of the disease's primary symptoms by the international scientific community. The aim of this study was to investigate the incidence of loss of smell and taste in a single center of Bangladesh whose SARS-CoV-2 infection with RT-PCR had confirmed.

Methods: Two hundred COVID-19 patients were included in this study who become RT-PCR positive in

Nasopharyngeal and oropharyngeal swabs between 5 June 2021 and 17 July 2021 in a single centre. All of them were interviewed by a structured questionnaire over the phone.

Results: Among two hundred COVID-19-positive patients smell and taste dysfunction appeared in 37.5% cases. Among them, 65% are male, and 35% are female. Only Anosmia occurred in 57% of patients, and Ageusia occurred in 34% of patients, and both symptoms were present among 9% of patients with or without other symptoms of COVID-19. The smell and taste recovery time was distributed as 63% recovered within less than a week, 20 % within 2 weeks, and 17% in 2 weeks. The predominant age group was 31-40 years, 44% was affected, followed by 21-30 years' age group (37%).

Conclusion: Early detection of COVID-19 infection requires recognizing sudden Anosmia or Ageusia to identify otherwise concealed carriers, allowing for an early isolation strategy that will limit the disease's spread.

Keywords: SARS-CoV-2, Anosmia, Ageusia, RT-PCR

Poster No. 22 (Abstract No. 11452R)

Prevalence of multidrug resistant enteric *Escherichia coli* isolated from apparently healthy children ≤ 5 years of age in Gouripur, Mymensingh

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Antibiotic resistance is a major global public health concern. *Escherichia coli* and non-typhoidal *Salmonella* (NTS) causes self-limited gastroenteritis in healthy individuals. NTS infection has been given less attention compared with that of *Salmonella enterica* serovar Typhi. The present study was conducted to isolate and identify *E. coli* and NTS from apparently healthy children below 5 years with their antibiogram. A total of 120 rectal swab samples were collected from male (60) and female (60) children upto 5 years of age. Swabs were initially enriched in BHI broth followed by streaking on EMB and SS agar media for isolation of *E. coli* and *Salmonella*, respectively. Both the species were identified by PCR using specific primers. Antibiogram was done against 19 and 16 commonly used antibiotics of nine classes for *E. coli* and NTS, respectively. Among 120 rectal swab samples, 53 isolates were confirmed as *E. coli* (44%) and 20 were confirmed as NTS (17%) by PCR, of which 7 were *S.* Enteritidis and 11were *S.* Typhimurium. The highest number of *E. coli* (93%) and NTS (67%) was isolated from children of 3-5 yrs of age. The isolation rate of *E. coli* was higher in male children (69%), whereas that of NTS was higher in female children (22%). A significant proportion (60-78%) of *E. coli* isolates were also found resistant to amoxicillin (64%), ampicillin (62%), azithromycin (72%), cephalexin (62%), cephalothin (78%), tetracycline (68%) and sulphamethoxazole (64%). All the *Salmonella* was found 100% resistance against clindamycin and erythromycin and 80-100% sensitive to ceftriaxone, gentamycin, imipenem, chloramphenicol and meropenem. Variation in resistance to different antimicrobial classes were observed by both *E. coli* and NTS isolated from children <5 yrs. It can be concluded that the presence of MDR *E.* coli and non-typhoidal *Salmonella* in apparently healthy children might be a source for environmental contamination and also threat for surrounding people.

Keywords: Children, *E. coli*, Non-typhoidal *Salmonella*, multiplex PCR, multidrug resistance

Poster No. 23 (Abstract No. 11047)

Immunobiotic lactobacilli modulate the respiratory antiviral innate immunity against SARS-CoV-2 infection

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Introduction: Immunoregulatory probiotics, also called immunobiotics, have proven health beneficial effects against infectious disease in animals and humans. In a previous work, we demonstrated that nasally administered immunomodulatory lactobacilli beneficially modulated the lung antiviral innate immune response induced by Toll-like receptor 3 (TLR3) activation and improved protection against the influenza virus and respiratory syncytial virus infection in mice. Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), the novel strain causing coronavirus disease 2019 (COVID-19), has badly affected the global human health during 2020 and 2021. To date, the potential beneficial effects of immunobiotics on SARS-CoV-2 infection and COVID-19 outcomes have been extrapolated from studies carried out in the context of other viral pathogens. Here, we evaluated the immunomodulatory effects of viable and non-viable *Lactiplantibacillus plantarum* strains in human respiratory epithelial cells (Calu-3 cells) and the capacity of these immunobiotic lactobacilli to enhance the innate immunity against in vitro infection of SARS-CoV-2.

Methods: The Calu-3 cells were treated with *Lactiplantibacillus plantarum* MPL16 and *L. plantarum* CRL1506 (5×10^7) for 24 h and then stimulated with polycytidylic acid [poly (I:C)] for and SARS-CoV-2 48 h. Calu-3 cells with no lactobacilli pretreatment were used as controls. Before and after poly (I:C) stimulation and SARS-CoV-2 infection, treated cells and the culture supernatants were collected for measuring cytokine expression by quantitative real time PCR and the concentration by ELISA.

Results: Immunobiotic *L. plantarum* MPL16 and *L. plantarum* CRL1506 strains differentially modulate IFN-b, IL-6, CXCL8, CCL5, and CXCL10 production and IFNAR2, DDX58, Mx1 and OAS1 expression in Calu-3 cells stimulated with TLR3 agonist, poly (I:C). Viable microorganisms of both *L. plantarum* MPL16 and *L. plantarum* CRL1506 strains were able to enhance the innate immunity of Calu-3 cells to the experimental infection of SARS-CoV-2. The MPL16 strain induced these beneficial effects more efficiently than that of the *L. plantarum* CRL1506 strain. Notably, neither non-viable immunomodulatory strains (*L. plantarum* MPL16 and CRL1506) nor the non-immunomodulatory strains (*L. plantarum* CRL1905 and MPL18) could modify the innate immunity to Calu-3 cells against SARS-CoV-2 infection or to poly (I:C) stimulation.

Conclusion: To the best of our knowledge, this is the first demonstration of the ability of immunomodulatory lactobacilli to influence the replication of the novel coronavirus. Further mechanistic studies and in vivo experiments in animal models of SARS-CoV-2 infection are necessary to identify specific strains of immunobiotic lactobacilli like *L. plantarum* MPL16 or CRL1506 for the treatment and control of the COVID-19.

Keywords: Lactobacilli, respiratory epithelial cells, probiotics, immunobiotics, SARS-CoV-2, COVID-19 pandemic

Poster No. 24 (Abstract No. 11054)

Sero-surveillance of SARS-CoV-2 specific antibody Immunoglobulin G among garment workers in Bangladesh

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Background: Since the detection of first corona virus infection in Bangladesh on 8th March 2020, it has been spread to the whole country quickly. Though there is lack of proper treatment facility, diagnostic facility, lack of awareness, unwillingness of people to follow the social distance guideline and lack of other containment strategies, the prevalence of COVID-19 infection especially severe and symptomatic infection among people of Bangladesh specially among working people like garment workers, people living in slum areas and rural areas are low.

Objectives: The study aimed to investigate the sero-prevalence of SARS-CoV-2 specific antibody (IgG) among garment workers in Bangladesh.

Methods: An observation and cross-sectional study was carried out among 402 garment workers (69.4% female; mean age = 28.9 ± 6.9 years) in Dhaka city. A semi-structured questionnaire including informed consent as well as, socio-demographics and COVID-19 related information, was used to conduct the survey. Likewise, blood samples of all participants were also collected to measure the SARS-CoV-2 specific antibody (IgG). Serum level of SARS-CoV-2 specific antibody (IgG) will be assessed by Chemiluminescent immunoassay technique as per instruction of manufacturer.

Results: The prevalence of sero-prevalence of SARS-CoV-2 specific antibody (IgG) was 80.8% which was slightly higher among females compared to male but not significant (82.1% vs. 78.0%, $p > 0.05$). It was notable that no significant differences were obtained in other socio-demographic information (e.g., age, education, marital status, residence, and economic status).

Conclusions: The findings reflect that the SARS-CoV-2 specific antibody (IgG) was more prevalent among garment workers in Bangladesh. It may be due to the virus itself, genetic factor of virus, people and presence of preexisting immunity specially COVID-19 specific antibody due to previous cross infections with other corona viruses in Bangladesh.

Keywords: Sero-surveillance; garment workers; Bangladesh; COVID-19; antibody

Poster No. 25 (Abstract No. 11201)

Detection of virulence genes and antibiogram profile of diarrheagenic, Extended-spectrum beta-lactamase producing *Escherichia coli* from high-touch surfaces at Mymensingh Sadar

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Introduction: *E. coli* is one of the major significant pathogens causing diarrhea in human. The present study investigated the virulence factors, phylogroup, antimicrobial susceptibility, and Extended-spectrum beta-lactamase (ESBL) genes in *E. coli* from publicly shared common touch surfaces during April 2022 to September 2022.

Methods: 105 publicly shared common touch surfaces of seven categories were sampled by cotton swabs from Mymensingh Sadar in Bangladesh. *E. coli* was isolated and identified by PCR targeting *malB* gene. Isolates were screened by PCR for the detection of major virulence genes (*stx1*, *stx2*, *eaeA*, *ipaH*, *bfpA*, *virF*, ST, LT, *aggR*, pCVD432 and *daaD*) of diarrheagenic *E. coli* followed by phylogenetic grouping. Antimicrobial susceptibility of the *E. coli* isolates was determined by disk diffusion test and double disk synergy test for detection of ESBL-producing *E. coli*. ESBL production was confirmed through molecular detection of *bla* TEM-1, *bla* SHV, and *bla* CTX-M genes.

Results: Microbial population density of the surface samples ranged from 6.4 to 8.56 Log10 CFU/cm^2 where the highest value was recorded from the keyboard of ATM machine's surfaces ($p < 0.05$). *E. coli* was isolated from 11.43% (12/105) of the surface samples from where only 16.66% isolates presented diarrheagenic virulence determinants *iapH* and *daaD*, and thus confirmed as EIEC and DAEC respectively. Isolates were distributed to all four phylogenetic groups with a predominance of group A (41.7%). Antimicrobial sensitivity testing exposed 83.3% (10/12) of the isolates as multidrug-resistant (MDR). Highest resistance was observed against ampicillin (100%) followed by cefotaxime (66.7%) and trimethoprim/sulfamethoxazole (50%), while imipenem, gentamicin, and chloramphenicol were found to most effective against the isolates. Double disk synergy test revealed 16.66% (2/12) isolates with ESBL producing ability. In contrast, 58.3% (7/12) isolates were confirmed to have at least one of the three ESBL-producing genes (*bla* TEM-1, *bla* SHV, *bla* CTX-M), with *bla* TEM-1 (50%, 6/12) being the most dominant type.

Conclusion: Findings of the present study indicate a potential threat of the likelihood of human infection with diarrheagenic *Escherichia coli* from publicly shared common touch surfaces. MDR pathogens from these surfaces might limit therapeutic options due to the dissemination of resistance determinants in the environment and simultaneously to human gut pathogens or commensal microfloral populations.

Keywords: High-touch surface, virulence genes, *E. coli,* PCR, ESBL

Poster No. 26 (Abstract No. 11202)

Identification, virulence characterization, and antibiogram study of *Escherichia coli* from betel leaf samples in Mymensingh city

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Introduction: Betel leaf is a product that is regularly consumed fresh and raw, but is difficult to decontaminate, as a result, like other fresh produces, can be a common vehicle of transmission of enteropathogenic bacteria. Contamination of fresh produce like betel leaf with *E. coli* O157:H7 pose great public health risk to the consumer. This study was designed to determine the virulence gene and antibiogram profile in *Escherichia coli* isolated from ready-to-eat and fresh betel leaf from roadside vendors and from different local market of Mymensingh city during April 2022 to September 2022.

Methods: A total of 100 samples were collected and screened for the detection of *E. coli* based on cultural properties on selective media, staining, and Latex agglutination test, followed by molecular characterization using genus-specific Polymerase Chain Reaction. Antimicrobial susceptibility of the *E. coli* isolates was determined by disk diffusion method.

Results: In this study, out of 60 fresh betel leaf samples and 40 ready to eat betel leaf samples, 4 samples were found to be positive for *E. coli* O157:H7 and 33 samples were positive for *E. coli* non-O157:H7. Among these 4 *E. coli* O157:H7 isolates, 1 was isolated from ready to eat betel leaf samples and 3 isolates from fresh betel leaf samples. Both *E. coli* O157:H7 and non-O157:H7 were detected by *mal*B promoter gene-based PCR. *E. coli* O157:H7 primarily confirmed by latex agglutination test and further confirmed by PCR using *rfb*E_{O157} promoter gene. From the results of stx_1 and stx_2 gene-based PCR, four isolates of *E. coli* O157:H7 and five isolates of *E. coli* non-O157:H7 were confirmed to be positive for the presence of the stx_1 gene, but no isolate showed positive for the stx_2 gene. In virulence gene detection, no isolate showed positive result in *eae*A and *hly*A gene-based PCR. The antimicrobial sensitivity test revealed that ciprofloxacin and ceftriaxone was the most sensitive antimicrobial agent against the Shiga-toxin-producing *E. coli* (STEC), followed by streptomycin (87.87%). On the other hand, amoxycillin and erythromycin were found to be 100% resistant.

Conclusions: From the current study, ceftriaxone and ciprofloxacin can be recommended as effective drugs to control STEC infections in humans.

Keywords: *E. coli*, detection, virulence characterization, AMR, betel leaf

Poster No. 27 (Abstract No. 11203)

Occurrence, virulence characterization and antibiogram study of *Campylobacter jejuni* from sugarcane juice in Mymensingh

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Introduction: *Campylobacter jejuni* is one of the major causes of food-borne bacterial infections in humans worldwide. This study was conducted to determine the occurrence of *Campylobacter jejuni* by isolation and identification from the sugarcane juice of 5 upzillas (Mymensingh, Trishal, Bhaluka, Muktagacha and Fulbaria) in Mymensingh district, and virulence characterizing and antimicrobial resistance profiling of isolated *Campylobacter jejuni* during the period of April 2022 to September 2022.

Methods: By using cultural, biochemical and molecular techniques, a total number of 50 sugarcane samples were subjected to *Campylobacter jejuni* isolation and identification. And then genus specific (16S rRNA gene) polymerase chain reaction (PCR) was performed for the identification of *Campylobacter* spp. and *hip*O gene-based PCR was performed for the identification of *C. jejuni*. Furthermore, for the virulence characterization of the *Campylobacter jejuni* isolates, *cdt* gene based multiplex PCR was performed by targeting *cdt*A, *cdt*B and *cdt*C genes. Finally, the isolated *Campylobacter jejuni* were characterized by antimicrobial susceptibility testing. In this study, antimicrobial susceptibility testing against commercially available eight antibiotics of different groups was performed by disk diffusion method.

Results: Among the 50 samples, 04 (08%) isolates were confirmed as *Campylobacter jejuni* and all 02 (50%) isolates are confirmed as virulent because all of them contain virulent cytolethal distending toxins. In the current study, it was observed that the majority of the *Campylobacter jejuni* isolates were resistant to tetracycline, erythromycin, and amoxicillin. Out of 04 *Campylobacter jejuni* isolates, 04(100%) were detected as multidrug resistant.

Conclusions: The results showed an alarming number of virulent and antibiotic resistant *Campylobacter jejuni* in sugarcane and thus there is a need to control and monitor the occurrence of virulent and multidrug resistant *Campylobacter jejuni*.

Keywords: *Campylobacter jejuni*, detection, virulence characterization, AMR, sugarcane juice

Poster No. 28 (Abstract No. 11220)

Prevalence and public health significance of *mcr E. coli* isolated from monkey (*Rhesus macaque*) in Bangladesh

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Colistin resistant *E. coli* (CREC) is an emerging global concern. CREC existed in a variety of environmental setting including wild animals. Monkey is most common among the wild animals residing at very close contact to human or invading localities due to destruction of their natural habitat. Monkey usually depends on the left-over foods or house hold sludge's making them exposed to a diverse group of pathogens. Recently occurrence of *mcr-1* CREC has been reported from urban sludge's in Bangladesh indicating potential threat of their exposure to CREC. Thus, this study was aimed at the determination of occurrence and characteristics of *mcr* CREC in monkey. A total of 68 rectal swab samples were collected from monkey and enriched in LB broth. CREC was isolated from the enrichment culture by streaking onto MacConkey agar containing colistin sulphate (1µg/ml) and identified by PCR targeting *E. coli* specific *malB* gene. CREC were screened for *mcr* genes by multiplex PCR. Antimicrobial resistances of the isolates were explored by disk diffusion method and MIC to colistin was determined by E-test. The isolates were further examined for virulence genes (*stx*, *eae* and *cdt*) and antimicrobial resistance genes by PCR. Out of 68 samples 25 samples carried CREC. A total of 75 *E. coli* isolates were recovered from the positive samples and found all of them carried *mcr-1* gene and showed a MIC of 2-4 µg/ml. None of the isolates showed positive amplification to the virulence gene (*stx*, *eae* and *cdt*) tested. On disk diffusion test all the *mcr-1* CREC showed multidrug resistance (MDR) with 100% resistant to amoxicillin, Ampicillin, ciprofloxacin, levofloxacin, enrofloxacin, moxifloxacin, nalidixic acid and tetracycline. PCR for antimicrobial resistance gene revealed 100% of the resistant isolates carried bla_{TEM-1}, *tetA* and *qnrS* genes, and 88% of the isolates carried both *qnrA* and *qnrS* genes. Occurrence of MDR CREC in monkey is critical which might threaten their existence through life threatening infection as well as potential to transmit to human.

Keywords: E. coli, Muti drug resistance, mcr gene

Poster No. 29 (Abstract No. 11221)

Molecular detection and characterization of *E. albertii* from broiler meat sold at the retail outlets in Mymensingh district of Bangladesh

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Introduction: *Escherichia albertii* is an enteric pathogen linked to food borne diseases. It has been reported from diverse environmental setting and food items including chicken. This bacterium was first described in Bangladesh from a diarrheic child in 1991. However, no further study was undertaken in Bangladesh since its first report. The present study was aimed to the molecular detection, isolation and characterization of *E. albertii* from broiler meat, the major protein source in Bangladesh.

Methods: Broiler meat was collected from the retail outlets of different location of Mymensingh district of Bangladesh. A total of 224 meat samples comprising 51 of each of breast, thigh, proventriculo-gizzard and liver were examined in this study. In addition, rectal swab samples (n = 35) of broilers and human hand swab (n = 11) was collected to identify the source as well as potential of transfer to human through handling during the act of slaughtering and dressing. Sample was homogenized in nine (9) times buffered peptone water and enriched overnight at 37^{o}C followed by detection of *E. albertii* by *Eacdt* gene PCR. *E. albertii* was isolated from the PCR positive samples onto *E. albertii* specific XRM-MacConkey agar media and further confirmed by PCR and sequencing of the *Eacdt* gene. Isolated *E. albertii* were subjected to ERIC PCR and PFGE to determine their genomic diversity as well as screened for *cdt*, *eae* and *stx* genes, the well-known virulence factors in this bacterium by multiplex PCR.

Results: 61.1% (149/244) of the meat sample, 68.6% (24/35) of broiler rectal swab and 36.4% (4/11) of human hand swab were positive for *E. albertii* by PCR. From the PCR positive samples 63 *E. albertii* colonies were recovered and on ERIC PCR and PFGE analysis four (4) different genotypes were identified. Isolates from human hand, meat and broiler feces from the same retail outlets showed same ERIC pattern. All the isolates carried *cdt* and *eae* but no *stx* genes.

Conclusion: From the findings it was evident that broiler meat carried *E. albertii* and has a potential to transfer to human during the act of slaughtering and/or dressing probably through fecal contamination.

Keyword: Escherichia albertii, broiler meat

Poster No. 30 (Abstract No. 11252)

Cockroaches: A suitable source of multidrug resistant pathogenic enteric bacteria for human

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Introduction: Cockroaches are considered as one of the most significant and objectionable pests for their nocturnal and filthy habits, ultimately act as a potential source for the transmission of pathogenic and antibiotic resistant bacteria.

Objective: The research was conducted to isolate and characterize human pathogenic strains of bacteria from external (mouth and leg) and internal (intestinal part) body parts of cockroaches, phenotypic and genotypic characterization of multidrug resistance pattern.

