



International Symposium 2023 (IS 2023)

on
Sustainable Development in Life Sciences

Date: 20 June 2023

Organized By

Faculty of Science

Noakhali Science and Technology University

Venue: IQAC Seminar Room

Prepared, Compiled and Edited by: Prof. Dr. Mohammad Safiqul Islam,
Chairman, Department of Pharmacy, Faculty of Science, Noakhali Science and
Technology University and Member secretary, IS 2023

with the support of

Organizing Committee, International Symposium 2023 (IS 2023)

Program at a Glance

Registration: 8:30 am – 9:30 am

Poster Set up Time: Start from 9:30 am

Inaugural session 10:00 am – 10:30 am

Anchoring: Prof. Dr. Firoz Ahmed, Chairman and Professor, Dept. of Microbiology, Noakhali Science and Technology University

Speech	Time
Address of Special Guests: Professor Dr. Newaz Mohammed Bahadur Treasurer Noakhali Science and Technology University	10:00 am – 10:10 am
Address of the Chief Guest: Professor Dr. Mohammad Abdul Baki Vice Chancellor (In-charge) and Pro-Vice Chancellor Noakhali Science and Technology University	10:10 am – 10:25 am
Address of the Session Chair: Prof. Dr. Md. Atiqur Rahman Bhuiyan Dean, Faculty of Science Noakhali Science and Technology University, Convener, Organizing Committee (IS 2023)	10:25 am – 10:30 am
Tea Break: 10:30 am – 10:45 am	

Plenary Session: 10:45 am – 11:45 pm

Session Chair: Prof. Dr. Mohammad Salim Hossain , Department of Pharmacy, Noakhali Science and Technology University		
Session Co-chair Prof. Dr. Jahangir Sarkar , Department of Fisheries and Marine Science, Faculty of Science, Noakhali Science and Technology University		
Plenary Speakers	Presentation Title	Time
Dr. A.R.M. Ruhul Amin Associate Professor Department of Pharmaceutical Sciences and Research, School of Pharmacy Marshall University, USA	Chemoprevention of Head and Neck Cancers by the Combination of Natural Compounds EGCG and Resveratrol.	10:45 am - 11:15 am

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Dr. Md Tofazzal Islam Professor and Founding Director, Institute of Biotechnology and Genetic Engineering (IBGE), Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur-1706 BANGLADESH	CRISPR-Cas Genome Editing for Sustainable Development in the Life Sciences	11:15 am –11:45 am
Poster session	P1-P24	12 pm-1:00 pm
Evaluation Team: <ol style="list-style-type: none"> 1. Dr. Subodh Kumar Sarkar, Associate Professor and Chairman, Department of Biochemistry and Molecular Biology, Noakhali Science and Technology University 2. Dr. Md. Mafizul Islam, Associate Professor and Chairman, Department of Biotechnology and Genetic Engineering, Faculty of Science, Noakhali Science and Technology University 3. Dr. Mohammad Mohinuzzaman, Associate Professor and Chairman, Department of Environmental Science and Disaster Management, Noakhali Science and Technology University 		

Scientific Session:

Oral Session 1: 11:45 pm -1:05 pm

Oral Session 2: 2:00 pm - 3:00 pm

Session	Time
Oral Session 1	11:45 am-1:05 pm
Session Chair Prof. Dr. Mohammad Safiqul Islam , Chairman, Department of Pharmacy, Faculty of Science, Noakhali Science and Technology University	
Session Co-chair Prof. Dr. Mohammad Hanif, Chairman , Department of Applied Mathematics, Faculty of Science, Noakhali Science and Technology University	
O1: Title: Association of NOS3 (rs 1799983) gene polymorphisms with increased risk of Chronic Kidney Disease in Bangladeshi patients Dr. Mafizul Islam , Chairman, Department of Biotechnology and Genetic Engineering, Faculty of Science, Noakhali Science and Technology University	11:45 am - 12:05 pm
O2: Title: Assessment of the Association of <i>CYP1A1</i> Gene Polymorphisms with the Susceptibility of Cervical Cancer: A Case-Control Study and Meta-Analysis Md Abdul Barek , Lecturer, Department of Pharmacy, Faculty of Science, Noakhali Science and Technology University	12:05 pm-12:25 pm
O3: Title: Identifying risk factors of preeclampsia among pregnant women in Bangladesh: A machine learning perspective Dr. Nazia Majadi , Associate Professor, Department of Computer Science and Telecommunication Engineering, Faculty of Engineering, Noakhali Science and Technology University	12:25 pm -12:45 pm