Methodology: A total of 123 cockroaches were collected from household, and girls' and boys' hostel premises (47), dining and kitchen areas (38), washroom (28) and laboratory (10). The collected cockroaches were processed and enriched in nutrient broth followed by inoculation in selective agar media for the isolation of enteric bacteria and detection by PCR using specific primers. Antibiogram with the detection of resistant gene in the selected isolates were also performed.

Results: Seventy-six *E. coli* was detected in the cockroaches of which 8 were identified as extraintestinal pathogenic *E. coli* (phylogenetic group B2 and D) and the rest as commensal *E. coli* (phylogenetic group B1 and A). Besides, 7 *Pseudomonas aeruginosa*, 3 *Aeromonas* spp. and 2 *Shigella* spp. were also isolated and identified from the cockroaches. Most of the isolates showed highly resistance to amoxicillin, colistin and moxifloxacin, and least resistance to ciprofloxacin and levofloxacin. The presence of tetracycline (*tetA* and *tetB*) and ESBL (bla_{TEM-1}, bla_{CMY-9},bla_{SHV-1}) producing genes in the isolates indicates that most of the isolates were multidrug resistant.

Conclusion: It is alarming that cockroaches of different sources carry multidrug resistant pathogenic enteric bacteria which can easily be transmitted to human and can cause disease.

Keywords: Cockroaches, enteric, pathogenic, resistant, multidrug

Poster No. 31 (Abstract No. 11255)

Detection and characterization of multidrug resistant *Escherichia coli* from livestock, poultry and human at domestic environment of Bangladeshi rural areas

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Introduction: Livestock farming is expanding world-wide because of increased demands for food of animal origin. Such farming practices pose a public health risk as livestock are reservoirs of several zoonotic pathogens. *Escherichia coli* is a zoonotic bacterium that is important for both public health and livestock economics.

Objectives: Isolation of *E. coli* from the livestock and poultry in a household system including human and identified at the phylogenetic and pathotypic levels with the determination of phenotypic and genotypic antibiotic resistance pattern.

Methodology: A total of 188 rectal, cloacal and hand swabs comprising of cattle (48), chicken (34), goat (32), sheep (5), duck (19), pigeon (13) and human (37) were collected from 30 rural households for the isolation of *E. coli* by culture, detection and differentiation by PCR, and antibiogram with resistant gene detection.

Results: One hundred and forty eight *E. coli* were recovered from samples with the prevalence of 79%, of which 20 (13%) were identified as extraintestinal pathogenic *E. coli* (phylogenetic group B2 and D) and the rest as commensal E. coli (phylogenetic group B1 and A). Enterotoxigenic *E. coli* (ETEC) was isolated from cow, hen, chick and duckling; Enterohemorrhagic *E. coli* (EHEC) was from calf, chick and goat; Enteroaggressive *E. coli* (EAEC) from sheep; Enteroinvasive *E. coli* (EIEC) from hen and kid; and Enteropathogenic *E. coli* (EPEC) from cow. Resistance was observed against amoxicillin, oxytetracycline, cefixime, amoxicillin-clavulanic acid, nalidixic acid and ciprofloxacin antibiotics. A majority of the examined *E. coli* isolates were found to carry the tetracycline and ESBL resistant genes, and 59% of all the isolates showed a pattern of multidrug resistance.

Conclusion: The isolation of ETEC, EPEC, and EHEC from chicken and duck suggests that *E. coli* may have transmitted from humans or cattle to poultry, whereas the isolation of EIEC and EAEC from chicken, goat, and sheep may suggests a possible transmission of *E. coli* from humans to animals.

Keywords: Antibiotic resistance, E. coli, pathotype, phylogenetic group, transmission

Poster No. 32 (Abstract No. 11283)

Working environment and occupational health problems among jute mill workers

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Occupational health problems identification, prevention, and control of them makes a good working environment, which is very imperative for the wellbeing of the working population. A cross sectional study was conducted from January to December 2022, among 290 jute mill workers in Narsingdi district to find out the working environment and occupational health problems among jute mill workers. A convenient sampling technique was used to collect data utilizing a pretested semi-structured questionnaire. Among the study respondents 36.2% were found in the age group of 31-40 years and mean age was 40.42 ±10. 02. Male participants were 67.2%, females 32.8% and 37.6% were illiterate. The average monthly salary was less than 8000 BDT for 50.7% respondents. Study showed that 32.4% job experience was between 15 to 24 years where 64.1% had permanent, 35.9% had temporary job and 71.7% did over time. Study revealed that 87.2% respondents were not available for outside work ,76.2% had no significant influence over work, 91.4% were not satisfied with their present salary structure and 54.8% were handled heavy loads at work. Study also revealed 79.7% had musculoskeletal, 33.1% skin, 27.9% respiratory, 19.7% had eye symptoms and 17.2% had minor cut or injuries in last 2 weeks. A significant relationship was found between age and musculoskeletal symptoms, gender and musculoskeletal symptoms, education and musculoskeletal symptoms and also handle heavy loads at work and musculoskeletal symptoms. Association between job nature and worried about becoming unemployed was shown to be statistically significant. The findings of the study may be helpful in eradicating problems and improving the precarious situation of the jute industry in Bangladesh.

Key words: Occupational health problem, working environment, jute workers, jute industry Bangladesh, industrial health hazard

Poster No. 33 (Abstract No. 11300)

Clinico-epidemiological features of animal bites among humans in Chattogram, Bangladesh - A hospital-based cross-sectional study

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Introduction: Animal bite particularly dog bite in humans is a neglected public health problem of worldwide distribution. In Bangladesh, an estimated 200,000 animal bite cases with more than 2,000 human rabies deaths are reported annually. The aim of this study was to determine the clinical and epidemiological factors associated with animal bites in humans in Chattogram, Bangladesh.

Methods: We conducted this cross-sectional survey among animal bite victims who visited at animal bite clinic under the Bangladesh Institute of Tropical and Infectious Diseases (BITID) from July to December 2021. Only confirmed animal bites by dogs, cats, jackals etc. were included in this study. Data were collected using a pre-designed case record form which possessed patient demography, bite pattern, clinical features, and treatment related information. Total 650 bites data were recorded where eight cases were found human to human bites and excluded from the study. Therefore, we used 642 patients' data for the final analysis.

Results: Among total animal bite cases, male patients (63.7%) were higher than females (36.3%). Students (33.2%) were mostly affected followed by service holders (24.5%). Below 18 years old children were frequently bitten (44.3%) followed by 32.3% from 18 to 40 years. Dog bite cases were higher (61.4%) than cat bite (37.1%). Of total, 30.4% of bites were recorded as category 3 and only 5.9% of them needed hospitalization. In head-neck region, 91.4% bites were caused by stray animal however, in upper limb areas, 67.8% were by stray animals and 32.2% had by pet animals. Incidents of bites were recorded during sleeping time of people where 70.8% had caused by stray animals and 29.2% by pet animals. People also got bitten by animals without any provocation. Among total non-provocative bites, 91.8% were caused by stray animals. Of total, 94.7% of stray animal bite victims required hospitalization. Among total admitted patients, 84.2% were getting routine treatment and released in time, whereas 10.5% needed surgery and 5.3% had become dead.

Conclusion: The results of our study provide baseline information for a further comprehensive nationwide survey of animal bites and also facilitate the rabies control and elimination program of the country.

Keywords: Animal bite, clinical features, Dog bite, Epidemiology, pattern of bite

Poster No. 34 (Abstract No. 11209)

Work related factors affecting quality of work life among secondary level hospital nurses

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Introduction: Nurses play a critical role in the delivery of healthcare. It is challenging to balance their work life with minimal facilities in secondary level hospital and it also unquestionably correlated with the standard of care they provide.

Methods: A cross sectional study was conducted to assess the quality of work life among nurses. 232 nurses were selected in this study who worked in secondary level hospital by using a pre-tested semi-structured questionnaire with WALTON's Quality of Work Life Scale.

Results: The largest group 31.5% of the respondents were between 40-49 years of age group. Most 96.6% of the respondents were female and 94.8% were married. In their 39.2% had less than 5-year work experiences in current hospital and 50% nurses completed their Diploma. Their monthly salary mean was 35909±10173.622 BDT. 33.6% respondents were posted in Medicine department, 31.9% were in Surgery department and 29.3% in Gynae & Obs department. Regarding individual perception of quality of work life, mean was 125.96±9.334, maximum score was 169 and minimum score was 93. Among 232 respondents 71.1% were experienced moderate quality of work life and 28.9% were experienced good quality of work life. Statistically significant was found with night shifts, ability to take break, sudden change in roster, ability to have meal in appropriate time, opportunity to spend time with family and friends, conflict with patients or their relatives.

Conclusion: In this study found majority of the respondents experienced moderate quality of work life. Modifying work related factors along with enhancing supportive working environment and facilities may improve quality of work life among nurses.

Keywords: Work related factors, Quality of Work Life

Poster No. 35 (Abstract No. 11237)

Awareness of mothers having 2-5 years children regarding milestones of motor development

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Background: Children's health is considered an investment and a source of societal benefit. Due to physical and psychological development benefits, interventions within the first five years are regarded as one of the most successful aspects of disease prevention and health promotion. All parents require information on healthy child development. Additionally, maternal knowledge is a crucial component of child-rearing. This cross-sectional study tries to assess the knowledge and awareness of mothers having 2-5 years of children regarding the milestone of motor development.

Methodology: The study was conducted from 1st January to 31st December 2023. Purposive sampling was used to choose 350 Mothers who visited the Dhaka Medical College and hospital and Institution of Child and Maternal Health in Dhaka. Mothers with children 2-5 years old who visited the health center and provided informed consent were included in this study.

Results: Out of 350 mothers, 169 (48.3%) had average knowledge, 140 (40%) had good, and 41 (11.7%) had a poor level regarding milestones of gross motor development. Out of 350 mothers, 171 (48.9%) had average knowledge, 118 (33.7%) had good, and 41 (11.7%) had a poor level regarding milestones of fine motor development. Among all respondents, 82.3% knew about Walking, 82% knew about Crawling and Sitting, 77.7% knew about Head Control, 65.4% knew about Turning of Head, and 60% knew Stair Climbing. There was an association between the mother's knowledge level and with father's age, the mother's highest education, the father's highest education, the mother's marital status, the mother's age during 1st pregnancy, family income, the child's sex, and children's vaccination status, which were statistically significant ($p < 0.05$).

Conclusion: Mothers had an average level of knowledge on milestones of gross motor development and an average level of knowledge on milestones of fine motor development. Health education and health promotion programs on early childhood development that employ the most effective method and media to reach the mother, as well as parenting programs that encourage early detection and intervention to protect children and maintain the strength of society, can help close this knowledge gap.

Key words: awareness, mother children, motor development

Poster No. 36 (Abstract No. 11297)

Screening of hypertension from selective area of Narayanganj City Corporation

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Backgrounds: Over recent year noncommunicable diseases' (NCD) here become an emerging pandemic global issue. Among the NCDs Hypertension is an important medical and public health issue because it is very common and increase the risk of cardiovascular and kidney disease. If hypertension (HTN) is detected early, we can easily treat the patient and prevent its complication. The objective was to find the prevalence, association with risk factors, awareness and establish referral system. The most significant risk factor, hypertension and obesity, is increasing at an alarming rate in most developing countries. As a result of demographic change, developing countries such as Bangladesh have quite a higher burden of NCDs such as hypertension and obesity. The purpose of this study would have been to assess the prevalence and awareness of HTN among young and middle-aged people from a particular population. It moreover explored into factors related to hypertension and obesity awareness.

Objective: We implemented this program to determine the prevalence and to aware the targeted population regarding hypertension and obesity in the selected areas of Narayanganj city corporation.

Methods: Purposive sampling was done to obtain data in 09 selected wards of NCC both male and female aged above 30 years and visible obese individual age 18 years and above. To evaluate the prevalence, awareness, treatment, and management of hypertension, descriptive data were used. A total of 11301 male and female-participants voluntarily came to the health point will be included in the study, randomly collected few sample for baseline study and after two month interval a post test was done over telephone with a same questionnaire. Hypertension was the dependent variable and it is defined as systolic blood pressure >140 mm of Hg and/or diastolic blood pressure >90 mm of Hg. And BMI >25-29.9 is overweight and BMI >30 is obese.

Results: Through the campaign, 11292 person's hypertension were evaluated. Proportion of hypertension of population was 8294 (73.5%) were found to be normal and 2998 (26.5%) were HTN. Proportion of gender of hypertension was 1734 (57.84%) were male and 1264 (42.16%) were female. Majority 2183 (72.81%) participant were no HTN who were smoke. The smoking status of the participant were significantly associated with their age and sex. The baseline survey showed that 1951 (65.07%) of the participant were hypertension who were using salt intake food. Majority of the respondents agreed that control measures for hypertension should be continued lifelong. Pre-hypertension condition improved in the endline assessment. No significant association was found between the ages of initiation of hypertension of the respondent status.

Conclusion: Since the prevalence of HTN is higher, The NCC authority should take necessary action to strengthening public health program so that NCDs specially Hypertension and its complication can be prevented.

Keywords: Hypertension, obesity, awareness

Poster No. 37 (Abstract No. 11294)

Multi-oocyte follicles and double nucleated oocytes in mammals and humans: as an unique model of twinning

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Introduction: Most follicles contain only a single oocyte. However, it has been manifested the presence of two or more oocytes or of two nuclei within the same follicle. We have revealed that the cotton rat (CR, *Sigmodon hispidus*) is a useful model for these unique folliculogenesis. This study examined the CRs as a model to study the folliculogenesis and discussed its disturbances in mammals and humans such as twinning.

Methods: The ovaries were collected from CRs at one month of age maintained at Hokkaido Institute of Public Health (HIS/Hiph) and Miyazaki University (HIS/Mz), and their sections were analyzed by light microscopy and transmission electron microscopy (TEM).

Results and Conclusion: Multi-oocyte follicles (MOFs) and double nucleated oocytes (DNOs) were observed in all developing follicles in HIS/Hiph strain whereas HIS/Mz had MOFs up to secondary stages but lacked DNOs. The estimated total follicles in HIS/Mz were almost half of the HIS/Hiph strain. Immunohistochemistry for PCNA and Ki-67 indicated the proliferative activities of oocytes and granulosa cells were higher in HIS/Hiph ovaries compared with HIS/Mz.

Taken together, we revealed the strain-differences in the folliculogenesis in the inbred CR, and comparison of these strains might shed light on the mechanisms of the folliculogenesis in mammals. We hypothesized the mechanism of formation of MOFs in both strains by failure of germ cell nest breaking or fusion, and HIS/Hiph DNOs are formed by nuclear division without cytoplasmic cleavage during nest breaking.

Key words: Multi-oocyte follicles, double nucleated oocytes, twinning

Emerging Infectious Diseases and Vaccines (animal health)

Poster No. 38 (Abstract No. 11020)

Community structure and functional annotations of mucosal microbiome in healthy and diseased *Heteropneustes fossilis*

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Introduction: Sustaining microbial balance is very important for preventing disease occurrence in fish. In this study, we report the mucosal microbiome composition from healthy and diseased stinging catfish (*Heteropneustes fossilis*) comparison of the inhabiting community clusters and the functional annotations of their genes based on 16S rRNA metagenomics.

Methods: For the present study healthy and diseased fishes were collected from Mymensingh (M), Narsingdi (N), Dinajpur (D) districts of Bangladesh from October 2019 to March 2020. Microbiome community from healthy and diseased fish mucus were compared by both culture dependent method using 16S rRNA gene sequencing and culture independent method (metagenomics).

Results: We have found 2174 operational taxonomic units (OTUs) annotated for genus where the healthy fishes had more OTUs than diseased. The OTUs consisted of four major phyla Proteobacteria, Bacteroidota, Actinobacteriota and Firmicutes. Among members of the predominant phyla, Proteobacteria were rich in healthy fishes but Bacteroidota and Firmicutes phyla significantly differentiated the healthy and diseased groups. Richer and more diversified microbiome was observed in the slime of healthy fishes but did not significantly differ from the diseased groups. At genus level, *Pseudomonas* showed the highest abundance in healthy fish and nearly absent in diseased fish, whereas the *Flavobacterium* showed the highest abundance in diseased fish. Linear discriminant analysis identified two phyla (Bacteroidota, Firmicutes) and two genera (*Flavobacterium*, *Allorhizobium*) that consistently labeled for the diseased fishes. Functional prediction analysis specified that the genes related to the activities of important physiological functions like metabolism, immune and digestive systems and environmental adaptations were high in diseased fishes.

Conclusion: Present study indicates that the compositions, richness and the functions of bacterial community influence the health status of cultured stinging catfish. Based on this report, aquaculture associated pathogenic bacteria may be identified and preventive measures can be taken for the surveillance of fish health.

Keywords: *Heteropneustes fossilis*, 16S rRNA metagenomics, Microbiome composition, Microbial gene functions

Poster No. 39 (Abstract No. 11026)

Prevalence and risk factor analysis of *Cryptosporidium* spp. in cattle at Sylhet, Bangladesh

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Introduction: *Cryptosporidium*, an enteric protozoon, is best known for infectious diarrhea in humans and animals. *Cryptosporidium* spp. are transmitted by faecal-oral route and is consider potential public health concern. This research aimed to investigate prevalence and risk factors of Cryptosporidium infection in cattle population of Sylhet District, Bangladesh.

Methods: In this study, 258 fecal samples were collected (Jan-Aug 2021) directly from the rectal region of cattle. Modified Ziehl-Neelsen (mZN) staining technique was used for initial screening followed by nested Polymerase Chain Reaction (nested PCR). A pre-tested questionnaire was developed to identify risk factor for *Cryptosporidium* infection. Risk factor analysis for the infection was explored by univariable analysis and multivariate logistic regression model at animal level. Each statistical analysis was accomplished by software R version 4.1.0.

Results: Through adopting mZN staining and nested-PCR methods, out of 258 samples 12 samples were confirmed as positive. Overall prevalence of *Cryptosporidium* infection in Sylhet District was 4.65% (95% CI 2.5-8.2). The multivariable logistic analysis identified age, breed, and deworming frequency were highly significantly ($p< 0.01$) associated with the *Cryptosporidium* infection. The risk of Cryptosporidium infection was significantly higher in young animal compared to aged animal. Exotic breeds (OR=11.38, 95%CI 2.46-85.50) were significantly associated with the infection than local. Deworming frequency, once in more than 3 months were significantly associated with the Cryptosporidium infection than once in a month.

Conclusion: Our results suggest that intervention strategy should be targeted in young exotic animal with establishing appropriate deworming frequency. Molecular characterization and epidemiological indices with wider geographical region and host-range will enhance better understanding the trend of *Cryptosporidium* infection, is needed to be explored from future studies.

Keywords: Cryptosporidium, Cattle, nested-PCR, Prevalence, Risk factors

Poster No. 40 (Abstract No. 11052)

Livability of Indian peafowl up to fledgling age in Bangladesh National Zoo

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Introduction: Livability is the potentiality of an individual to survive up to its normal life, which affects the productive and reproductive performance of poultry and other birds. The fledgling age considered in the present study was 3 months, because by this time they grow full feathers. Therefore, this research was conducted with the aim to explore the livability and mortality up to fledgling age of Indian peafowl under captive condition in Bangladesh National Zoo.

Methods: The study was done from April 2015 to December 2018, by direct interacting, observing, using structured questionnaire and finally taking records on the data sheets.

Results: During the study period we observed a very high livability of peachicks for all the year round. The overall livability was found 95.82% (*n*=263) up to fledgling age. Livability (97.5%; *n*=40) was the highest in 2018, whereas it was the lowest (93.75; *n*=16) in 2016. On the other hand, the mortality was found low in all the listed years; the average was found 4.18% (*n*=263) up to fledgling age. The mortality was the lowest (2.50%; *n*=40) in 2018, and the highest (6.25%; *n*=16) in 2016. The major infectious diseases that affected the peachicks were colibacillosis (46%; *n*=5) and salmonellosis (27%; *n*=3); other noninfectious accidental injury (27%; *n*=3) follows the most considerable death. In the early stage of life (1-15 days), the mortality rate was remarkably high (82%; *n*=9) than (18%; *n*=2) in the later stage of life (16-90 days).

Conclusion: Considering the livability of the species in captivity, it is possible to acclimatize them in the semi-wild habitat and eventually release them in the wild in order to re-establish the wild population in Bangladesh.

Keywords: Indian Peafowl, livability, fledgling age, Bangladesh National Zoo

Poster No. 41 (Abstract No. 11055)

Molecular detection of lumpy skin disease virus in cattle in selected district of Bangladesh

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Introduction: Lumpy skin disease (LSD) is a contagious viral disease of cattle caused by the lumpy skin disease virus (LSDV). The disease first appeared in Bangladesh in the Chattogram district in 2019 and quickly spread across the country. This study aimed to investigate and confirm the recent outbreaks and provide LSDV molecular characterization in different regions of Bangladesh.

Methods: The research was carried out from July 2021 to November 2021. A total of 17 LSDV-affected bovine samples (scab, pus, blood, and edema fluid) were collected from Rajshahi and Mymensingh districts in Bangladesh. The samples were collected aseptically and delivered to the laboratory of the Department of Medicine at Sylhet Agricultural University via a cool box. The samples were stored at -80°C for further processing. The DNA was extracted using a DNA extraction kit (Monarch® Genomic DNA Purification Kit, UK) and kept at -20°C until further analysis. Extracted DNA was used in a PCR test to detect the presence of LSDV, with specific primers targeting the LSDV gene for viral attachment protein. The primers LSD-F (5'-TCCGAGCTCTTTCCTGATTTTTCTTACTAT-3') and LSD-R (5'- TATGGTACCTAAATTATATACGTAAATAAC-3') were used to detect LSDV with the amplicon size of 192bp. The amplified products were then visualized by gel electrophoresis using 1.5% agarose gel and viewed under UV trans-illumination in a gel documentation system.

Results: From 17 samples 64.70% (n= 11/17) were found LSDV positive by polymerase chain reaction (PCR). In PCR test, 75% samples (n= 9/12) found positive from Mymensingh district and 40% samples (n= 2/5) found positive from Rajshahi district of Bangladesh. The results additionally showed that 100% of scabs (n= 5/5), 40% of blood (n= 2/5), 75% of pus (n= 3/4), and 33.33% of edema fluid (n= 1/3) samples from affected animals were found positive for LSDV by PCR test.

Conclusion: Genetic analysis of partial sequences of viral attachment protein genes might be a helpful and practical strategy in the early molecular characterization of LSDV strains involved in the LSD outbreak in Bangladesh, according to our findings.

Keywords: Lumpy skin disease virus, PCR, Molecular Identification, Cattle

Poster No. 42 (Abstract No. 11096)

Infrared thermography to measure negative emotions in dairy cows

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In commercial dairy cows, the conditions in which they are kept may lead to negative emotional states associated with the development of chronic physiological and behavioral abnormalities that may compromise their health, welfare and productivity. Such states include fear, stress or anxiety. Behavioral rather than physiological tests are more likely to be used to indicate these states but can be limited by their subjectivity, need for specialized infrastructure and training (of the operator and sometimes the animal), and the time-consuming nature of data collection. Popularly used physiological measures such as blood cortisol may be more appropriate for acute rather than chronic assessments but are easily confounded, for example by a response to the act of measurement *per se*. More sophisticated physiological measures such as functional magnetic resonance imaging (fMRI) and electroencephalography (EEG) may be impractical due to cost, time and, like blood cortisol, have the confounding associated with the act of measurement. By contrast, infrared thermography of external body surfaces is remote, non-invasive, easily repeated and follows an objective methodology, allowing longitudinal data acquisition for the inference of changes in chronic emotional state over time. In lactating dairy cows, maximum IRT of the eyes and coronary band of the limbs seem to be most representative of thermoregulatory changes, are repeatable and correlate with behavioral and physiological indicators of emotional state. IRT methodologies have the potential to become a fundamental tool for the objective assessment of welfare state in dairy cows, which will impact positively on human health.

Keywords: One Health, body temperature, non-invasive, stress, cow welfare

Poster No. 43 (Abstract No. 11208)

Human and dairy cattle brucellosis in military farms of Bangladesh

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Brucellosis is the most widespread bacterial zoonotic disease throughout the world. WHO estimates only half a million cases annually being registered as human brucellosis distributed in more than 170 countries and the true prevalence is estimated at 5.0 to 12.5 million cases annually. In animals: mainly affects reproduction and fertility, with abortion and reduced milk yield. In humans: the clinical picture resembles many other febrile diseases, but sacroiliitis and hepato-splenomegaly are the most prominent. The brucellosis has been reported to be associated with bovine infertility for the first time in 1967 from Bangladesh. Most of the research on brucellosis was limited on the sero-epidemiology during the last 50 years in Bangladesh and recently molecular techniques have been initiated to study brucellosis. The objectives of this study were to determine sero-molecular prevalence, identify risk factors and detect *Brucella* species associated with bovine and human brucellosis in Bangladesh. Serum and milk samples from 1003 lactating dairy cows of eight military dairy farms and 715 serum samples of dairy farm workers and hospital patients were collected. All the collected sera and milk samples were tested with four different commercial diagnostic test kits to detect the prevalence of *Brucella* infection. The four sero-positive milkers' sera and milk and all animal samples collected from aborted cases were tested for *Brucella* genus-specific RT-PCR and *Brucella* species-specific DNA (*B. abortus* and *B. melitensis*) Multiplex PCR. The overall 2.39% sero-prevalence of *Brucella* infection was recorded with all the CFT, SAT and ELISA assay and 3.09% with RBT, whereas only 0.20% tested milks samples showed positive with MRT in the lactating dairy cows. The *B. abortus* DNA was amplified from all of the four RBT positive human serum samples tested. Phylogenetic tree of partial 16S ribosomal RNA sequences of the PCR products was closely matched with *B. abortus.* Three variables (age, parity and abortion) were found to be significantly associated with *B. abortus* infection in lactating cows. *B. abortus* is the causal agent of bovine brucellosis which is identified as the first time as an etiological agent of human brucellosis in occupationally exposed dairy farm workers in Bangladesh.

Keywords: Brucellosis, PCR, Human, dairy cows, military farms

Poster No. 44 (Abstract No. 11212)

Evidence of exposure to Nipah virus among domestic and peridomestic animals living in human outbreak sites in Bangladesh

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Background: A previous study has reported the exposure of domestic animals to NiV-like viruses in Bangladesh, although their role in transmission in Bangladesh remains unclear. Our objective was to detect infections among domestic and peri-domestic animals living in close proximity to bat roosts associated with human NiV cases in Bangladesh.

Methods: From Oct-13 to Oct-15 in six confirmed human Nipah outbreak sites we collected bat roost urine and collected blood samples from animals along with their feeding habits. All animal serum samples were sent to the CDC, Atlanta, where a human IgG ELISA was adapted and optimized to test animal sera by using alternative positive and negative control sera and horseradish peroxidase conjugated Pierce Recombinant Protein A/G.

Results: Of the five bat roosts sampled, roost urine from four had NiV RNA. No animal deaths were reported nearby human cases. We sampled 604 domestic (cattle, sheep, goat) and 552 peridomestic (rat, shrew, dog, cat) animals from 369 households. Cattle (3/274; 1%), dogs (5/189; 3%), and cats (4/85; 5%) had evidence of antibodies to NiV in their serum. 33% of cattle (91/274) and goats (110/330) were fed dropped fruit; two cattle with antibodies were fed dropped fruit.

Conclusions: NiV spillovers occur in ruminants and carnivores without obvious increases in mortality which may allow opportunities for the virus to evolve and transmit in other species. Surveillance for spillovers should include multiple species to truly understand the ecology of NiV and risks for transmission.

Keywords: Nipah virus, Spillover, Domestic and peridomestic animals

Poster No. 45 (Abstract No. 11226)

Isolation, identification and antibiogram of bacteria associated with cat oral cavity: a neglected issue

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Introduction: In modern days, people pass their time alone to some extent. Hence, keeping pet animals has been increasing globally including Bangladesh. Cat is one of the most popular pet animals in the world. Approximately 600 million cats live with human worldwide. Therefore, this study was conducted to isolate, identify and antibiotic profiling of bacteria found in pet cat's oral cavity in Dhaka city.

Methods: Forty oral swab samples were collected aseptically from cats at Central Veterinary Hospital (CVH), Dhaka and transported to National Institute of Biotechnology. Total bacterial count (TBC) was done by 10 fold dilution method. The confirmation of bacterial genera/species was performed by necessary cultural tests, Gram's staining methods and biochemical tests. Molecular identification and sequencing was also conveyed to some extent. Finally, antibiogram study of the isolated bacteria was done by disk diffusion method against seven different antibiotics.

Results: All samples showed positive result in TBC, therefore, the microbial prevalence was 100%. The highest TBC was 1.199×10^{13} and the lowest TBC was 3.60×10^{2}. The prevalence of *Escherichia coli, Salmonella* spp*.,* *Staphylococcus aureous* and *Staphylococcus epidermidis* were 100%, 5%, 60% and 7.5%, respectively. The presence of both pathogenic and non-pathogenic *E. coli.* were confirmed. Afterwards, the antibiotic sensitivity pattern was performed where *E. coli* showed the highest sensitivity to gentamycin (80%), followed by azithromycin (70%) and showed the highest resistance against ampicillin. *Salmonella* isolates showed the highest (100%) sensitivity to gentamycin, followed by azithromycin (50%) and highest resistance against ampicillin (100%). *Staphylococcus aureous* isolates showed the highest sensitivity to gentamycin (80%) and the highest resistance against ampicillin (100%), followed by erythromycin (80%), tetracycline (60%). *Staphylococcus epidermidis* showed the highest (100%) resistance against ampicillin and showed 100% sensitive to gentamycin.

Conclusion: The findings from study indicate that pet cats in Dhaka city contain multi-drug resistant *E. coli, Salmonella* spp*.,* *Staphylococcus aureus* and *Staphylococcus epidermidis. This multi-drug resistant phenomenon* can cause a potential public health hazard through transmission to humans through direct contact or the evolved way of life.

Keywords: Prevalence, Antibiogram, Multi-drug resistant, Public health

Poster No. 46 (Abstract No. 11254)

Developed Reverse Transcriptase - Polymerase Chain Reaction protocols using designed primers to detect circulating Peste des Petits Ruminants Virus from goats at slaughter houses in Bangladesh

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Introduction: The Peste des Petits Ruminants (PPR) are a highly contagious, deadly and economically significant transboundary viral disease affecting small ruminants, mainly goats and sheep. It is a common practice among poor goat owners that if the goats were infected, they could have sold to the local market. The infected goats were sometimes slaughtered at the meat market; this source could have transmitted PPR from slaughtered goats to farmer's sheds. This study aimed was to investigate pathology and develop Reverse transcriptase- Polymerase Chain Reaction (RT-PCR) protocols using designed N gene based primer sets to detect PPR virus (PPRV), and phylogenetic analysis of the circulating PPRV of slaughtered goats.

Methods: A total of 200 slaughtered goats were investigated in Mymensingh, Sherpur, Jamalpur and Netrokona districts from January 2019 to March 2021. Lungs, spleen and mesenteric lymph nodes were examined by the naked eye and collected for histology and molecular study. RT-PCR was carried out using designed primer sets (PPRV NF- gctctgtgattgcggctgagc and PPRV NR- cctggtcctccagaatcttggcc). The selected PPRV isolates were sequenced and submitted to GenBank. CLC sequence viewer was used for phylogenetic analysis.

Results: Pneumonic lungs in 80 goats, fibrinous covering with shrinkage spleen in 33 goats and enlarged mesenteric lymph nodes in 92 goats were recorded. Both intracytoplasmic and intranuclear inclusion bodies were seen in lymphocytes of the mesenteric lymph node, spleen and lungs. Among 200 slaughtered goat samples in the Mymensingh division, PPRV was detected in 37 goats (18.5%) by RT-PCR test using designed primer sets. 402bp amplicon was generated in PPRV-positive cases. The nucleotide sequence of PPRV isolates searched in BLAST nucleotide and found the highest percent homology with Bangladesh/2016/OK274194 (98.28%-99.78%) followed by China/2007/KX421388 (96.73%-98.15%), India/2016/KX033350 (96.48%-97.87%), Dubai/2018/MN369542 (95.42%-96.83%) and Israel/2014/OL310704 (95.15%-96.56%). The phylogenetic analysis revealed that the studied PPRV isolates of the Mymensingh division belonged to lineage IV.

Conclusions: Developed RT-PCR protocols successfully amplified the PPRV in goats at slaughter. Restricting free animal movement within the country, mass PPR vaccination campaigns, increased awareness among livestock producers through participatory training and education, and improved biosecurity in the meat market may lessen the incidence of PPR in goats and sheep.

Keywords: PPRV, designed primers, RT-PCR protocols, goats, slaughter house

Poster No. 47 (Abstract no. 11258)

Ectoparasites infesting companion animals living in close contact with humans in Sylhet, Bangladesh

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The number of companion animals living with humans is rapidly increasing in parallel with an increased risk of transmission of the pathogens they might carry. By sharing a common environment, ticks (Ixodida) and fleas (Siphonaptera) are considered amongst the most important arthropod of public health concern due to their ability to transmit vector-borne diseases. This study aimed to determine companion animal-associated ticks and fleas based on morpho-molecular approaches. Between December 2021 and May 2022, 74 animals (62 cats and 12 dogs) were examined, of which 17 (27.4 %) cats and 9 (75.0 %) dogs had ectoparasitic infestations, with 35.1% overall prevalence. After a comprehensive morphological and molecular study of representative specimens, the fleas and ticks were identified as *Ctenocephalides canis* in dogs, *Ctenocephalides felis* in cats, and *Riphicephalus sanguineus* in dogs. The PCR targeting the cox1 mitochondrial gene of *Ctenocephalides* species using the universal cox1F/cox1R primers yielded a specific amplicon approximately at 601 bp and 735 bp. When compared with the reference data in Genbank records, the cox1 sequences of flea specimens showed 99.4% homology to *Ctenocephalides canis* (MN173764) and 99.7% homology to *Ctenocephalides felis* (KF684876). The cox1 sequences of ticks showed 99.0% homology to *Rhipicephalus sanguineus* (KU214592). Ectoparasites occurrence varied according to the host's breed, age, and sex. A wide distributive area of ectoparasitic infestation in companion animals was observed in this study; however, 35.14% of owners had no concerns about the ectoparasitic infestation of their animals. Wide-spread screening of these ectoparasites should not be underestimated, considering their role as vectors of pathogens of medical and veterinary concern. The findings of the study might help in establishing effective control programs for ectoparasitic infestation in companion animals in Sylhet city.

Keywords: Ectoparasites, Companion animals, Morpho-molecular approaches, Awareness, One Health

Poster No. 48 (Abstract No. 11288)

Whole genome sequencing of a thermostable and Vero cell adapted candidate Newcastle disease vaccine strain for its molecular integration

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One avirulent strain, APMV/northern pintail/Japan/Aomori/2003 (dk-Aomori/03, NDV261) of Newcastle disease virus (NDV) was isolated from field in Japan and selected for its excellent thermostability. The strain was heat-treated at 56℃ for 30 min during each passage into Vero cells to maintain thermostability and to adapt to Vero cells. The intracerebral pathogenicity index (ICPI) test score was 0. After serial 20 passages in Vero cells, it was named NDV-Vero20. When growth curves were tested in Vero cells, NDV-Vero20 grew well in comparison to the original NDV261. NDV-Vero20 showed lower titer drops at 37 ℃ up to 10 days and it was immunogenic potential. Whole genome sequencing against NDV-Vero20 and NDV261 viruses using next-generation sequencing was carried out for molecular evaluation after heat treatment and adaptation on Vero cells to confirm its genome organization, protein length and phylogenetic analysis. The results showed that there is no significant variance in the genome sequences of NDV-Vero20 and the original NDV261. Especially no sequence variance in F and HN genes which are responsible for virulence and thermostability respectively. So, candidate vaccine strain is thermostable, Vero cell adapted, and has immunogenic potential which would make it an advisable alternative to the traditional embryonated chicken eggs-based vaccine.

Keywords: Newcastle disease virus, Thermostable, Vaccine candidate

Poster No. 49 (Abstract No. 11291)

Traditional healers matter in One Health approach to rabies control in Bangladesh

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Rabies is a zoonotic viral disease that has huge impact on human and animals in Bangladesh. According to the Ministry of Health and Family Welfare, there are 4 million people seek for rabies vaccine each year due to dog bites which indicates a significant risk of rabies to the country. Not to mention the fact, many dog bite victims (59%) visit traditional healers to receive primary treatment rather than going to a hospital. Traditional healers offered treatment comprises the use of oils, salt, herbs, red chilies on dog bite wounds and eating medicated bananas (locally called as "Kola Pora") and drinking water (locally called as "Pani Pora"). But they are often neglected and left out from 'Rabies Prevention and Control Program in Bangladesh". They don't know the importance and value of immunization and thereby contribution to the prevention and control of Rabies. As there are persisting myths and false beliefs on traditional healers regarding the management of dog-bite cases among people with low socioeconomic status in rural areas, so it is crucial to implement an outreach communication initiative to engage and educate traditional healers on rabies prevention measures in both animals and humans. This will be a way where they can learn about rabies, its infectiousness and the importance of early PEP and dog vaccination in controlling the disease, both in dogs and humans. This effort aims to reduce the number of human rabies cases and deaths in Bangladesh by educating and motivating traditional healers and improving dog vaccination coverage and collaborating with multi-sectoral partners to achieve a rabies-free country by 2030.

Keywords: Traditional Healers, Rabies, Awareness, Control, Bangladesh

Poster No. 50 (Abstract No. 11401R)

Gut microbiome analysis revealed that pet birds carry bacteria having potentials to do human infection

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Introduction: The gut microbiota of animal may have a significant impact on health and disease and vary depending on their genetic makeup, environment, diet and behavior. Little is known about the gut microbiota of pet bird species popular in Bangladesh. This is crucial to comprehending the effects of microorganisms on health and is pertinent in the context of zoonoses.

Methods: Gut content of pet birds of order Psittaciformes: Budgerigar (Bud) (*Melopsittacus undulatus*), Lovebird (LoB) (*Psittacus* spp*)*, Cockatiel (Coc) (*Nymphicus hollandicus*); and Passeriformes: Finch (Fin) (Fringilla coelebs) were collected. Besides, droppings of five types of pigeons (*Columba livia*) of Columbiformes order were also collected. For each species three samples were analyzed. DNA was extracted using microbiome kit and sequenced from Novogene Bioinformatics Technology Co., Ltd. (Beijing, China) on an Illumina Nova sequencing platform. 16S rRNA gene (V4 region) was amplified by a specific primer (515F-806R). Data were analyzed using different softwares.

Results: An average of 65,509 reads and 64,507 tags per sample were measured, and subsequently 100,115 clean tags were calculated. An average of 27,784,575 nucleotides per sample was found. Average Q20 and GC% were 99 and 52, respectively. The sequences were clustered into operational taxonomic units (OTUs) with 97% identity and a total of 1,188 OTUs were obtained. The average OTUs were 271. Makshi racer harbored most OTUs (387) followed by Black racer (BR3) and Budgerigar (Bud3) each with 368 OTUs. The core OTUs among group were 300. *Psittaciformes, Columbiformes* and *Passeriformes* had 382, 184 and 62 unique OTUs. A total of 14 phyla, 30 classes, 80 orders, 132 families, 278 genera, and 219 species were identified. Population and diversity of microbiome is evident. *Columbiformes* and *Passeriformes* had higher and lowered microbiota, respectively. *Psittaciformes* and *Columbiformes* had higher and lowered observed species, respectively. Significantly different β-diversity was found between *Passeriformes-Columbiformes* and *Psittaciformes-Columbiformes*. But no significantly different β-diversity was found between *Passeriformes-Psittaciformes*. About 54 bacteria including *Raoultella ornithinolytica* have been identified those have potentials to infect human.

Conclusion: Differences in composition of gut microbiota were observed among the species and many bacteria that could potentially infect humans have been identified.

Keywords: Pet birds, Gut microbiome, Zoonoses, Bangladesh

Poster No. 51 (Abstract No. 11451R)

Characterization of *Escherichia coli* and *Salmonella* spp. isolated from fecal materials of popular pet birds with emphasis on antimicrobial profiling

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Introduction: Pet birds rearing have been increasing with the increased socio-economic condition. Pets may be a potential source of risk for its owner including spread of zoonotic pathogen as well as drug-resistant bacteria. *Salmonella* spp. and *Escherichia coli* are considered as the most common zoonotic pathogen in the world. Moreover, bacterial resistance to antibiotics has been extensively studied because it is a matter of health concern. This study assessed the occurrence of *Salmonella* spp. and *E. coli* in caged birds along with their antimicrobial profiling.