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<p>Q4: Title: Combating multidrug resistant pathogens: Development of antibiotic resistance breakers and the way forward Dr. Murad Hossain, Associate Professor, Department of Biotechnology and Genetic Engineering, Faculty of Science, Noakhali Science and Technology University</p>	12:45 pm -1:05 pm
<p>Lunch Break: 1:05 pm – 2:00 pm</p>	
<p>Oral Session 2</p>	<p>2:00 pm-3:00 pm</p>
<p>Session Chair: Prof. Dr. Firoz Ahmed, Chairman, Department of Microbiology, Faculty of Science, Noakhali Science and Technology University</p>	
<p>Session Co-Chair: Prof. Dr. Abdullah-Al Mamun, Chairman, Department of Fisheries and Marine Science, Faculty of Science, Noakhali Science and Technology University</p>	
<p>Q5: Title: Genetic differentiations in sparid fishes inferred from mtDNA control region analysis Dr. Rakebul Islam, Professor, Department of Fisheries and Marine Science, Faculty of Science, Noakhali Science and Technology University</p>	2:00 pm -2:20 pm
<p>Q6: Title: Phytochemical screening, Antioxidant activity and detection of bioactive compounds present in water, methanol and ethanol extracts of Japanese Peach Fruit and their antibacterial study Dr. Subodh Kumar Sarkar, Chairman and Associate Professor, Department of Biochemistry and Molecular Biology,</p>	2:20 pm -2:40 pm
<p>Q7: Title: An In Silico Approach to Identify the Conserved Virulent Proteins of Campylobacter species Explores Potential siRNA Candidates as a Novel Therapeutic Strategy against Campylobacteriosis Md. Abdul Kader, Lecturer, Department of Biotechnology and Genetic Engineering, Faculty of Science, Noakhali Science and Technology University</p>	2:40 pm-3:00 pm

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GENERAL TRACKS:

1. Track 1: Pharmacology and Biomedical Sciences
2. Track 2: Approaches in Biotechnology, Molecular Biology and Microbiology
3. Track 3: Food Safety and Security
4. Track 4: The Fourth Industrial Revolution (4IR) in life sciences

We believe that scientific discussions and presentations by leading global and local experts as well as new research being carried out by young scientists, will contribute to improving life science technologies in both basic and clinical research.

Symposium committee:

1. Prof. Dr. Md. Atiqur Rahman Bhuiyan, Dean, Faculty of Science, NSTU- **Convener**
2. Prof. Dr. Mohammad Salim Hossain, Dept. of Pharmacy, NSTU
3. Prof. Dr. Mohammad Hanif, Chairman, Dept. of Applied Mathematics, NSTU
4. Prof. Dr. Md. Jahangir Sarkar, Dept. of FIMS, NSTU
5. Prof. Dr. Abdullah-Al Mamun, Chairman, Dept. of FIMS, NSTU
6. Prof. Dr. Firoz Ahmed, Chairman, Dept. of Microbiology
7. Dr. Subodh Kumar Sarkar, Chairman, Dept. of Biochemistry Molecular Biology, NSTU
8. Dr. Mafizul Islam, Chairman, Dept. of Biotechnology and Genetic Engineering, NSTU
9. Dr. Mohammad Mohinuzzaman, Chairman, Dept. of Environmental Science and Disaster Management
10. Director (Acting), Research Cell, NSTU.
11. Prof. Dr. Mohammad Safiqul Islam, Chairman, Dept. of Pharmacy, NSTU- **Member Secretary**

Accepted Abstracts

Tracks

PBS- Pharmacology and Biomedical Science

BMM- Approaches in Biotechnology, Molecular Biology and Microbiology

FSS-Food Security and Safety

4IR- 4th Industrial Revolution

Plenary Session

Sl No	Presenting author	Title	Group	Accept/reject	Page No.
PS-1	Dr. A.R.M. Ruhul Amin Associate Professor Department of Pharmaceutical Sciences and Research, School of Pharmacy Marshall University, USA	Chemoprevention of Head and Neck Cancers by the Combination of Natural Compounds EGCG and Resveratrol.	PBS	Accepted	10
PS-2	Dr. Md Tofazzal Islam Professor and Founding Director, Institute of Biotechnology and Genetic Engineering (IBGE), Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur-1706 BANGLADESH	CRISPR-Cas Genome Editing for Sustainable Development in the Life Sciences	BMM	Accepted	15