Methods: A total of 45 fecal samples were collected from caged birds like Pigeon (n=20), Budgerigar (n=15) & Lovebird (n=10) from pet shops of Katabon market, Dhaka. Samples were directly collected from the tray under the cage where several birds of each species were kept in one cage. Hence it was possible to mark fecal samples of each species. Bacteria were isolated using selective media and identified by biochemical and molecular test using 16S rRNA gene of *E. coli* and *invA* gene of *Salmonella* spp. Antimicrobial profiling was performed against the commonly used antibiotics by disk diffusion method. Besides, AMR genes were detected by PCR in *E. coli*.

Results: *E. coli* and *Salmonella* spp. were isolated and identified from 48.9 and 17.8% samples, respectively. The occurrences of *E. coli* were 35.0, 73.3 and 40.0% in pigeon, budgerigar and lovebird, respectively. *Salmonella* spp. could not be isolated from samples of budgerigar & lovebird. The antibiotic profiling study revealed that 100% *E. coli* isolates were resistant to tetracycline, ampicillin & colistin but sensitive to ciprofloxacin, norfloxacin, amikacin, azithromycin & gentamicin. Predominant resistance gene/s detected by PCR were tetA and tetB (100%) for tetracyclines, dfrA1 (30%) for trimethoprim. But ampicillin (blaSHV), gentamicin [aac(3)-IV], fluoroquinolones (qnrA) and colistin sulphate (mcr1 and mcr3) resistance genes were not detected. On the other hand, all the *Salmonella* spp. showed resistance to tetracycline & trimethoprim but sensitive to amoxicillin, amikacin & gentamicin.

Conclusion: This study reveals that the companion birds may contribute in spread of AMR bacteria through feces and thus poses potential risk for humans.

Keywords: Pet birds, *Escherichia coli*, *Salmonella* spp., Zoonosis, Antimicrobial resistance

Poster No.52 (Abstract no.11019)

Antimicrobial resistance genes in *E. coli* isolated from frozen broilers

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Introduction: Antimicrobial agents have been used to improve animal welfare, food security and food safety. However, it is noticed that inadequate selection, overuse and misuse of antibiotics promoted the growth of antimicrobial resistance (AMR) in various bacteria. The level of AMR in *E. coli* has been used as an indicator of resistance dissemination in bacterial populations, and the selective pressure imposed by antimicrobials used in food animals and humans. Therefore, continuous surveillance of AMR in bacteria is necessary.

Methods: A total of 160 frozen broilers were purchased from different supermarkets in Dhaka city. *E. coli* were isolated from surface muscle of these chickens and identified by biochemical test and PCR. Antimicrobial profiling of these isolates was done against seven antimicrobials of six classes by disk diffusion method. These included Aminoglycosides: Gentamicin (10µg) & Streptomycin (10µg), Tetracyclines: Tetracycline (30µg), β-lactam: Ampicillin (10µg), Macrolides: Erythromycin (15µg), Phenicols: Chloramphenicol (30µg), and Sulfonamides: Sulfonamide (300µg). Ten antimicrobial resistance genes (ARGs) viz. *aadA1, aac(3)-IV, tet(A), tet(B),* bla_{SHV}, bla_{CITM}, *ereA, catA1, cmlA* and *sulI* were investigated using gene specific primers.

Results: *E. coli* was isolated and identified from 31.25% (50/160) samples. All the isolates were found resistant to one or more of seven antimicrobial agents used in the study. The most commonly observed resistance phenotypes were to tetracycline (66.0%), erythromycin (42.0%), ampicillin and streptomycin (38.0%), and sulfonamide (28.0%). On the other hand most commonly identified resistance genes were *tet(A)* (66.0%), *ereA* (64.0%), *tet(B)* (60.0%), *aadA1* and *sulI* (56.0%), bla_{CITM} (48.0%) and bla_{SHV} (40.0%). About 84.0% of the isolates were multi-drug resistant (MDR) and 61.9% of the isolates showing resistance to 4–7 antimicrobial agents. Multiple (4-9) ARGs were detected in 84.0% of the isolates. Strong positive associations were found in AMR phenotypes and the corresponding resistance genes.

Conclusion: *E. coli* isolated from frozen broiler carried MDR phenotypes as well as resistance genes. Therefore, cautions are required for personnel hygiene during processing and handling of frozen broiler to prevent transfer of MDR *E. coli*. The study also highlighted the necessity of thoughtful use of antimicrobials in chickens to minimize the development of antibiotic-resistant bacterial strains.

Key words: AMR, broiler, E Coli, MDR

Poster No. 53 (Abstract No. 11005)

Detection and molecular characterization of *mcr-1* gene positive *Salmonella* isolated from dairy cattle

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Introduction: The mcr-1 gene has been identified in bacterial isolates obtained from humans, animals, the environment, and food, including *Salmonella* spp., which is one of the major foodborne pathogens having a public health impact worldwide. The main objectives of this study were to determine the in-vitro antimicrobial susceptibility status of *Salmonella* and to identify the *mcr-1* gene in *Salmonella* isolated from the feces of dairy cattle.

Methods: This research was carried out on the different selected dairy farms in the Sylhet district of Bangladesh. A total of 200 fresh feces samples were collected directly from the rectum of dairy cattle. Conventional bacteriological methods were used to isolate *Salmonella* from the sample. The DNA was extracted using a DNA extraction kit and kept at -20°C until further analysis. Extracted DNA was subjected to PCR for the confirmation of Salmonella isolates using specific primers targeting the invA gene. For the detection of mcr-1 genes, DNA extracts of Salmonella isolates were subjected to PCR using designed primers. The amplified products were visualized by gel electrophoresis using 1.5% agarose gel and viewed under UV trans-illumination in a gel documentation system. Antibiograms were obtained for *Salmonella* isolates by the Kirby–Bauer disk diffusion method utilizing Mueller Hinton agar.

Results: Among 200 fecal samples, 24 (12%) were found positive for Salmonella based on their morphological and biochemical properties. Out of 24 isolates, 10 Salmonella isolates were randomly selected for further confirmation by PCR for the presence of the *invA* virulence gene, and the *invA* gene was found to be positive in all ten *Salmonella* isolates. Antibiotic resistance in *Salmonella* isolates was found to be significantly high to Amoxicillin (87.50%), Trimethoprim/Sulfamethoxazole (75%), and Tetracycline (45.83%), respectively. In addition, the largest percentages of Salmonella isolates were sensitive to Gentamycin (75%) and Neomycin (66.66%). One out of 10 randomly selected Salmonella isolates obtained from dairy cattle were found positive for *mcr-1* and deposited into the GenBank for accession number. The obtained sequences showed 100% similarity to the allele retrieved from the NCBI database.

Conclusion: The presence of the *mcr-1* gene in *Salmonella* emphasizes the necessity of monitoring AMR in the food supply chain and promoting appropriate antibiotic usage in livestock.

Keywords: *mcr-1* gene, *Salmonella*, Antimicrobial Resistance, Dairy cattle

Poster No. 54 (Abstract No. 11006)

Identification of oral and periodontal disease pathogens and antimicrobial resistance pattern of children in Bangladesh

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Introduction: Oral cavity is an important part of the body and protection against antimicrobial infections. The most common oral and periodontal diseases (OPD) are oro-pharyngeal cancer, mouth sores, congenital anomalies, gum diseases, dental caries, periodontitis and other disorders such as HIV/AIDS which are major public health problems worldwide. This study was conducted to investigate the oral and periodontal disease pathogens in children and to determine their antimicrobial resistance pattern in Bangladesh.

Methodology: A total of 131 oral swab samples were collected from the age group 4−10 years of children in outdoor dental unit of Mymensingh Medical College Hospital, Mymensingh during October 2019 to March 2020. The isolation and identification of OPD pathogens were performed based on morphology, cultural, staining, biochemical properties and PCR (conventional and real-time). The isolates were subjected to antimicrobial susceptibility test using 12 commonly used antibiotics in dentistry by disk diffusion method. Finally the relation of the pathogens were analyzed by phylogenetic analyses.

Results: Five major pathogens were identified which were *Staph. aureus* (64/49%), *S. salivarius* (60/45.8%), *S. mutans* (22/16.8%), *L. fermentum* (18/13.7%) and *S. sobrinus* (1/0.8%) and *Staph. aureus* was the highest (49%). Antibiotic sensitivity test showed that 100% of *Staph. aureus* were resistant to metronidazole, 95.3% were found resistant to cephradine and 90.6% were resistant to amoxicillin. For *Lactobacillus* 100% were resistant to amoxicillin, 94.4% were resistant to metronidazole and 88.9% were resistant to cephradine. For *Streptococcus* sp. 98.8% were resistant to metronidazole, 97.6% were resistant to cephradine and 96.6% were resistant to amoxicillin. However, none of the isolates were 100% sensitive to any tested antibiotics. Overall, 100% of *Lactobacillus* spp, 95.2% of *Streptococcus* spp. and 92.2% of *Staph. aureus* were multidrug resistant. There were two resistance genes identified which were β−lactamase gene *blaTEM* and *cfxA*. There were *blaTEM* gene positive for *L. fermentum* (11/18); *Streptococcus* sp. (10/83) and *Staph. aureus* (3/64). Detection of *cfxA* gene by real-time PCR were positive for *Streptococcus* sp. (79/83); *Staph. aureus* (60/64) and *L. fermentum* (13/18). However, metronidazole belongs *nim* gene was not detected in tested isolates. We also identified methicillin resistance gene (*mecA*) from *Staph. aureus* (8/12.5%). In phylogenetic analyses of the organism/gene found that Bangladeshi isolates showed genetic variation among themselves but similar to the global isolates.

Conclusion: Antibiotics have to be used judiciously to prevent AMR in children

Keywords: AMR, OPD, PCR, sequencing

Poster No. 55 (Abstract No. 11022)

Engaging communities to address antimicrobial resistance: A novel initiative towards identifying contextualized and sustainable community led solutions in low resource settings

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Introduction: Community engagement (CE) approaches that have impacted health outcomes are often intensive, small-scale and usually require high levels of financial and human resources. They can be difficult to sustain and scale-up in low resource settings. Our recent study explored the process of developing an embedded approach to CE taking the global challenge of antibiotic resistance (AMR) as an example. We identified the Community Dialogue Approach (CDA) as having potential to address antibiotic consumer behavior through CE. The present ongoing research is based on the previous experience of involving CE in a 'One Health' perspective to combat AMR. Our focus is (i) to assess the effectiveness of the CDA approach to impact on AMR in Bangladesh (ii) Costing study and process evaluation to explore the potential for sustainability and implementation at scale (iii) Look at reliability in a new context (Nepal)

Methods: The CDA involves training of community-based volunteers to facilitate regular community meetings where specific 'One Health' issues will be explored and local solutions around AMR and relevant One Health issues will be identified. The One Health team has a strong capacity-building focus. A research uptake strategy has been implemented to engage a wide range of local, national and international stakeholders across the One Health sphere. We hope to develop a sustainable approach to tackling AMR at community level. These methods will be combined and implemented at a larger scale in Bangladesh and partly in Nepal.

Results: The expected output of the project will include (i) identification of the key drivers of AMR within rural communities in Bangladesh and Nepal (ii) development of new contextualized CDA materials (iii) better understanding of the extent to which our CDA approach to CE impacts on knowledge, attitudes and reported behaviors in relation to AMR (iii) Increased knowledge/ recommendations regarding contextually appropriate mechanisms for replicating the approach in new settings (Nepal).

Conclusion: The CDA has the potential to contribute to a body of urgent action recommended by the WHO and 'National One Health Action Plan' of Bangladesh to prevent AMR. However, observations revealed a need to strengthen communities' capacity to plan and put decisions into action and monitor progress. Additionally, multi-sectorial collaboration is required to expand the content of the CDA to incorporate One Health dynamics.

Keywords: Community engagement, Community Dialogue Approach, One Health, Animal health, Antimicrobial resistance

Poster No. 56 (Abstract No. 11024)

A survey on knowledge, attitude and practices of large animal farmers towards antimicrobial use, resistance and residues in Mymensingh division of Bangladesh

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Introduction: The widespread use of antimicrobials in food animals is a key contributor of antimicrobial resistance and antimicrobial residue which has become a growing public and animal health concern in developing countries like Bangladesh. This study was aimed to assess the knowledge, attitude and practices of the large animal farmers towards antimicrobial use (AMU), antimicrobial resistance (AMR) and antimicrobial residue (AR) and to relate these results with their biosecurity management system of farm.

Method: A cross-sectional survey was conducted with a structured and pretested questionnaire in Mymensingh division of Bangladesh. A total of 212 large animal farmers (Including dairy, beef fattening, buffalo, sheep and goat farmers) were surveyed.

Results: Result shows that most of the farmers are male (85.8%) and are belonging to 18-30 age group (37.3%). 20.3% had no formal education and close to half participants (48.1%) received training regarding antibiotic use and resistance. Penicillin is the most common class of antibiotics used (61.79%) in study area followed by other antibiotics. Only 37.7% farmers used antibiotics by the recommendation of veterinarian. Overall, 41.5%, 42.5% and 21.7% farmers possess adequate knowledge, satisfactory attitude and perform desirable practices, respectively. 31-40 years and 41-50 years aged group farmers have adequate knowledge, attitude, doing desirable practice and good management of farm compared to 18-30 years' age group farmer. Farmers having formal education scored better in relation to knowledge, attitude and practice than that of illiterate farmers. Analysis revealed that farmers who received training on AMU and AMR had 10.014 times (ORs = 10.014, 95%CIs =5.252-19.094), 10.3 times (ORs = 9.409, 95% CIs =4.972-17.806) and 25.994 times (ORs = 25.994, 95% CIs =7.73-87.414) better knowledge, attitude and performance, respectively compared to their counterparts. A significant proportion of farmers (97.2%) dispose leftover antibiotics inappropriately. Biosecurity management of the farm significantly associated with farmer's level of education (p=0.001), training received (p=0.000), farm type (p=0.001) and population size of the farm (p=0.000).

Conclusion: Results of the study could be used to intervene education and training of the farmers which will help to limit the indiscriminate and irrational use of antibiotics as well as to reduce the chances of developing AMR.

Keywords: Large animal farmers, KAP, survey, AMU, AMR

Poster No. 57 (Abstract No. 11025)

Assessing informal veterinary healthcare provider's perspective regarding antimicrobial usage, antimicrobial resistance and antimicrobial residues in Mymensingh division, Bangladesh

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Introduction: Indiscriminate use of antibiotics contributes to the development of antibiotic resistance in bacteria in countries like Bangladesh where both human and veterinary health systems are not well regulated. Informal veterinary health providers (IVHP) are strongly involved in a significant portion of primary veterinary healthcare in Bangladesh but there is no information in the literature on their level of knowledge, attitudes, and practices. This study was intended to assess the knowledge, attitude and practices of IVHP pertaining to antimicrobial use, resistance and residues.

Method: A cross-sectional survey of 128 informal veterinary health providers (Govt. veterinary paraprofessionals, Village animal doctor, veterinary drug sellers, medicine company professionals and NGO artificial insemination workers) were conducted with structured and pretested questionnaires from four upazilas of each district of Mymensingh division of Bangladesh.

Results: All of the IVHP were male with experience of 1-33 years in this field. 30.5% of them had HSC degree followed by 25% had graduation and 60.9% received training. Results revealed that 100.0%, 82.8% and 66.4% informal veterinary healthcare providers have heard about antibiotics, antimicrobial knowledge and antimicrobial residue respectively but surprisingly when they have asked about "what antibiotics do?", only 36.7% answered correctly, whereas, 81.2% and 61.6 % described antimicrobial resistance and residue satisfactorily). Above half of the IVPH (54.7%) didn't believe that antibiotic residue may be the cause of antibiotic residue. 61.0% informal veterinary healthcare providers answered that antibiotic should only be prescribed by veterinarian. Most of the IVPH showed good attitude about antibiotic use neither as growth promoter nor for preventive purpose. About 61.7% IVPH practices extra-level dosing of antimicrobials. It was very alarming that a significant percentage of IVPH (88.3%) did not suggest farmers to maintain withdrawal period of antimicrobials, even no veterinary drug seller maintained records of antibiotic sell.

Conclusion: The results of the study highlight the incompatibility between knowledge, attitude and practices among different informal veterinary healthcare providers who need to train up in order to minimize the irrational AMU in large animals for the reduction of AMR.

Keywords: Informal veterinary health providers, knowledge, attitude and practices, survey

Poster No. 58 (Abstract No. 11041)

Influence of knowledge on the attitude and practice of poultry farmers on the use of antimicrobial drugs in Mymensingh, Bangladesh

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Introduction: The poultry sector is a major force in the agricultural sector of Bangladesh that is soon preparing to export its products to international market. Thus the knowledge, attitude, and practice of the stakeholders in poultry production should be of high standard. The aim of this study was to assess the knowledge, attitude, and practice (KAP) of poultry farmers towards the use of antimicrobials (AMU), antimicrobial resistance (AMR) and antimicrobial residue.

Method: Seventy-five poultry farmers (layers, broilers and ducks' farmers) were surveyed in a cross-sectional study that included both open-ended and closed-ended questions across four districts of Mymensingh division.

Result: Most of the farmers had formal education (92%). Nearly half of them (46.66%) had flock size between 1001-5000 birds. 93.3%, 52% and 49.3% farmers heard about antibiotics, antimicrobial resistance and antimicrobial residue, respectively. However, only few farmers (17.33%) answered correctly when they were asked about "what antibiotics do?", whereas 46.6% and 41.33 % described antimicrobial resistance and residue properly. About 42.6% farmers used antibiotics by veterinarian's prescription only, whereas, rest of them took suggestion about antibiotic use from either single informal veterinary healthcare providers or more than one prescribers including veterinarian. About 22.66% antibiotics were only used for treatment purpose, the remaining were used for prevention or as growth promoter or for both purposes. A significant proportion of farmers (90.7%) did not add antibiotics in poultry feed. On the other hand, most of the farmers did not follow withdrawal period of antimicrobials (82.7%). In addition, 22.7% and 25.33% farmers stored antibiotics in right way and kept the record of antibiotic use respectively.

Conclusion: The anticipated data would help future interventions to increase knowledge among poultry farmers which would definitely change their attitude and practices towards irrational or indiscriminate use of antimicrobials as well as to combat with antimicrobial resistance which are considering a major One Health approach concern.

Keywords: Poultry farmers, KAP, survey, AMU, AMR

Poster No. 59 (Abstract No. 11062)

Accessible veterinary care in poultry farms and antimicrobial resistance in Bangladesh: a qualitative investigation

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Background: The poultry sector is one of Bangladesh's fastest-growing industries. With this growth, providing quality products and services to the growing number of poultry farms across the country has become a significant challenge. One of the most critical challenges is the timely provision of required veterinary services. This study aims to determine the extent to which veterinary services are available in dealer-dependent and company-regulated poultry farms, assess farmers' understanding of antibiotics, and how these circumstances can contribute to the emergence of antimicrobial resistance (AMR).

Methods: A qualitative study has been conducted through semi-structured interviews with exotic broiler and Sonali poultry farmers (n=35), feed dealers (n=29), and veterinarians (n=41) in 10 districts of Bangladesh into disease management practices on farms, access to veterinary services, antibiotic usage, and the breadth of farmers' antibiotic understanding.

Results: For most farms relying on credit provided by feed dealers, the first course of treatment typically begins with the farmer's or dealer's own experience, followed by seeking out veterinary counsel if the desired results are not attained. Some farmers are hesitant to accept the veterinarian's suggestions due to their supposition of having superfluous prescriptions and unwillingness or inability to pay for the medications. Contrarily, veterinarians encounter difficulties reaching farmers in remote areas due, in some instances, to reliance on feed dealers to gain access to farms. This resulted in farmers' dependency on non-expert advice for veterinary care. This gap between farmers and veterinarians and the engagement of intermediary stakeholders has increased the misuse of various medications, including antibiotics. In contrast, a low incidence of illness or use of medications in company-regulated contract farms is attributed to the designated representative's routine farm visits, management inspections, and swift supply of veterinary services. The study further revealed the farmers' insufficient knowledge about antibiotic usage, misuse effect, and AMR. The cumulative effect of these factors increases the usage of a wide range of antibiotics, and raises concerns about AMR.

Recommendations: Making veterinary services more accessible, improving awareness about antimicrobial usages and resistance, and adopting legislation prohibiting antibiotic abuse with effective monitoring system can help address the rising threats.

Keywords: AMU, AMR, Veterinary service, Farm

Poster No. 60 (Abstract No. 11073)

Bacterial predominance and antimicrobial susceptibility patterns of blood culture in adult and child group at a tertiary care hospital, Bangladesh

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Background: Determine bacterial profiles and the change of antimicrobial resistance provides an important guidance for effective and optimized use of antibiotics in local healthcare systems.

Objective: The purpose of this study was to evaluate the antimicrobial susceptibility pattern of predominant isolated bacterial in blood culture.

Methodology: This cross-sectional study was conducted in the department of Microbiology at Monno Medical College, Manikganj, Bangladesh during the period from January 2019 to December 2019 for duration of one year. A total number of 178 respondents were selected. In adult patient 5-10 ml blood was collected and inoculated into BacT/ALERT FA plus aerobic blood culture bottles with 0.025% of sodium polyanethol sulfonate (SPS) as anticoagulant and in pediatric cases 1-2 ml of blood was inoculated in BacT/ALERT PF plus pediatric blood culture bottles. After collection these bottles were immediately incubated in BacT/ALERT 3D (manufactured by bioMerieoux, France) a fully automated blood culture system. The positive bottles were then subculture on Blood Agar, Chocolate Agar and Mac Conkey Agar. Antimicrobial susceptibility test was done for all isolated bacteria by disk diffusion method.

Results: Among 178 cases, 12 (7%) yielded growth of different bacteria. Among them culture positive cases were found 7 (4%) in child age group and 5 (3%) in adult age group. The most predominant identified bacteria in child group was Escherichia Coli (3 out of 7) which showed highly sensitive to Imipenum, Amikacin, Linezolid, Gentamicin (N=3, 100%). In adult group the most predominant isolated bacteria was Streptococci (3 out of 5) which showed high sensitive to Imipenum, Linezolid, Gentamicin (N=4, 80%).

Conclusion: There were a high percentage of bacteria resistant to several antibiotics. Antibiotic susceptibility testing is a prerequisite guide for the selection of appropriate antibiotic therapy for bacterial infections.

Keywords: Blood cultures, Blood stream infections, Bacterial isolates, Antibiotic sensitivity, BacT/ALERT

Poster No. 62 (Abstract No. 11104)

Can multisectoral coordination mitigate antimicrobial resistance in Bangladesh? Collaborative interventions of USAID Medicines, Technologies, and Pharmaceutical Services Program with Government of Bangladesh

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Antimicrobial resistance (AMR) is a huge concern for public health in Bangladesh, and globally where AMR caused 1.27 million deaths in 2019. There is also a high prevalence of AMR in the country causing ineffectiveness of first-line drugs, reduced success of antimicrobial treatment and higher healthcare expenditure. To mitigate AMR, the World Health Organization (WHO) has recommended multi sectoral coordination (MSC) as an effective approach worldwide. USAID Medicines, Technologies, and Pharmaceutical Services (MTaPS) Global Health Security Agenda program supports the Ministry of Health and Family Welfare (MOHFW) to implement effective MSC on AMR through regular review and improvement of joint external evaluation (JEE) capacities and increased achievement of the WHO benchmarks for International Health Regulations in Bangladesh.

MTaPS has been collaborating with the Communicable Disease Control (CDC) program of the Directorate General of Health Services (DGHS) under MOHFW since 2019 to improve the MSC mechanism on AMR. MTaPS supported the completion of 25% of actions at the limited capacity level, 100% at the developed capacity level and 50% at the demonstrated capacity level, bringing the country to 47% overall MSC benchmark achievement. MTaPS contributed to the restart of regular meetings of the National Technical Committee on AMR through continuous communication, advocacy and agenda setting. During the last two years of collaboration, MTaPS assisted CDC, DGHS to develop a Monitoring & Evaluation framework for the National Action Plan (NAP) on AMR Containment 2017-2022, and update the National Strategic Plan and NAP for AMR Containment. MTaPS continues to support joint stakeholder meetings to accelerate achievement of the NAP-AMR objectives, including developing a costed operational plan for the NAP-AMR and establishing an in-country agenda for World Antibiotic Awareness Week. The program’s initiatives have helped MOHFW make progress towards higher WHO JEE benchmark levels.

Given the crucial importance of MSC in combating AMR with a One Health spirit, USAID MTaPS will continue its support to the government to strengthen national MSC mechanisms and achieve progress towards higher capacity levels in the JEE indicator P.3.1 (effective MSC on AMR). Additional coordinated initiatives and partnerships, funding and capacities are needed to further institutionalize and sustain these gains.

Keywords: Multisectoral Coordination, Antimicrobial Resistance, Joint External Evaluation, National Technical Committee, WHO Benchmark

Poster No. 63 (Abstract No. 11204)

Genomic insights of an emerging multidrug-resistant non-aureus *Staphylococcus* sp. isolated from murine mastitis

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Introduction: Mastitis is one of the most prevalent and economically important diseases in the dairy industry worldwide. The disease is caused by a plethora of emerging, opportunistic, and commensal microbes, including *Staphylococcus* spp. This study aimed to elucidate the genomic characteristics, antimicrobial resistance repertoire, virulence, and metabolic functional potentials of a non-aureus *Staphylococci* (NAS), *Staphylococcus warneri*.

Methods: We characterized a non-aureus *S. warneri* G1M1F strain from the feces of mastitis-induced pregnant mice using both culture-dependent and -independent (16S rRNA and whole genome sequencing; WGS) methods, antibiogram, virulent gene(s) and metabolic functional profiling.

Results: Out of 101 isolates screened, 41 (40.60%) were found positive for *Staphylococcus* spp., including *S. aureus* (46.34%), *S. warneri* (34.15%) and *S. haemolyticus* (19.51%). The non-aureus *S. warneri* was confirmed through biochemical tests and ribosomal gene (16S rRNA) sequencing. The *in vitro* antibiogram profiling revealed that *S. warneri* strain G1M1F was a multidrug-resistant (resistant to ≥ 5) strain showing the highest resistance against gentamicin, tetracycline, ampicillin, oxacillin, cefoxitin, nalidixic acid, and sulfonamide antibiotics. The WGS of *S. warneri* strain G1M1F yielded a genome size of 2.5 Mbp with 32.5% GC content,100% BUSCO completeness, and 60.0% genome coverage. The *S. warneri* G1M1F strain possessed 32 contigs, 2426 protein-coding sequences (CDSs), and 38 RNA genes, including 31 tRNA, 3 rRNA, and 4ncRNA genes. Twenty-seven antimicrobial resistance genes including *blaZ*, *mecA*, *mgrA*, *norA*, *msrA*, *gyrA* etc. were predicted in the draft genome. The *S. warneri* G1M1F also harbored 112 virulence factors and 278 SEED subsystems with 34% subsystem coverage.

Conclusion: This study, for the first time, identified a multidrug-resistant non-aureus *S. warneri* G1M1F strain from murine mastitis that showed a diverse evolutionary origin. The draft genome contained virulent and antimicrobial resistance genes and metabolic functional potentials similar to other clinical isolates of *Staphylococci*. These findings of this study will help to develop a species-specific diagnostics for rapid and accurate diagnosis of mastitis and optimize therapeutic schemes for better prevention and control.

Keywords: Murine mastitis, *Staphylococcus warneri*, whole genome sequencing, multidrug resistance, virulence

Poster No. 64 (Abstract No. 11207)

Putting the principles of One Health into practice through a private sector approach: Lesson learned from a leading animal health company to promote antimicrobial resistance stewardship in the livestock sector

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Introduction: Indiscriminate Antimicrobial Use is a global threat to animal and human health, resulting in an alarming increase in Antimicrobial Resistance (AMR) development. This is an acute issue in Bangladesh, as the livestock sector is a major source of nutrition. To address the issues, the USAID funded Livestock and Nutrition Activity adopted a private sector approach with ACME Laboratories Ltd. to implement the principles of One Health. The paper discusses their systemic commercial approach to reduce AMR as an opportunity to promote non-antimicrobial immunity booster products while changing the behaviors of market actors at various tiers**.**

Methods: Primary sources are utilized to compile the findings. During February 2023, KII interviews were conducted with various stakeholders including livestock farmers, veterinarians, local service providers (LSP), and stockiest in Jashore and Barishal. All promotional channels at various tiers were evaluated. A significant number of veterinarian prescription and the company's sales report were also analyzed to draw the findings.

Results: Through the approach, ACME aims to provide quality animal health inputs and services to 100,000 farmers through over 2000 LSPs trained in AMR and good farming practices. They engaged more than 500 veterinarians in the target areas and different relevant professionals through vet conferences. After the prescription analysis, ACME observed promising early symptoms that veterinarians are prescribing fewer antibiotics and recommending more vitamins, minerals, and probiotics products. ACME is collaborating with local chemist shops where vets make regular visits and conducting animal health campaigns to educate farmers and LSPs about AMR and promote non-antimicrobial product lines in regions with limited access to animal health inputs and services. As a result, ACME found a 29 percent rise in sales of prebiotics and probiotics in the Activity Areas, and a 23 percent increase in sales of nutritional/vitamin-mineral supplements in locations where sales were negative before the intervention.

Conclusion: The private sector approach has demonstrated that there is a market for non-antimicrobial product lines if they are placed in an integrated manner. Hence, the private sector can play a significant role by incorporating AMR strategies into their core business plans in order to promote non-antimicrobial product lines.

Keywords: Antimicrobial Resistance (AMR), Livestock Service providers, USAID Livestock and Nutrition Activity, animal health campaign, commercial approach

Poster No. 65 (Abstract No. 11215)

Phenotypic characterization and whole genome analysis of bacteriophage BAU.Micro_SLP-22 against multidrug resistant avian *Salmonella* spp.

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Background and objective: Multidrug resistant (MDR) *Salmonella* spp. associated with Salmonellosis causes huge economic losses in poultry industries. Applying bacteriophage therapy as an alternative option of antibiotics is a prominent step to cope with the crisis. In this study a novel lytic bacteriophage BAU.Micro_SLP-22 was isolated from sewage water as a therapeutic agent against MDR *Salmonella* spp. and was characterized by *in vivo* and *in vitro* approaches.

Methods: Isolation of the bacteriophage has been performed by enrichment method with host bacteria, spot test and plaque assay and then characterization has been performed by pH and heat survivability test, one step growth curve, *in vitro* antibacterial, *in vivo* toxicity test and Next generation sequencing.

Results: The phage exhibited a broad host lytic activity, remarkable thermal stability from 0°C to 60°C and pH survivability from 4 to ≥ 9. According to one step growth curve analysis, the isolated phage has relatively shorter latent period of < 20 min and larger burst size of >300 PFU, which indicates its strong lytic activity. The phage BAU.Micro_SLP-22 exhibited strong antibacterial activity against *Salmonella* spp.by *in vitro* antibacterial activity investigation. No toxicity was observed in case of toxicity investigation test as the phage was injected into BALB/c mice model. More over in vivo efficacy test of the isolated phage revealed the successful recovery report of the *Salmonella* spp. infected experimental mice by the phage treatment. From Next generation sequencing (NGS) analysis data, the double stranded phage DNA length is 2,42,090 bp which contains 51% GC content and 373 coding sequences and does not contain any toxin producing or virulent gene.

Conclusion: All the findings suggest that, BAU.Micro_SLP-22 is a potential candidate for phage therapy against MDR *Salmonella* spp. to combat against Salmonellosis as well as antibiotic resistance.

Keywords: Antimicrobial resistance, Phage therapy, Salmonellosis, NGS, *in vitro, in vivo*

Poster No. 66 (Abstract No.: 11218)

Potential therapeutic targets identified in Shigella through genome-wide investigations of antibiotic resistance gene sharing networks

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Introduction: Investigations on how bacteria evade antibiotics and eventually develop resistance could open new avenues for novel therapeutics development and diagnostics. It is therefore critically important to develop a comprehensive genome-wide understanding of what are the antibiotic resistance gene (ARG) repertoire in a genome, how they develop resistance, and what could be the potential targets. Due to the global increase in antibiotic resistance, the treatment and management of Shigella-causing diarrheal diseases in humans are currently critical.

Methods: We performed a comprehensive analysis of 45 whole genome sequences of four Shigella species, including S. flexneri (n = 17), S. dysenteriae (n = 14), S. boydii (n = 11), and S. sonnei (n = 13) to detect ARGs, elucidate gene-drug and protein-protein interactions and functional pathways for screening of novel therapeutic candidate. The coverage and size of the selected genomes were ≥ 40x and ≥ 4.5 Mbp, respectively. A maximum-likelihood phylogenetic tree showed three distinct clades among the circulating strains of Shigella worldwide, with less genomic diversity.

Results: We detected 2,146 ARGs in 45 genomes, and of them, only 91 ARGs were found to be unique. By comparing the mechanisms of resistance, we found that the majority of ARGs conferred their resistance through antibiotic efflux pump (51.0%), antibiotic target alteration (23%), and antibiotic target replacement (18%). We also identified 13 hub-protein using, of which only four hub-proteins were found to be shared among the study genomes. Of the shared hub-proteins, tolC and mdtA operate antibiotic efflux mechanisms, while acrR and gyrA modulate antibiotic target alteration mechanisms to inhibit antibiotic sensitivity. The ARGs were significantly enriched in 24 gene ontology terms including biological process, molecular function and cellular component. Besides, pathway analysis reveals that primary metabolic process, and nitrogenous compound metabolism were the most enriched metabolic pathways to confer resistance in Shigella spp.

Conclusion: Screening of sequenced clinical Shigella isolates demonstrates a greater number of ARGs encoding for antibiotic efflux pumps and antibiotic target modification, which must be considered in future research. Moreover, the identified hub-proteins could be exploited to develop and formulate novel therapeutics against this MDR human pathogen.

Keywords: *Shigella*, Antibiotic efflux pump, Antibiotic resistance, Comparative Genomics

Poster No. 67 (Abstract No. 11223)

Antimicrobial resistance in poultry farms and live bird markets in Bangladesh

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Introduction: Antimicrobial resistance (AMR) is a worldwide global health problem. AMR in the poultry food value chain is a growing concern in Bangladesh. The study was undertaken to assess flock-to-flock variation of AMR phenotypes and associated antimicrobial resistance genes (ARGs) in fecal commensal enteric bacteria (*E. coli* and *Salmonella*) in poultry farms and live bird markets (LBMs).

Methods: A total of 567 samples including 243 cloacal swabs and 243 drinking water from different broiler, layer and Sonali poultry farms and 81 cecal contents from LBMs were collected from Gazipur, Narsinghdi, Bogura, Joypurhat, Barishal, Sylhet, Chattogram, Cox's Bazar and Jessore district during 2021-22. Samples were collected from poultry prone districts of Bangladesh to assess the AMR patterns regarding the areas. Bacteriological analysis was conducted to detect *E. coli* and *Salmonella*. Antimicrobial susceptibility testing was performed through disk diffusion for 12 different antibiotics according to the CLSI (2020). The bacteria and resistant genes were confirmed by PCR.

Results: The overall *E. coli* recovery and prevalence of *Salmonella* was 78.5% and 11%, respectively. At farm level, *E. coli* was 58.9% and *Salmonella* 10%. At market, *E. coli* from cecal content was 98% and *Salmonella* 11%. Out of 12 different tested antibiotics, ampicillin, tetracycline, ciprofloxacin and nalidixic acid showed highest resistance pattern in both *E. coli* and *Salmonella* isolates ranging from 75-81%. For *E. coli*, tetracycline was the highest resistance ranging from 80 to 88% in all sampling site. In *Salmonella*, ampicillin was the highest resistance ranging from 82 to 92% in all sampling site. 98% of *E. coli* and 88% of *Salmonella* isolates were MDR. 4 resistance genes have been identified from phenotypically resistant *E. coli* and *Salmonella* isolates. $\mathrm{bla}_{\mathrm{TEM}}$ was predominant in *Salmonella* and *sul*2 was highest in *E. coli*.

Conclusion: AMR patterns in farms and LBMs are almost similar in all sites. MDR *Salmonella* and *E. coli* are circulating in farms and LBMs that is concerning for public health. Spatio-temporal surveillance should be continued throughout the country in poultry farms and LBMs to draw the AMR scenario.

Keywords: E. coli, Salmonella, MDR, Poultry farms, LBMs

Poster No. 68 (Abstract No. 11224)

Antimicrobial resistance in poultry farms and environment Interface

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Introduction: The emergence of multidrug resistance (MDR) in *Escherichia coli*, *Salmonella*, and *Klebsiella pneumoniae* are an important concern in the human, animal, and environmental interface. Considering the backdrop, the study conducts antimicrobial resistance (AMR) surveillance by monitoring the Extended-spectrum beta-lactamases (ESBL), Carbapenemase, and colistin-resistant genes in *E. coli*, *Salmonella*, and *Klebsiella pneumoniae* in poultry farms and environment interface.

Methods: AMR surveillance in layer farms and environment interface has been started since August 2022 in Dhaka, Rajshahi, and Chattogram divisions. From each division, 36 layer farms have been selected. We collected one pooled cloacal swab and environmental sample (soil and water) from each layer farm. Individual farm will be visited thrice in a year. A total of 648 samples (216 pooled cloacal swabs, 216 soils and 216 water) collected from 216 layer farms and surrounding environments during the last two visits. Bacteriological analysis was conducted to detect the target bacteria. Antibiotic susceptibility testing was performed via disk diffusion for 12 different antibiotics according to the CLSI, 2021. For colistin, micro broth dilution was performed. The targeted bacteria and resistant genes were confirmed by PCR.

Results: The overall occurrence of *E. coli*, *Salmonella*, and *Klebsiella* were 79.2%, 15.7% and 12.5%, respectively. In *E. coli*, the highest resistance was observed in tetracycline (88%) followed by ampicillin (85%), and ciprofloxacin (65%). *Salmonella* showed 89% of isolates were resistant to ampicillin followed by tetracycline (83%), ciprofloxacin (62%), and gentamicin (48%). In *Klebsiella*, ampicillin was the highest resistance (91%) followed by ciprofloxacin (81%) and tetracycline (73%). For colistin resistant, 18 isolates of *E. coli*, 12 of *Klebsiella* and 7 of *Salmonella* were ranging from MIC value, 4-16 µg/ml. *E. coli*, *Salmonella*, and *Klebsiella* were 95%, 88%, and 91% MDR. A number of antibiotic resistant genes (*bla*$_{\text{TEM,}}$ *tet*A, *tet*B, *Sul*1, *Sul*2), ESBL (*bla*$_{\text{CTXM,}}$ *bla*$_{\text{PSE1,}}$ bla$_{\text{SHV}}$), Carbapenemase (*bla*$_{\text{OXA1,}}$ *bla*KPC) and colistin resistant (mcr-1) has been identified.

Conclusion: MDR genes in E. coli, Salmonella, and Klebsiella isolates in poultry farms and environments could pose a severe public health threat. It is high time to monitor antibiotic usage in poultry farms and encourage the farmers to practice excellent farming systems.

Keywords: MDR, E. coli, Salmonella, Klebsiella, Poultry farms and Environment

Poster No. 69 (Abstract No. 11225)

Antimicrobial usage patterns in small- and medium-sized commercial poultry farms in Bangladesh

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Introduction: Antimicrobial resistance (AMR) has become a serious health risk for both humans and animals, and is also thought to be a major result of irrational and reckless antimicrobial usage (AMU) in poultry. Bangladesh's commercial chicken businesses provide the majority of the country's animal proteins and the substantial use of antimicrobials in the farms is essential to the food value chain. We, therefore, carried out this investigation to comprehend the AMU patterns and associated factors in Bangladeshi commercial chicken farms.

Methods: Between September and December 2021, we conducted a cross-sectional survey on 340 commercial poultry farms comprising broilers (109), layers (109), and Sonali (122) farms in seven districts of Bangladesh. We collected the data via in-person interviews with a pre-tested semi-structured questionnaire. Using descriptive statistics and mixed model multivariable logistic regression, we examined the AMU patterns and their underlying causes, respectively.

Results: We identified 62.4% (212/340) of farms that used at least one antibiotic on chickens within the last 14 days. Of them, meat-type birds including broiler (78%) and Sonali (67.2%) received larger antibiotic doses than layer chickens (41.3%). We found that 31 antibiotics from 11 distinct classes—12 of which belonged to the WHO's most significant and critically vital antimicrobials—were being administered on the farms. We also noticed the reserved group antibiotic, colistin sulfate, was also being used (3.6%). We also observed the use of colistin sulfate (3.6%) which is the reserved group antibiotic. Moreover, antibiotics use was significantly associated with the type of chickens, and the farmer's perception of antibiotics that can be used anytime even without any purposes.

Conclusion: The results showed that a significant number of chicken producers used antibiotics, which may have resulted in increased residues and resistance that may be endangering public health. We advise farmers to receive training on the responsible use of antibiotics and the effects of antibiotic misuse on the ecosystem, human health, and animal health.