Oral Presentation

Sl No	Presenting author	Title	Group	Accept/reject	Page No.
O1	Dr. Mafizul Islam	Association of <i>NOS3</i> (rs 1799983) gene polymorphisms with increased risk of Chronic Kidney Disease in Bangladeshi patients	BMM	Accepted	17
O2	Md Abdul Barek	Assessment of the Association of <i>CYP1A1</i> Gene Polymorphisms with the Susceptibility of Cervical Cancer: A Case-Control Study and Meta-Analysis	PBS	Accepted	18
O3	Dr. Nazia Majadi	Identifying risk factors of preeclampsia among pregnant women in Bangladesh: A machine learning perspective	4IR	Accepted	19
O4	Dr. Murad Hossain	Combating multidrug resistant pathogens: Development of antibiotic resistance breakers and the way forward	BMM	Accepted	20
O5	Dr. Rakebul Islam	Genetic differentiations in sparid fishes inferred from mtDNA control region analysis	FSS	Accepted	21
O6	Dr. Subodh Kumar	Phytochemical screening, Antioxidant activity	PBS	Accepted	22

	Sarkar	and detection of bioactive compounds present in water, methanol and ethanol extracts of Japanese Peach Fruit and their antibacterial study			
O7	Md. Abdul Kader	An In Silico Approach to Identify the Conserved Virulent Proteins of Campylobacter species Explores Potential siRNA Candidates as a Novel Therapeutic Strategy against Campylobacteriosis	BMM	Accepted	24

Poster Presentation

Sl No.	Author	Title	Group	Accept/reject	Page No.
P1	Anik Roy	Influence of <i>Clerodendrum infortunatum</i> leaf extract on Anti-inflammatory and Anti-obesity gene expression in high-sugar diet-induced obese mice	PBS	Accepted	25
P2	Mahbuba Afrin Sworna	Pharmacovigilance in the Fourth Industrial Revolution: Enhancing Drug Safety and Surveillance	PBS	Accepted	26
P3	Tasfiya Bhuiyan	Inhibition of mPGES-1 with trans-Ferulic acid and catechin derivatives from <i>Zingiber capitatum</i> Roxb rhizome reduces pyrexia via downregulating PGE ₂	PBS	Accepted	27
P4	Marjanur Rahman Bhuiyan	Antidiabetic Potential of Whole Plant Extract of <i>Fimbristylis aestivalis</i> : Chemical Profiling, <i>in-vitro</i> , <i>in-vivo</i> and <i>in-silico</i> Approach	PBS	Accepted	28
P5	Rumaisa Saifee	Association of the single nucleotide polymorphism rs2241766 in ADIPOQ gene with type 2 diabetes mellitus	BMM	Accepted	29
P6	Md Salahuddin	Re-sensitizing multidrug-resistant <i>E. coli</i> and <i>K. pneumoniae</i> through investigation of antibiotic resistance breakers from traditional medicinal plants and antibiotic combination therapy	BMM	Accepted	30
P7	Farjana Akter	Identification and molecular characterization of microbial community with heavy metal tolerance patterns of some bacteria in textile effluents from Chattogram municipal area, Bangladesh	BMM	Accepted	31
P8	Tahomina Mitu	Assessment of bacterial load in a street food (Fuchka) in Noakhali with their characterization and study on antibiotic-	BMM	Accepted	32