Keywords: Chickens, Bangladesh, antimicrobial usage, antimicrobial resistance

Poster No. 70 (Abstract No.: 11228)

Prevalence of colonization with antibiotic-resistant organisms in hospitalized and community individuals in Bangladesh, a phenotypic analysis: Findings from the Antibiotic Resistance in Communities and Hospitals study

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Introduction: Measuring the prevalence of multidrug-resistant organism (MDRO) colonization is critical to understand burden and guide prevention strategies. We assessed the colonization prevalence of three MDROs in hospitals and the surrounding community: Enterobacterales with resistance to extended-spectrum cephalosporins (ESCrE) or carbapenems (CRE) and methicillin-resistant *Staphylococcus aureus* (MRSA).

Methods: Stool and nasal samples were collected from adults in three hospitals and from community dwellers within the hospitals' catchment area. Samples were plated on CHROMagar™ ESBL, mSuperCARBA, or MRSA agar plates. Up to three morphotypes per plate underwent identification and antibiotic susceptibility testing using Vitek® 2. Isolates were confirmed as ESCrE when resistant (R) to ceftriaxone and susceptible or intermediate to all tested carbapenems, CRE when R to at least one tested carbapenem, or MRSA when R to oxacillin or positive by cefoxitin screen.

Results: Of 743 enrolled participants in hospitals, all provided nasal swabs and 719 (97%) provided stool samples. Among 768 community participants, all provided nasal swabs and 714 (93%) provided stool samples. Participants' median age in years was 40 (IQR: 30-55) and 35 (IQR: 25-40), among hospital and community participants, respectively. Three hundred ninety-eight (54%) hospital and 274 (36%) community participants were male. MRSA colonization was similar ($p=0.43$) in both hospital 21% (154) and community 22% (172) participants. The prevalence of ESCrE was higher in hospitalized participants compared to community [82% (591) vs. 78% (554); $p=0.03$] and a similar pattern was observed for CRE colonization [37% (266) vs. 9% (66), respectively; $p\leq0.001$]. The most frequently identified resistant Enterobacterales were *Escherichia coli* and *Klebsiella pneumoniae* for hospital (73% and 22%, respectively) and community (75% and 18%, respectively). Fewer hospitalized participants had no MDRO identified compared to community [7% (50) vs. 16% (117); $p\leq0.001$].

Conclusion: Most hospital and community participants were colonized with at least one clinically important MDRO, putting them at risk for developing antibiotic resistant infections and facilitating continued spread of MDROs in both the community and hospital.

Key words: Antibiotic-resistance, prevalence, colonization, community, hospital

Poster No. 71 (Abstract No. 11229)

Regional antimicrobial resistance surveillance in regional animal health diagnosis laboratory in Barishal, Bangladesh: A One Health local initiative

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Antimicrobial resistance (AMR) is a growing concern worldwide, and One Health (OH) approaches have been proposed to address the issue. In this context, Field Disease Investigation Laboratory (FDIL), a regional animal health laboratory, Barishal has initiated an AMR surveillance program with the aim of understanding the animal disease and antibiotic use pattern through local OH initiative in Barishal region of Bangladesh.

The surveillance program launched on January 30, 2023 and samples are collecting from nine districts under the FDIL. A structured questionnaire including demographic, management and biosecurity practices, clinical history and clinical signs was developed with the AMR experts at home and abroad. A tertiary care medical college (Sher-E Bangla Medical College) Microbiology department provided technical support for the antibiotic sensitivity test, while the Livestock and Dairy Development Project (LDDP) supplied the necessary antibiotic disks. The animal health laboratory scientists and laboratory technicians are working in this program. Animal samples with a tentatively diagnosed as bacterial etiology in the postmortem examination are being collected for the antibiotic sensitivity test. The samples are grown in the respective culture media, and isolate the bacteria and grow it on Muller-Hinton agar for the test.

In this program, disease, antibiotic uses, and AMR pattern and their epidemiological linkage will be identified, which could be used to develop an antibiotic stewardship program. Furthermore, it could create an example of establishing surveillance at the local level, following the OH approach to solve other public health risks.

This initiative demonstrates that OH approaches can be successfully implemented at the local level to address complex health challenges like AMR, and it can serve as an example for other regions to follow. Overall, our program contributes to the global effort to address AMR and promotes the health and well-being of both humans and animals.

Keywords: AMR, Surveillance, One Health, Animal health laboratory, Barishal

Poster No. 72 (Abstract No. 11230)

Pattern of antibiotics usage among the dental patients in selected tertiary hospital of Bangladesh

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Background: Antibiotics are medications used to kill the bacteria or inhibit its activity. Antibiotics have saved and still saving a huge number of lives. But, the problem of antibiotic resistance emerged as a public health issue. In dentistry, antibiotic misuse and over use is one of the most threatening healthcare problems which ultimately leading to antibiotic resistance.

Objective: The main objective of this study was to assess the pattern of antibiotics usage among the dental patients in selected tertiary hospital of Bangladesh.

Methods: From July 2020 to June 2021, a cross-sectional study was carried out at the Dhaka Dental College Hospital among 195 dental patients by purposive sampling technique and face to face interview was done. Patients who consumed antibiotics for their dental problems were included in this study. Data were collected via face-to-face interview utilizing a pretested semi-structured questionnaire and checklist following the receipt of informed written consent. SPSS 26 was used to analyze the data.

Results: Among the 195 dental patients majority (33.8%) of the patients were from 31-45 years age with male (52.8%) predominant and nuclear family (65.6%). Most of the patients (42.1%) suffered from dental caries and a large number of them (69.2%) were prescribed Cephradine for their current treatment. Among the patients, 34.9% consumed antibiotic 2 to 5 times in the last 5 years (except their current antibiotic), 45.1% were prescribed previous antibiotic by pharmacy man and 21.9% by *Polli* physician. This study showed that, more than one-third (35.9%) of the patients had not completed dosage and duration of their previous antibiotics. In respect of influencing factors, 41% consumed antibiotics without prescription due to financial crisis and 65.6% used indiscriminately due to severity of their oral disease and majority (72.3%) of them were able to buy required antibiotics easily without prescription.

Conclusion: This study revealed the improper antibiotic usage pattern among a large number of dental patients. Mass awareness program should be enhanced focusing on rationale antibiotics usage to reduce antibiotic resistance.

Keywords: antibiotic, usage pattern, dental patient, tertiary hospital

Poster No. 73 (Abstract No. 11233P)

Molecular detection of super-antigenic Methicillin-resistant *Staphylococcus aureus* from commercial cheeses

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Introduction: Cheese is a popular fermented dairy product known for its versatility in human consumption due to its ability to promote gut health equilibrium and overall body immunity. In Bangladesh, the number of cheese consumers is increasing day by day, but the prevalence of common food-borne pathogens like Methicillin-resistant *Staphylococcus aureus* (MRSA) is yet to well define. Due to overwhelming challenges of AMR (antimicrobial resistance) and ARGs (antimicrobial resistance genes) transmission through MRSA, One Health approaches are needed to address these problems.

Objectives: The objective of this study was to identify MRSA encoding super-antigens producing genes available in commercial cheese in Sylhet.

Methods: In this study, 12 commercially available cheeses were collected from different chain supermarket in Sylhet District, and analyzed using standard microbiological, biochemical, and PCR tests for the identification of *Staphylococcus aureus*. The experiment was performed through collecting the same samples for three times (based on different Batch number) to justify the CFU of *S. aureus* above the safety margin. Then, the antimicrobial sensitivity testing was performed using the (K-B) disk-diffusion method. Finally, the isolates were characterized for MRSA (mec*A* gene), staphylococcal enterotoxins (SEa, SEb, SEc, SEd, SEe), and toxic shock syndrome toxin (tsst-1) using Multiplex PCR.

Results: The results of this study indicate that all cheese samples were positive for *Staphylococcus aureus*, with CFU count levels exceeding the standard safety margin (2.7 log cfu/gm) in five samples. Out of 12 samples, three samples were positive for MRSA (mec*A* gene), and all isolates were 100% resistant to several antibiotics like Oxacillin, Cefoxitin, Penicillin, Tetracycline, etc. The prevalence of SEa was 16.7%, and the prevalence of SEc and tsst-1 was also 16.7%. No other super-antigenic genes (SEb, SEd, SEe) were found in our study.

Conclusions: It is concerning that cheese is often consumed raw or as a snack, making MRSA contamination a major public health concern. Both the tsst-1 and SEa/SEc are heat-stable toxins, so heating has no effect on their virulence. Thus, the presence of MRSA in cheese is a significant health risk. One Health approaches are needed to address the transmission of AMR and ARGs through MRSA.

Keywords: Cheese, Methicillin- resistant *Staphylococcus aureus*, Staphylococcal enterotoxin, toxic shock syndrome toxins-1.

Poster No. 74 (Abstract No. 11259)

Pattern of antibiotic use among hospitalized patients according to World Health Organization's Access, Watch, Reserve classification: Findings from a point prevalence survey in Bangladesh

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Introduction: For supporting antibiotic stewardship interventions, World Health Organization (WHO) classified antibiotics naming AWaRe (**Access, Watch, Reserve**) classification. Inappropriate use of antimicrobials among hospital admitted patients exposes them to vulnerability of developing resistant organisms which are difficult to treat. We aimed to describe the prevalence of antibiotic use (ABU) based on WHO AWaRe classification in tertiary and secondary level acute care hospitals in Bangladesh.

Method: A point prevalence survey (PPS) was conducted adopting WHO PPS design, among inpatients of two tertiary and two secondary level public hospitals in Bangladesh from February to April 2021.

Findings: Among the enrolled 1417 inpatients, 52% were female and 63% were from the 15-64 years age group. Nearly, 78% of patients received at least one antibiotic during the survey period. Proportioning for different departments, 91.2% of pediatric patients, 81.4% of gynae and obstetric patients, 78.0% of surgery patients, and 66.2% of medicine patients received at least one antibiotic. Third-generation cephalosporins (44.6%), penicillins (12.3%), imidazoles (11.8%), aminoglycosides (7.2%), and macrolides (5.8%) were documented as top 5 antibiotics. Overall, 64.0% of Watch, 35.6% of Access, and 0.1% of Reserve group antibiotics were used for treatment. In medicine wards, 78.7% of patients were treated with Watch antibiotics and 20.7% with Access antibiotics. About 62.9%, 36.4%, and 0.2% of patients were treated with Watch, Access, and Reserve group of antibiotics, respectively, in surgery wards. Among the patients of gynae and obstetric wards, 55.4%, 44.4%, and 0.2% patients were treated with Watch, Access, and Reserve antibiotics, respectively. Moreover, among pediatric patients, 60.7% and 39.3% of children received Watch and Access antibiotics, respectively. Use of Watch antibiotics was found more in secondary hospitals (71.5%) compared to tertiary hospitals (60.2%) (p-value of <0.0001). On the contrary, Access antibiotics were used more in tertiary hospitals (39.4%) compared to secondary hospitals (28.3%).

Conclusion: The use of watch group antibiotics is quite high in public hospitals with predominant use in secondary level hospitals. Our PPS findings underscores the need for urgent nationwide antibiotic stewardship progam for physicians, along with development of local guidelines and in-service training on ABU for the containment of AMR.

Keywords: Antibiotic use, hospital, point prevalence survey, AWaRe classification

Poster No. 75 (Abstract No. 11286)

Caspase activation capacity of mutant meningococcal lipopolysaccharide

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Neisseria meningitidis typically produces a very potent hexa-acylated lipopolysaccharide (LPS) which is too toxic for therapeutic applications. Previously we have developed a panel of meningococcal LPS mutants having different levels of TLR4 agonist activity from wild type maximum to practically zero. Recent studies have identified the non-canonical inflammasome pathway as an additional recognition system for LPS. Here, we report on the characterization of the caspase-mediated non-canonical inflammasome activation potential of our set of meningococcal LPS mutants.

We transfected both human and mouse macrophage-derived cell lines with wild-type and different mutant LPS species and measured capacity to induce the cell death, IL-1β and TNF-α production and caspase-1 activity. Additionally, the direct caspase-4 binding capability of wild-type and different mutant LPSs was investigated by an in vitro oligomerization assay.

Wild-type meningococcal LPS provoked strong caspase-mediated inflammatory signaling in terms of cell death and cytokine production. Surprisingly, removal of phosphoethanolamine in lipid A by deletion of lptA slightly increased the activity of hexa-acylated LPS in terms of IL-1β production, but this increase was evident more with human THP-1 cells than murine J774A.1 cells. Penta-acylated LPS mutants showed decreased caspase-mediated responses, similar to what was found for TLR4. Expression of PagL deacylase in LptA or LpxL1 mutants further decreased LPS activity in terms of IL-1β production and caspase-1 activation. Incubation in vitro of the different LPS species with purified caspase-4 resulted in a variety of molecular sizes, with all LPS structures inducing at least dimerization of caspase-4. Wild-type and LptA LPS induced the largest aggregates, relating to their effect on with IL-1β and TNF-α secretion. Further to our previous report on TLR4 activation, our present results highlight that the mutant meningococcal LPSs also mediate graded non-canonical inflammasome activation.

We conclude that combinatorial engineering of LPS can be exploited to generate a spectrum of bioactive variants of immunostimulatory molecules which can be used as vaccine adjuvants or for other therapeutic applications.

Keywords: *Neisseria meningitidis*, LPS, TLR4, Caspase, Vaccine adjuvants

Poster No. 76 (Abstract No. 11287)

Bacteriophage as a potential weapon for killing extensively drug resistant and Colistin-resistant *E. coli*

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Introduction: In the era of the increasing emergence of drug resistant including multidrug resistant (MDR) bacteria and a lack of new effective antibiotics, scientific effort has been put into developing new technologies to combat bacteria. Bacteriophages have been proposed as an alternative strategy to antibiotics for poultry, and thus for food safety and public health. Bacteriophages are a group of viruses abundant in nature whose life cycle is strictly associated with the bacterial cell. We have isolated several phages those can infect MDR *Escherichia coli* and one of the potential phages was reported here.

Methods: Environmental waste water was collected and processed for bacteriophages isolation. Equal volume of *E. coli* suspension and processed wastewater was mixed incubated at room temperature for 5 min, and then added with 5mL of molten top agarose and plated onto a bottom agar plate. The plates were incubated overnight at 37^0C and examined the next day to identify clear lytic bacteriophage plaques. Plaque purification and characterization was done following standard procedures. DNA was extracted from purified phages and whole genome sequencing of a selected phage was done and analyzed different softwares.

Results: The isolated phage NAP06K shows adsorption time <6 min, a latent period of 23 min and burst size of 154 PFU per bacterial cell. This was confirmed by monitoring phage lytic development by a one-step growth experiment. The phage exhibits considerable stability in a wide pH 5-11 and survives an hour at 55°C. The genome of the phage comprises dsDNA, 86,81,895bp in length, with a GC content of 38.72%. It contains 96 putative open reading frames (ORFs). Among them, the putative functions of only 35 ORFs were predicted (36.5%), whereas 61 ORFs (63.5%) were classified as hypothetical proteins. The prediction of the ORFs identified protein-coding genes that are responsible for functions that have been assigned such as cell lysis proteins, DNA packaging proteins, structural proteins, and DNA replication/transcription/repair proteins. Importantly, genome analysis suggested that this *E. coli* phage is free of toxins and other virulence factors.

Conclusion: Our results indicate that studied phage has potentials for phage therapy and/or food protection against Shiga toxin-producing *E. coli*.

Keywords: Bacteriophage, Characterization, Genome sequence, *Escherichia coli,* Bangladesh

Poster No. 77 (Abstract No. 11292)

Epidemiology and molecular characterization of multidrug-resistant *Escherichia coli* isolated from fish

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Introduction: AMR turns into incredibly alarming, especially for the rapid spread of multi-drug resistant (MDR) bacteria throughout the world, which cause infections that exert thriving challenges to cure with existing antibiotics. Augmented use of antimicrobial compounds in the human, animal, and agricultural production system and their subsequent release into the environment has promoted the emergence of MDR bacteria as a natural bacterial phenomenon. A cross-sectional study was designed to investigate the MDR *E. coli* prevalence, MDR pattern, MDRI and ARG pattern in fish samples.

Methods: Field sampling was done over a 6-month period from March to August 2022, on randomly selected ten prominent fish markets in Chattogram. A total of four hundred and fifty (450) fish samples were purchased from randomly selected vendors of the wet markets. Bacteriological culture-based technique, disk diffusion method according to established Clinical and Laboratory Standard Institute (CLSI) guidelines for the evaluation of phenotypic resistance, simplex (SimpPCR), and multiplex Polymerase Chain Reaction (mPCR) assay were used to determine the occurrence of resistance genes in MDR *E. coli* isolates. Isolates that exhibited phenotypical resistance against at least one agent in three or more antimicrobial categories were classified as MDR.

Results: This study revealed an overall 41.78% (188/450) MDR *E. coli* prevalence in the tested samples. The generated multiple antibiotic resistance indices ranged between 0.25 to 1.00, with the highest value seen in one MDR *E. coli* isolates from catfish. The ESBLs and p$_{\text{AmpC}}$ resistance determinants detected were bla$_{\text{TEM}}$ [36.7% (69/188)], bla$_{\text{SHV}}$ [16.49% (31/188)], bla$_{\text{CTX}}$ [4.79% (9/188)], bla$_{\text{OXA-1-like}}$ [6.91% (13/188)], bla$_{\text{OXA-2-like}}$ [7.98% (15/188)], bla$_{\text{CMY-1-like}}$ [3.19% (6/188)],bla$_{\text{CMY-2-like}}$ [3.72% (7/188)], bla$_{\text{ACC-1}}$ [0.00% (0/188)], P$_{\text{ampC}}$ [7.98% (15/188)]. The frequencies of the non-β-lactam genes detected were *tet*-A [60.11% (113/188)], *tet*-B [3.19% (6/188)], *tet*-C [0% (0/188)], and *tet*-D [5.85% (11/188)], *sul*-I [18.62% (35/188)] and *sul*-II [55.85% (105/188)].

Conclusion: The research's conclusions highlighted the significance of fish as sources of MDR *E. coli* and resistance genes along with the possible risk to consumers' health. Also, the data of the current study could be useful for the development of mitigation strategies for AMR to avert the potential horizontal transfer of AMR genes to humans via animal-sourced food.

Keywords: Fish, MDR *E. coli* prevalence, MDR pattern, Multiple Antibiotic Resistance Index (MDRI), Antibiotic Resistant Genotype Pattern (ARG Pattern)

Poster No. 78 (Abstract No. 11301)

Molecular detection and antibiotic sensitivity of *Pseudomonas* spp. isolated from feces of wild and migratory birds

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Introduction: *Pseudomanas* spp. is widespread in the environment, resistant to unfavorable conditions, and may spread between humans and other mammals. Migratory birds and captive wild birds are a very common source of spreading of this bacterium. Given the lack of knowledge on MDR bacteria in migratory and captive wild birds, we examined fecal and cloacal samples of migratory and captive wild birds in Sylhet, Bangladesh, to find MDR *Pseudomanas* spp.

Methods: The current research was carried out in Sylhet division, which is located in the northeastern part of Bangladesh. A total of 219 feces and cloacal sample were collected from migratory and captive wild birds. The DNA was extracted using a DNA extraction kit (Addbio Inc. Ltd., Korea) according to the manufacturer's instructions and stored at -20°C until further analysis. The PCR test was used using the 16srDNA-based primer sets (PA-GS-F: GACGGGTGAGTAATGCCTA, PA-GS-R: CACTGGTGTTCCTTCCTATA; PA-SS-F: GGGGGATCTTCGGACCTCA, PA-SS-R: TCCTTAGAGTGCCCACCCG). The antimicrobial resistance genes were also detected by PCR using the designed primers sets. The PCR products were then run on a 1.8% agarose gel for analysis. According to the Clinical and Laboratory Standard Institute (CLSI), the qualitative agar diffusion method (Kirby-Bauer method) was employed for antibiotic sensitivity testing utilizing Mueller Hinton agar.

Results: Overall prevalence of *Pseudomonas* spp. was estimated at 18.72% (95% CI 13.78%-24.53%) through conventional cultural and molecular test. Pseudomonas was higher in migratory birds (24.11 %, 95% CI 16.53%-33.10%) and lower in wild bird (13.08 %, 95% CI 7.34%-20.98%). On the other hand, the prevalence of *Pseudomonas* spp. was 21.28%, 38.89%, 16.9%, and 5.56% in Tanguar Hoar, Horipur, Sreemongal, and Tilaghor Ecopark respectively. However, *Pseudomonas aeruginosa* was present in 10.05% (95% CI 6.40%-14.81%) in migratory and captive wild bird populations. Disk diffusion method was used for antimicrobial sensitivity test against 11 antibiotics. Phenotypically 100% sensitivity was showed by Levofloxacin, Ciprofloxacin, Tetracycline, Colistin Sulphate, Meropenem and Gentamicin. Multiple antibiotic resistance was found (77.27%; 95% CI, 54.63%-92.18 %) while MDR was 63.64% in this study. Though, genotypically the resistance gene with the highest percentage was blaTEM (90.91%), while the genes with the lowest percentage were blaOXA and blaSHV (4.54%). In the present investigation, tet A 13.64% is common.

Conclusion: The study found that MDR *Pseudomonas* spp. are likely to be present in migratory and wild birds, where they can easily spread to humans, other animals, and the environment. Therefore, to reduce and prevent the spread of resistance genes, we strongly propose that the national AMR monitoring program surveillance and monitor these birds.

Keywords: Migratory Birds, Captive Wild birds, MDR, *Pseudomonas* spp., One Health

Poster No. 79 (Abstract No. 11303)

Antibiotic usage practices and its drivers in commercial chicken production in Bangladesh

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Introduction: Inappropriate use of antibiotics in commercial chicken production can play an important role for the emergence of antibiotic resistance. Increasing information on current antibiotic usage practices in commercial chicken production is crucial for the design of effective interventions to minimize the animal and public health impact of antibiotic resistance. We aimed to assess antibiotic usage and identify factors in commercial chicken.

Methods: We conducted a large-scale cross-sectional study to collect information on antibiotic usage in commercial chickens. Adjusted odds ratios (aOR) were calculated to measure the association between antibiotic usage and related factors.

Results: The proportion of farms, irrespective of the production type, having used antibiotics in the 24 hours, 72 hours, 14 days preceding each farm visit and since the start of their production cycle was 41% (n=314, 95% CI: 37-44%), 45% (n=344, 41-48%), 86% (n=658, 83-88%) and 98% (n=753, 97-99%), respectively. Doxycycline, oxytetracycline, ciprofloxacin and amoxicillin were the most frequently used antibiotics. The usage of antibiotics in the last 24 hours was significantly associated with the occurrence of illnesses in broiler (aOR 41.2, 95% CI:13.6-124.6), layer (aOR 36.4, 9.5-139.4) and Sonali chicken (aOR 28.4, 4.9-162.9). Antibiotics were reported to be used for both treatment and prophylactic purposes on most farms (66%). Antibiotic usage was mainly advised by veterinary practitioners (45-71%, depending on production type), followed by feed dealers (21-40%) and farmers (7-13%).

Conclusions: This study's findings emphasized that improvement of chicken health through good farming practices along with the changes of the relevant stakeholder attitudes (farmers, feed dealers and practitioners) can help in reducing the levels of antibiotic use and contribute to reduction in resistance.

Key words: antibiotic, resistance, chicken, Bangladesh

Food Safety, Food and Nutrition Security

Poster No. 80 (Abstract No. 11001)

Broiler and native chicken: Comparison for productivity and global nutrition security

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Chickens belongs to poultry and contribute much as a source of meat and egg for human. There is no restriction to consume meat and eggs from chicken considering religion, nation, cast, health status etc. Since early history the chickens are jungle fowl and have different varieties distributed throughout the globe. Considering lower productivity but increasing demand due to growing population researchers has studied to improve their productivity. Finally two types of commercial chickens has innovative separately for egg and meat production. Broiler is specialized for higher meat production within short period consuming less feed. Due to innovation of broiler the nutrition security improved more than 300 times globally in comparison to all others sources of meat. It contributes nutrition security for poor people in developed countries as well as for peoples in developing countries, because of low price and easy access. Its contribution is mentionable because it is a good source of animal protein containing all the essential amino acids required for growth and development of body. It covers not only food security but also nutrition security globally. But, in many countries its production challenges due to some rumor and unethical business manner which need to be addressed for sustainable development of this sector considering importance of animal protein and food security.

Key words: broiler, native chicken, productivity, nutrition, security

Poster No. 81 (Abstract No. 11010)

Additional activities influencing food insecurity and school absenteeism among rural children

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Introduction: Food insecurity refers to limited or uncertain availability of nutritionally adequate and safe foods or limited or uncertain ability to acquire food in socially acceptable ways. Food insecurity has substantial detrimental effects on children, but little is known about the mechanisms through which these effects occur. This study investigated some possible mechanisms by examining associations of food insecurity reported by children with daily activities and school absenteeism.

Methods: A school based cross-sectional study was conducted among 460 school going children (class 4 to class 10) in Saltha upazila of Faridpur district, Bangladesh from January-December, 2019. Semi-structured questionnaire was used to collect data on the food insecurity and additional activities through face-to-face interview.

Results: Among 460 study population those who helped their parents in raising food crops, household food shopping, cooking food for family members in home and taking care of siblings were found 48.7%, 53.1%, 58.2% and 80.9% moderately food insecure respectively. Those who used to playing during school recess time, walking to and from school, doing sports in school, watching television during leisure time and taking nap in evening were found 87.5%, 83.2%, 87.2%, 89.0% and 91.9% moderately food insecure respectively. There was a significant association between taking care of siblings, playing during school recess time, walking to and from school, doing sports in school, watching television during leisure time and taking nap in evening with level of food insecurity ($p<0.05$).

Conclusion: Planners and policy makers may take necessary action to improve food insecurity status to reduce school absenteeism by improving socio-demographic and socio-economic status of rural families and improve the academic performance of rural school going children.

Keywords: Food Insecurity, School Absenteeism, Additional/Altered Activities, Rural School-going Children

Poster No. 82 (Abstract No. 11011)

Higher gross domestic product in agriculture does not ensure food security of a nation

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To secure food of a nation there is no alternative to get food from agriculture (e.g., crop, fishing, forestry, livestock etc.). There are many countries contribute large part of their national gross domestic product (GDP) from agriculture. Now it become a question either countries those producing more food and GDP contribute in agriculture is higher secured in food or not. In this connection the study has conducted to relate the GDP contribution in agriculture and food security of those nation. Food Security Index related data has collected from Economist Intelligence Unit (EIU) Global Food Security Index of 2020. Data on contribution of agriculture in GDP has collected from World Bank (2020). Percent of employment involved in agriculture has collected from FAO Statistical Yearbook, 2020. All data have inserted in Microsoft Excel Sheet chronologically for further processing and statistical analysis. Regression and correlation value have calculated to express the relationship among GDP and food security as well as other related parameters (employment in agriculture and per capita income). According to the data, it's become clear that those country are secured in food don't have higher GDP in agriculture. When we consider the top 10 countries with higher GDP in agriculture, it shows that GDP in agriculture is 32.58 % negatively related with Food Security Index and 0.7 % negatively related with per capita income where 13.87 % positively related with percent employment in agriculture. But when top 10 countries with lower GDP in agriculture is considered, it express. That lower GDP in agriculture is positively correlated with Food Security Index (4.24%) and percent employment in agriculture (13.71%) but negatively related with per capita income. After considering all about 113 countries, it becomes absolutely clear that percent GDP in agriculture is negatively related with food security index (96.66%) and per capita income (004%) but 41.02 % positively correlated with percent employment in agriculture. That means the more people involved in agriculture may have low per capita income and lower food security index. So, the data proved that those countries have higher GDP in agriculture are less secured in food but per capita income has much more effects on food security of those nations.

Keywords: Food security, food producing countries, global, income

Poster No. 84 (Abstract. No. 11027)

Molecular identification of *Escherichia coli* from apparently healthy pigeons in Sylhet division of Bangladesh

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Introduction: *E. coli* is a common intestinal microbiota of a variety of animals, including pigeons. Pigeons are particularly effective in transmitting *E. coli* to people because their feces contain *E. coli* O157:H7, a source of infection for birds, animals, and humans. The present study was conducted with the aim of molecular identification and characterization of *E. coli* and determination of prevalence from apparently healthy pigeons in the Sylhet division of Bangladesh.

Methods: A total of 103 samples (50 oral and 53 cloacal) were collected with sterile cotton buds from apparently healthy pigeons. The obtained swabs were then transported to the Department of Medicine, Sylhet Agricultural University, Bangladesh. They were quickly inoculated into the nutrient broth to provide maximum nutrition for the desired organisms. Using traditional bacteriological methods, *E. coli* was isolated from the samples. The DNA extraction was performed using a DNA extraction kit (AddBio Inc. Ltd., Daejeon, Korea) and kept at -20°C for further study. Extracted DNA was subjected to PCR to confirm *E. coli* isolates targeting the 16S rRNA gene. The primers ECO-1F (5'-GACCTCGGTTTAGTTCACAGA-3') and ECO-1R (3'- CACACGCTGACGCTGACCA-5') were used to detect *E. coli.* The amplified products were visualized by gel electrophoresis using 1.5% agarose gel and viewed under UV trans-illumination in a gel documentation system.

Results: The prevalence rate of *E. coli* by primary isolation on EMB agar was found to be 54% (n=27/50) in oral swabs and 56.6% (n=30/53) cloacal swabs, with an overall prevalence rate of 55.34% (n=57/103). The prevalence rate of *E. coli* in pigeons varied among locations; 60.71% (n=34/56) in Rural, 45.45% (n=10/22) in Semi-urban and 52% (n=13/25) in Urban areas. The prevalence rate also varied among rearing systems; 68% (n=17/25) in Intensive, 40% (n=4/10) in Semi-intensive, and 52.94% (n=36/68) in Free range. Total 12 (60%) out of 20 samples were found to be positive by PCR, where they amplified at a region of 585-bp segment.

Conclusion: The study suggests that the prevalence of *E. coli* infection in pigeon is higher in the study area which is a major concern for human health. Necessary steps should be taken to mitigate the infection of apparently healthy pigeon to ensure the sound health of pigeon as well as human.

Keywords: Pigeons, *E. coli*, Molecular identification, Prevalence

Poster No. 85 (Abstract No. 11028)

Molecular identification of *Salmonella* spp. from apparently healthy pigeons in Sylhet division of Bangladesh

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Introduction: Pigeons (*Columbia livia*) have an essential role in disseminating bacterial pathogens to free-range poultry and are a fecal contaminant of drinking water supplies and rural harvests. Salmonellosis is one of the most important bacterial diseases in pigeons. This research work was conducted to isolate and identify Salmonella spp. from apparently healthy pigeons.

Methods: The study was conducted in two districts (Sylhet and Moulvibazar) of the Sylhet division of Bangladesh. Using sterile cotton, 206 samples of nasal swab (162) and cloacal swab (44) from apparently healthy pigeons were collected. The obtained swabs were promptly inoculated into nutrient broth for better nourishment of the desirable organisms, and then transported to the Department of Medicine, Sylhet Agricultural University, Bangladesh, where the laboratory work was completed. *Salmonella* spp. was isolated from the samples using conventional bacteriological approaches. The DNA was extracted using a DNA extraction kit (AddBio Inc. Ltd., Daejeon, Korea) and kept at -20°C until further analysis. Extracted DNA was subjected to PCR for the confirmation of *Salmonella* spp. isolates using specific primers targeting the *Histidine Transport Operon* gene. The primers SP1-F (5'-ATACCAAAATGTGGATGGTGGAA-3') and SP1-R (5'-TAATCCTGCTACTGGGTTATACCAATT-3') were used to detect *Salmonella* spp. The amplified products were visualized by gel electrophoresis using 1.5% agarose gel and viewed under UV trans-illumination in a gel documentation system.

Results: The prevalence rate of Salmonella was found to be 6.81% (n=3/44) in cloacal swabs and 8.02% (n=13/162) in pharyngeal swabs, with an overall prevalence rate of 7.77% (n=16/206). The prevalence rate of Salmonella in pigeons varied among locations; 11.53% (n=6/52) in live bird markets, and 6.49% (n=10/154) in villages and city dwellers. The prevalence rate of Salmonella also varied among places; it was 7.006% (n=11/157) in Sylhet district, and 10.20% (n=5/49) in Moulvibazar district. Molecular detection of 16 Salmonella samples isolated from primary isolation was performed by genus specific PCR, where all of them amplified a region of 496-bp segment. In PCR, all the samples that were taken to be tested came out positive.

Conclusion: The prevalence of salmonella in the apparently healthy pigeons in local market has significant zoonotic importance. Our study suggests to take necessary steps to mitigate the disease in pigeons which is the major concern of One Health.

Keywords: Molecular identification, *Salmonella* spp., Pigeons, Prevalence

Poster No. 86 (Abstract No. 11042)

Raw milk: an important source of multidrug resistant bacteria for human

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Introduction: The increasing prevalence of antimicrobial resistance (AMR) is a significant threat to global health. The widespread use of antibiotic is increasingly shortening the time for resistant strains to develop and multi-drug-resistant bacterial strains cause life-threatening infections. Antibiotic resistance genes (ARGs) in raw milk can be transferred from non-pathogens to pathogens via horizontal gene transfer. The present study was focused on antibiotic resistant bacteria isolation and detection from milk of cattle, buffalo, goat and sheep.

Methods: A total of 80 raw milk samples (20 milk samples from each species) were collected for the isolation of *Escherichia coli*, *Salmonella* spp., *Staphylococcus aureus* and *Streptococcus* spp. Each milk sample was inoculated in nutrient broth followed by streaked on EMB, SS, MS and KF streptococcal agar media for growth of target bacteria. Chromosomal DNA was extracted from pure culture and each species was detected by PCR using specific primers. Antibiotic sensitivity test was performed for the detection of antibiotic resistance pattern of each isolate by disk diffusion test. PCR was also performed to detect *tet*A, *tet*B and *tet*C genes in the isolates.

Results: All the target species were detected in the raw milk samples of cattle, buffalo, sheep and goat. Most of the isolates of *E. coli* were found resistant to ampicillin, amoxicillin, tetracycline and streptomycin; whereas most of the isolates of *S. aureus* were found resistant to ampicillin, amoxicillin and tetracycline. Variation in antibiotic resistance pattern was observed for other isolates. Most of the isolates were found to contain *tet*A gene.

Conclusion: It can be concluded that presence of multidrug resistance pathogens in raw milk can be a threat for public health.

Keywords: raw milk, antibiotic resistance, *tetA*, *Streptococcus*, *E. coli*

Poster No. 87 (Abstract No. 11046)

The impact of COVID-19 on food and nutrition security among the urban poor in Bangladesh

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Introduction: The COVID-19 pandemic exposed new vulnerability in global food system and nutrition status specially for urban poor. The purpose of the study was to explore the impact of COVID-19 on food and nutrition security among infant and young children (0-59 months) and their families living in slums of Gazipur and Dhaka.

Methods: A population-based cross-sectional household survey was conducted in 2 large slums at 2 city corporations in Bangladesh (Dhaka North and Gazipur) under urban health and demographic surveillance (UHDSS) sites. Initially, randomly selected 42 respondents from each clusters were approached and collected data from 773 mothers having children under the age of 5 years between February and March, 2021. Using Tablet based semi-structured questionnaires data on household income, food security, dietary diversity, health seeking behavior, and nutritional status of children was collected. Descriptive statistics and graphical representations were used for analysis.

Results: Almost 90% of the respondents reported changes in their household income due to reduced pay (86%), delay in receiving payment (52%), and complete loss of job (39%). Adverse changes in food access were reported by 76% of the respondents in terms of number of meal (93%), amount of food (89%) and dietary diversity (93%). Better access to safe drinking water were reported by 30% of the respondents. Around one-third reported sickness of their children during the pandemic. Regarding health care seeking behavior; delayed decision-making (14%), delayed arrival at the health facility (13%), and delayed provision of adequate care at the facility (12%) were reported by the respondents.

Conclusion: It is evident that COVID-19 pandemic has disproportionately affected urban slum population in Dhaka and Gazipur. They have been affected financially which have influenced their food and nutrition security and also health care seeking practices. As one of the One Health perspective greater research will need for food system.

Keywords: COVID-19; food security; health-seeking behavior, food diversity; nutrition security

Poster No. 88 (Abstract No. 11051)

Economic impact of COVID 19 lockdown on the dairy farming in Bangladesh: Recommended a coordinated action for resilience

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Introduction: The country-wide lockdown caused by the COVID-19 Pandemic imposed a range of impacts on the socio-economic condition of the country. In Bangladesh, more than 70 % of rural livelihoods depend on livestock farming and it generates direct employment for 20% of the total population. The livestock sector, especially the dairy farming producing 32,800 Ton milk per day has been hit hard. The aim of this paper was to measure the effect of COVID-19 associated lockdown on the performance of dairy farming and advocacy for enhancing resilience.

Methods: A list of dairy farmers was collected from the Upazila livestock office and veterinary hospital, Sadar, Noakhali. Data were collected from medium-scale dairy farm owners through telephone interviews on the production cost and earnings before and after the lockdown. In this study, we focused on the first 66 days of lockdown effective from 26th March 2020 to 30th May 2020. Only complete responses were taken into account and analyzed using SPSS software. Time series analysis had been done to show the difference between the earnings before lockdown and after lockdown. Multivariate regression analysis was used to reveal the relation between the earnings of dairy farmers and the average cost of feed, medicine, labor, and other costs.

Results: Based on the data of 60 dairy farms this study found a negative relation between lockdown and dairy farming. Of the total, 13.3% farms were permanently closed and another significant number temporarily paused the production. A decrease in market demands for dairy products and increased price of feed, medicine, and labor due to shortage of supply were the potential reasons for their loss of capital. The milk price decreased by 17% whereas feed price had increased by 3.7%.

Conclusion: Besides financial support, the government should prioritize increasing the resilient capacity of farmers for sustainable development of the sector. In this regard, the One Health approach could play a potential role in strengthening this industry by creating a secure supply chain, value addition of products, and proper marketing channels through multidisciplinary collaboration.

Key words: Impact of COVID-19, Dairy industry, Livestock economy, Milk production, Multivariate analysis

Poster No. 89 (Abstract No. 11072)

Food borne parasitic infection: a neglected food safety hazard in Bangladesh

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Introduction: Food borne parasites are common worldwide. Unhygienic food supplies and changes in culinary habits are associated with the food-borne parasitic disease in developing world including Bangladesh. This study illustrates the important food-borne parasitic infections to understand the current status of parasitic contamination of food and their multiple transmission pathways in Bangladesh.

Food borne parasites and their transmission: Parasitic contamination of food are not uncommon in Bangladesh. Parasites that may be transmitted through fecal contamination of foods are *Toxoplasma gondii* and *Echinococcus* spp. Humans may get infected by ingestion of raw or undercooked vegetables/foods contaminated with infective stages of these parasites. Meat is the source of infection of a number of parasites such as *Taenia* spp., *Trichinella* spp, *T. gondii* and *Sarcocystis* spp.. Fish can be a source of infection of variety of parasites including trematodes (*Opisthorchis* spp., *Clonorchis sinensis*), cestodes (*Diphyllobothrium* spp.), nematodes (*Gnathostoma* spp., anisakine parasites), and pentastomids that can cause infections in humans when consumed raw or undercooked. *Paragonimus* spp. may also transmit to humans through contaminated crabs or fish. These parasites are common in a number of Asian countries because of the particular food habits. Meat harbors the infective stages and meat inspection is mandatory to avoid this meat borne parasitic infection. There is no precise information about the food borne parasites in Bangladesh. Toxoplasmosis and cystic echinocoocosis were reported from different areas of Bangladesh. There is also evidence of Taeniasis and Cysticercosis in Bangladesh. Due to limitations of routine diagnosis and monitoring or reporting of the food borne parasites, the incidence of parasite in food is underestimated.

Conclusion: Food safety hazard caused by parasites are neglected in Bangladesh although it has significant impact on public health. It’s necessary to take initiative for better monitoring and control of food-borne parasites using advance technologies.

Keywords: Parasites, food, transmission, Bangladesh

Poster No. 90 (Abstract No. 11077)

An assessment of food safety knowledge, attitude and practices of restaurant food handlers in Mymensingh city, Bangladesh

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Introduction: Food safety is an important strategy with a view to controlling foodborne diseases and subsequently improving the overall health status of the community.

Aim: This study aimed at evaluating the knowledge, attitudes and practices regarding food safety among restaurant food handlers in the district of Mymensingh, Bangladesh.

Methods: A cross-sectional study was conducted from April to June, 2019 among 115 ready to eat restaurant food handler by using an interviewer-administered, semi-structured pretested questionnaire to evaluate their knowledge, attitude, and practices on food safety and foodborne pathogens at different restaurants of Mymensingh city, Bangladesh. The data were collected by face-to-face interview through the questionnaire & analyzed by using software SPSS (Version 20).

Findings and discussion: The mean (SD) scores of knowledge, attitude and practices of the respondents were 9.10±4.16, 12.83±2.57, 10.78±8.87 respectively. There was significant correlation between food safety training and knowledge, knowledge and attitude or knowledge and practices ($p < 0.001$). The results showed that a considerable number of vendors were primary school leaver (62%) followed by illiterate (16%) and secondary school degree (37%) and no one had any food safety training and health certificate. The food handlers in our study were well-versed in sanitary techniques, cleaning, and sanitation processes. Almost all food handlers were aware of the need of general hygienic measures in the workplace, such as hand washing (90.43% accurate answers). On disease transmission, the results indicated that, only (26.95%) percent of food handlers were aware that Salmonella is a foodborne pathogen. Absent from work due to food borne illness (78.02%), check the shelf life of foods at the time of delivery (60.8%), storing any left-over's of cooked meal in a cool place within two hours (58.2%) were the areas with the maximum unsatisfactory practice. However, the food handlers had a relatively positive attitude towards food safety but their knowledge and practice level were not satisfactory.

Conclusion: For food handlers to enhance their food safety knowledge and practices, they should receive ongoing education, hands-on food safety training, awareness and enthusiasm.

Keywords: Knowledge, Attitudes, Practices, Ready-to-eat food, Food handlers

Poster No. 91 (Abstract No. 11088)

Mini scale production of Brazilian cherry fruits (*Eugenia uniflora* L.) for the first time in Noakhali Science and Technology University campus and their phytochemical screening, Thin-Layer Chromatography analysis and antioxidant activities in water, methanol and ethanol extracts

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Introduction: This research is carried out to cultivate Brazilian Cherry Fruits (*Eugenia uniflora* L.) Plants in Noakhali Science and Technology University (NSTU) Campus, Noakhali for fruits production which is one of the sweet finest nutritionally rich foreign fruits and their phytochemical, Thin-Layer Chromatography (TLC) analysis, antioxidant activities and total phenolic content of different solvent extracts (Water, Methanol and Ethanol) of Ripe and Non-Ripe Brazilian Cherry Fruits.

Methods: Phytochemical screening was carried out by standard laboratory method, Compounds were detected by TLC, the antioxidant activity was determined by DPPH method while the total phenolic content was determined by FC method.

Results: Based on the phytochemical screening, the water, methanol and ethanol extracts of Ripe and Non-Ripe Brazilian Cherry Fruits in Red (BC-RC) and Green Colors (BC-GC), respectively showed the presence of Alkaloids, Tannins, Saponin, Flavonoids, Cardiac Glycosides, Carbohydrates, Proteins and Amino Acids. The purple color compound present in the water, methanol and ethanol extracts of both Ripe and Non-Ripe Brazilian Cherry Fruits may be Vitamin C or unknown nitrogenous compound and the white color compound is absent in water, methanol and ethanol extracts of BC-RC, it is only present in water, methanol and ethanol extracts of BC-GC. The result of Antioxidant test indicated that all extracts of Brazilian Cherry Fruits contain high antioxidant compounds. Among all extracts, in both Ripe and Non-Ripe stage, the water extract of non-ripe Brazilian Cherry Fruits showed the highest DPPH radical scavenging activity (73.66%) and showed the lowest IC_{50} of DPPH scavenging activity (1.01 µg/ml) which indicates the presence of high content of Vitamin C. Among all extracts of Ripe and non-ripe, the methanol extract of non-ripe Brazilian Cherry Fruits in Green Color was found to be highest total phenolic content 111.52 mg GAE/100g, and the ethanol extracts of Ripe Brazilian Cherry Fruits in Red Color was found to be lowest total phenolic content, 106.004 mg GAE/100g.

Conclusion: overall results may be one of the important key strategies by adding this fruit in the diet chart to prevent and fight against infection recently caused by COVID-19 and other infectious diseases by increasing our body immunity and this fruits also will be useful as a raw materials in the pharmaceutical and food industries to prepare drugs and food products.

Keywords: Brazilian Cherry Fruits, Phytochemicals, Antioxidants, DPPH, Phenolic

Poster No. 92 (Abstract No. 11107)

Risk-based food inspection in Bangladesh - challenges and obstacles for Food Safety Inspectors

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Introduction: Risk-based food inspection (RBFI) is the modern inspection technique that categorize food items and Food business operators (FBOs) based on selected criteria for ensuring optimum inspection compliance and strengthening combating capacity against food borne illness. In addition, RBFI provides opportunities to build effective food regulatory system to prevent food adulteration and contamination, thus plays pivotal role in maintaining food safety. In 2015, Bangladesh shifted from end product-based inspection to this modern RBFI by adopting new food safety law. This study identifies challenges and obstacles in implementing RBFI, by the frontlines of food regulatory systems, Food safety Inspectors (FSIs), while practicing inspection procedure.

Methods: A representative sample of forty-eight Sanitary Inspectors from 48 Upazila of eight districts in Bangladesh, participated in eight focus group discussion (FGD) sessions, during early May to mid-August 2019. They identified the barriers they face and demand they had when implementing the new Food inspection procedure. Data validation were done through the cross-validation method. Constant comparison and classical content analysis methods were used in data analysis. Transcription procedure, coding, and themes were prepared by anthropologists whereas synopsis on each FGD and final report were prepared by researcher.

Results: The challenges of FSIs in implementing the new Food inspection procedure (RBFI) included a complex risk categorization process for foods and FBOs, a burdensome inspection checklist, high job risk, little enforcement capacity, and sample collection and transportation. In addition, the major obstacles in practicing enforcement at RBFI were high non-compliance penalty and overlapping regulatory bodies and laws.

Recommendations: We recommended hands-on training for FSIs on risk categorization of food and FBOs, tailoring the inspection checklist to food business operators, need based equitable supply of logistics and coordinated food safety activities between regulatory bodies.

Keywords: Risk-based Food Inspection, Food Safety Inspectors, Food safety, Food risk categorization

Poster No. 93 (Abstract No. 11114)

Lead poisoning outbreak investigation and its driving factors in livestock, Dinajpur

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Introduction: Bangladesh is an agriculture-based country. The livestock sector is an integral component and plays a crucial role in the agricultural production system of Bangladesh. Farmers face many challenges in livestock rearing to contribute GDP. Heavy metals poisoning especially lead poisoning is one of them. Industrial residues e.g., Recycling battery factories are one of the sources of lead poisoning. The mode of exposure is spreading the lead to the grass field and paddy land when battery plates melt at high temperatures in those factories. In cattle usually, two forms- (acute and subacute) lead poisoning occurred. The main clinical signs in acute forms are staggering movement, show muscle tremor especially at the head and neck, Head pressing to objects, blinking eyelids, cattle wandering aimlessly, circling movement, pupil dilatation, tetany, and convulsion. In case of subacute form dullness, complete anorexia, blindness, gait abnormalities, muscle tremor, and hyperesthesia may occur. Due to its heaviness of toxicity in animals, the meat and other accessory organs are also infected with lead which may create a public health hazard. The last outbreak of lead poisoning in cattle happened in the Dinajpur district in December 2021.

Methods: We have collected demographic, animal health-related information by interviewing face to face with a structured questionnaire and physical samples to find out the other risk factors associated with lead poisoning. The blood samples were collected from exposed living individuals of cattle and meat and liver from a dead animal. Some environmental samples were also collected from exposed soil, water, grasses, and paddy land straw with paddy.

Results: In the vicinity of the factory, some samples of straw showed the following results, Straw_DFN_004A (73113.79 ppb), Straw_DFN_006A (57848.71 ppb), Straw_DFN_002A (20170.63 ppb). The result of beef of dead cow was 2957.51. In the case of the environmental sample, Grass leaf (102851.85 ppb), water (286.71 ppb), soil (108360.75 ppb).

Conclusion: All the results are much higher than the acceptable level. We need to be aware of farmers to prevent this sort of outbreak in cattle and also need to further study to establish the public health hazard by One Health approach.

Keywords: Cattle death, Lead poisoning, One Health approach

Poster No. 94 (Abstract No. 11115)

Effects of xylanase supplementation on production performance, hemato-biochemical parameters and digestibility co-efficient in broiler chicken

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The present study was conducted to analyze the effects of dietary xylanase supplementation on broiler performance, digestibility, hemato-biochemical parameters in broiler chicken. For this purpose, a total of 90 one-day-old broiler chickens (Arbor Acres strain) were randomly divided into three equal groups each having 30 birds. All chickens were fed a corn-based formulated broiler mash feed during study period. Xylanase was given orally @ 0(Control), 0.5gm/kg (T1) and 1.0 g/kg (T2) for 28 days. The blood samples with and without anticoagulant (EDTA; 1mg/ml) were collected from all the birds for hematological and serum biochemical analysis. the body weight of the broiler chicken was extremely significant ($p<0.001$) than the control group. the low energy diet reduced feed intake, consequently a rise in feed efficiency enzyme supplementation in the corn-based diet ($p< 0.067$) and feed conversion ratio was also extremely significant. The effects of xylanase on digestibility of non-starch polysaccharides (NDF, ADF, ADL) was extremely significant ($p<0.001$). Likewise, statistically significant was recorded in dry matter and crude fibre in all treated groups. Also, non-significant result was recorded for red blood cells, leukocytes, hemoglobin concentration, and hematocrit values. Similarly, the liver enzymes (ALT, AST) and ALP and ammonium concentration were not significantly different in all treated groups as compared to control. In broiler chicken fed low energy diets, the xylanase supplementation of exhibited positive effects on growth, nutritional digestibility and hemato-biochemical response. The results of current study exposed that xylanase actions had non-significant effects on kidneys, heart and blood forming tissues exhibiting its safety for food applications.

Keywords: Xylanase, growth performance, hematological, biochemical, broilers

Poster No. 95 (Abstract No. 11205)

Influence of reproductive phase on *in vitro* maturation of abattoir-derived bovine oocytes

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Introduction: Abattoir-derived ovaries constitute a cost-effective source of oocytes for *in vitro* production (IVP) of embryos for commercial and research purposes. However, such oocytes are extremely heterogenous in terms of the quality and developmental competence. The reduction of variability of the oocytes quality is very important when they are selected as recipients for somatic cell nuclear transfer (SCNT) to produce genetically modified animals or for research purposes This study aimed to investigate the influence of reproductive phase of oocyte donor originated from abattoir-derived ovaries on *in vitro* maturation (IVM) of bovine oocytes.

Methods: IVM of oocytes was evaluated by observing the degree of cumulus cell (CC) expansion and extrusion of first polar body as well as both nuclear progression (NP) and cytoplasmic maturation (CM). For NP, after 24 h of IVM, oocytes were denuded and stained with DNA fluorochrome, Hoechst 33342 and observed under epifluorescence microscope. The male or female pronucleus (PN) forming ability of an oocyte following *in vitro* fertilization (IVF) were considered as CM. For CM, the fertilized zygotes after 24 h post-insemination were stained with Hoechst 33342 and observed under epifluorescence microscope.

Results: Results revealed that maturation rate was significantly influenced by the reproductive phase of the oocytes donor, luteal phase ovaries (LPO) versus follicular phase ovaries (FPO) based on the presence or absence of corpus luteum (CL), respectively. The significantly higher CC expansion (2°; 44.9 ± 4.9% vs. 35.9 ± 2.7%) and first polar body extrusion (58.3 ± 1.7% vs.46.7 ± 2.4%) were observed with LPO than FPO oocytes, respectively. Significant ($p<0.05$) effect of reproductive phase was also noted with LPO oocytes progressing higher rate of mature metaphase II stage (MII; 58.3 ± 1.7% vs. 46.7 ± 2.4%) and PN (54.9 ± 2.3% vs. 44.4 ± 3.0%) formation following IVF than FPO oocytes that imply better NP and CM of oocytes, respectively.

Conclusion: The present study therefore, indicates that the reproductive phase of oocyte donor notably from LPO positively influences the IVM of bovine oocytes to produce higher number of viable embryos *in vitro.*

Keywords: Bovine, Abattoir, Reproductive phase, Oocyte, IVM

Poster No. 96 (Abstract No. 11222)

Polymorphism in *CatSper1* gene in crossbred (Holstein Friesian x Deshi) and native cattle in Bangladesh

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Bangladesh Government is promoting sustainable improvements in milk, meat and eggs production. Artificial insemination (AI) with semen from high yielding animals is using to increase milk production. The widespread use of AI has revealed great variation in fertility. The success of AI significantly depends on quality of semen. Assessment of male fertility is traditionally based on microscopic evaluation of semen. However, some of the priced males have a low fertility even when classical semen parameters (i.e. viability, motility, abnormal forms, etc.) are normal. Many genes are known to control sperm motility, among them Cation channel of sperm (*CatSper*) family mutations resulted in male infertility. This study was therefore, undertaken to identify the polymorphism of *CatSper1* gene in crossbred cattle. A total of 94 blood samples were randomly collected from crossbred cattle (Holstein Friesian x Deshi) (54) from Sirajganj district and native cattle (40) from 5 different districts of Bangladesh. Nucleotide variation in CatSper1 gene at position 482 encompassing exon 3 and 4 was evaluated using PCR-RFLP. DNA was extracted from blood samples followed by PCR with targeted primer and restriction analysis *with Pvu*II, *Rsa*I (exon 3 and 4). Each of the enzymes cuts the PCR product and generated (403 and 79 bp) and (229, 152 and 103 bp) bands respectively against the restriction enzymes. Findings of this study indicate that CatSper1 gene in examined crossbred and native cattle has no polymorphism in selected position with respect to restriction enzymes used and show the conserveness in these exons in the studied samples.

Keyword: *CatSper1* gene, Crossbred cattle, Native cattle, Polymorphism, Semen

Poster No. 97 (Abstract No. 11251)

Isolation and molecular characterization of specific bacteriophages against Methicillin-resistant *Staphylococcus aureus* recovered from cow's Milk

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Background: The emergence of antibiotic resistance in bacterial pathogens has become a major concern in healthcare and agriculture. Methicillin-resistant *Staphylococcus aureus* (MRSA) is a notorious bacterial pathogen that has become resistant to multiple antibiotics, posing a significant threat to public health as it is ubiquitous in nature and circulating in the human-animal-environmental interfaces. In the scenario of rising antibiotic resistance among bacterial pathogens, the use of alternative therapy with bacteriophage has brought hope and can be a potential alternative therapy to combat MRSA infections.

Objectives: This research aimed to isolate and molecularly characterize specific bacteriophages (T2 virus) against methicillin-resistant *Staphylococcus aureus* (MRSA) isolated from cow's milk.

Methods: In this research, we recovered MRSA strains based on standard microbiological procedures and molecular detection of the fem*A*, nuc, and mec*A* gene. We identified 31 MRSA isolates out of 263 cow's milk samples (11.8%), and based on higher CFU production traits, we further selected 05 MRSA isolates for the isolation of specific bacteriophages from sewage samples. Double Agar Overlay Plaque Assays were performed to determine plaque formation, and purified phages were undergone for determining of the minimum inhibitory concentration (MIC). The MIC of bacteriophages was determined using microdilution method where prophages were serially added (9 log PFU – 3 log PFU, as 100 ul/ well) to the seeded MRSA (5 log cfu/ml @ 200 ul per well) in microtiter plates. The lowest concentration of phage at which no turbidity was seen was regarded as the MIC.

Results: The formation of plaques (clear zones of inhibition) on the lawn of the plates of MRSA was confirmed. Based on higher PFU yield (>10 log PFU/ml) we identified a total of five (05) lytic phages, and further characterized for MIC against MRSA. The phages exhibited excellent lytic activity against MRSA with a range of MICs of 0.0136 - 0.000272. According to our findings, we found all five bacteriophages are helpful to prevent the growth of *S. aureus*.

Conclusion: The overall findings showed that bacteriophages isolated from sewage had excellent lytic activity against MRSA strains. In conclusion, bacteriophages can be a promising candidate for phage therapy against MRSA instead of chemical-based antibacterial agents with no side effects in the future.

Keywords: MDR *Staphylococcus aureus*, bacteriophage, MIC

Poster No. 98 (Abstract No. 11268)

Antibacterial properties of *Lactobacillus* spp. against common multidrug resistant food-borne bacteria

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Introduction: Probiotic bacteria are widely known for their health benefits as dietary supplements. Lactic acid bacteria (LAB) are well known for their probiotic properties and are commonly used in food preservation and fermentation. This study aimed to assess the inhibitory potential and anti-biofilm activity of LAB against multi-drug resistant (MDR) bacteria like *Staphylococcus aureus*, *Salmonella enteritidis*, *Klebsiella pneumonia,* and *Escherichia coli.*

Methods: We isolated *Lactobacillus* spp. from yogurt samples and identified them by cultural, biochemical, and molecular methods (PCR). The viability of the *Lactobacillus* spp*.* was tested by exposing them to different pH levels (3, 5, 7, 9) and bile salt concentrations (0.3, 0.5 and 1%). Antibiotic susceptibility of the *Lactobacillus* spp*.* was demonstrated by the (K-B) disk diffusion method. The MDR pathogens were isolated from mastitic milk and identified through standard microbial, biochemical, and mPCR. Then, the non-specific bacteriocins (cell free supernatants) produced from *Lactobacillus* spp. were tested for antimicrobial activity against *E. coli, S. aureus, K. pneumonia,* and *S. enteritidis* having MDR traits.

Results: The results showed that *Lactobacillus* spp. had good growth in acidic conditions, with the most growth (9.53×10^{9} CFU/ml) seen at pH 5. They also had good viability at 0.3% bile salt concentration, which is the highest amount present in the human gut. *Lactobacillus* spp. showed strong antagonistic activity against MDR foodborne pathogens, and the bacteriocin extracted from them was able to inhibit the growth of *Staphylococcus aureus*, *Salmonella enteritidis*, *Klebsiella pneumonia* and *Escherichia coli*. Bacteriocin's inhibition zones against *Klebsiella pneumonia* was 14.66 ± 3.05 mm and *E. coli* was 9.66 ± 2.08 mm, respectively. The antibacterial activity of the bacteriocin was also noticeable against *Staphylococcus aureus and Klebsiella pneumonia.* Although *Lactobacillus* spp. showed resistance to various antibiotics, no antibiotic resistance genes (ARGs) were found through PCR testing, indicating that antibiotic resistance is an intrinsic characteristic of *Lactobacillus* spp.

Conclusion: The study suggests that instead of using antibiotics to combat MDR food-borne pathogens, *Lactobacillus* spp.*'s* bacteriocin can be a promising alternative. However, further research is required to determine their potential benefits to public health. Overall, the study concludes that *Lactobacillus* spp. isolated from yogurt could be promising probiotic strains due to their pH tolerance and intrinsic antibiotic resistance.

Keywords: Lactic acid bacteria (LAB), bacteriocins, food-borne MDR bacteria.

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Prof. Dr. Md. Taohidul Islam	Bangladesh Agricultural University
Prof. Dr. Mohammad Mahmudul Hassan	Chattogram Veterinary and Animal Sciences University
Prof. Dr. Mst. Minara Khatun	Bangladesh Agricultural University
Prof. Dr. Rokshana Parvin	Bangladesh Agricultural University
Prof. Dr. Sukumar Saha	Bangladesh Agricultural University
Prof. Dr. Zakir Hossain Habib	Institute of Epidemiology, Disease Control and Research
Dr. Ariful Islam	EcoHealth Alliance
Dr. Himel Barua	Chattogram Veterinary and Animal Sciences University
Dr. M. Salim Uzzaman	Institute of Epidemiology, Disease Control and Research
Dr. Mahbubur Rahman	Institute of Epidemiology, Disease Control and Research
Dr. Md. Abdullah Yusuf	National Institute of Neurosciences & Hospital
Dr. Md. Abdus Samad	Bangladesh Livestock Research Institute
Dr. Md. Abul Kalam	USAID
Dr. Md. Ahaduzzaman	Chattogram Veterinary and Animal Sciences University
Dr. Md. Giasuddin	UNIDO
Dr. Mohammad Mushtuq Husain	Institute of Epidemiology, Disease Control and Research
Dr. Mohammad Rafiqul Islam	Bangladesh Agricultural Research Council

Dr. Monalisa	Institute of Epidemiology, Disease Control and Research
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