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		resistant pattern			
P9	Nilufa Yasmin	Micro RNAs expression analysis shows key affirmation of ESR1 (Estrogen Receptor 1) as a novel prognostic and therapeutic biomarker for cervical and liver cancers.	BMM	Accepted	33
P10	Adnan Munim	Phenotypic and Genotypic Detection of Multi-drug Resistant Gramnegative Bacteria from Gut and Rectal swab of Poultry Chickens in Noakhali	BMM	Accepted	34
P11	Md. Mubarak Hossain	Exploration of endophytic fungi from <i>Allium cepa</i> along with its in-vitro antioxidant, antimicrobial and cytotoxic potential	BMM	Accepted	36
P12	Khadijatul Kubra Riya	Prevalence and characteristics of microplastics in surface water of urban river, Bangladesh	FSS	Accepted	37
P13	Meer Md. Rahad	Morphological variation among different eel fish species in Bangladesh	FSS	Accepted	38
P14	Arman Hossain Patwary	Determination of Antioxidant Activity in Some Fresh Fruits Commonly Consumed at Noakhali, Bangladesh.		Accepted	39
P15	Sweety Bhowmik	Determination of Harmful Algal Bloom and Their Subsequent Effects on the Food System Security in Noakhali, Bangladesh.	FSS	Accepted	40
P16	Salma Sultana	Accumulation and human health risk assessment of micro and mesoplastics in some coastal and marine water fishes from Bangladesh	FSS	Accepted	41
P17	Partho Banik	Quantification and characterization of microplastics from five major estuaries of Bangladesh	FSS	Accepted	42
P18	Najmul Hossain	Morphological and physico-biochemical characterization of diversified Tomato (<i>Solanum lycopersicum</i>) genotypes in Bangladesh	FSS	Accepted	43
P19	Nilima Tuz Jamal	Accumulation and characterization of microplastics in some commercially important marine fishes from the Bay of Bengal	FSS	Accepted	44
P20	Atiqur Rahman Bhuiyan	Evaluation and performance analysis of some inbreed and hybrid cotton varieties in coastal areas	FSS	Accepted	45
P21	Gazi Mohsin	Gene effects for the traits contributing to yield in pumpkin (<i>Cucurbita moschata</i> Duch. Ex. Poir)	FSS	Accepted	46
P22	Maeen Uddin	Impact of Tobacco Farming on the Micro	FSS	Accepted	47

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		Algal Community and Food Security in Chakaria, Bangladesh			
P23	Mohima Khanom	The linkage between IL-6 rs1800797 Polymorphism and breast cancer susceptibility in Bangladeshi women	PBS	Accepted	48
P24	Shahana Akter	Bioactive molecule(s) of Kalanchoe pinnata synergistically act to re-sensitize multidrug-resistant <i>Klebsiella pneumoniae</i>	BMM	Accepted	49

PS-1

Chemoprevention of Head and Neck Cancers by the Combination of Natural Compounds EGCG and Resveratrol.

*Adeoluwa Adeluola¹, Lukmon Raji¹, Saroj Sigdel¹, A.S.M. Anisuzzaman², A. R. M. Ruhul Amin¹.
¹Marshall University, Huntington, WV, USA; ²Winship Cancer Institute of Emory University, Atlanta, GA, USA*

Head and neck cancer (HNC) is a devastating disease and the 6th most common cancer worldwide. Most HNC patients are diagnosed with advanced-stage disease for which the 5-year survival is below 50%, stressing the need for chemoprevention. Recently, we have reported that the combination of resveratrol and EGCG induces synergistic apoptosis and inhibits xenografted HNC growth by inhibiting the AKT-mTOR pathway. This study investigated the chemopreventive efficacy of resveratrol, EGCG, and their combination using the 4NQO-induced oral carcinogenesis model. C57BL/6 mice were exposed to 4-NQO (50 µg/ml) via drinking water for 10 weeks, followed by treatment with vehicle (50% sweetened condensed milk), resveratrol (30 mg/kg), EGCG (30 mg/kg) and their combination for 8 weeks, 5 days/week. The mice were sacrificed on week 24, and the number of visible and microscopic lesions was counted. Resveratrol alone and in combination with EGCG significantly inhibited the number of visible lesions. In contrast, the number of microscopic lesions and lesion area was significantly inhibited only in the combination group. The expression of Ki-67 was also significantly inhibited in resveratrol and combination groups when compared with untreated control. Furthermore, RNASeq and qPCR analysis using an HNC cell line identified GDF15, ATF3, p21, p27, and Bim as significantly upregulated genes, with GDF15 being the most upregulated one. Expression of GDF15 and ATF3 proteins was confirmed by western blotting. Our data strongly demonstrate the chemopreventive potential of the combination of EGCG and resveratrol and pave the way for further clinical developments. *(Supported by NIH Grant P20GM103434 to the West Virginia IDeA Network for Biomedical Research Excellence)*

Curriculum Vitae

A.R.M. Ruhul Amin, B. Pharm, M. Pharm, Ph.D.

Associate Professor of Pharmacology (Tenured)

Marshall University School of Pharmacy

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Tel # 1-304-696-7371 (O), 1-404-210-2102 (C), E-mail: amina@marshall.edu

Education

- 1990 B. Pharm. (Hons.), University of Dhaka, Bangladesh.
1991 M. Pharm., University of Dhaka, Bangladesh.
2003 Ph.D. (Medical Sciences), Nagoya University School of Medicine, Japan.

Postgraduate Training

- 05/2004-07/2007 Postdoctoral Fellow, Case Western Reserve University, OH. Dissect the molecular basis of p53-dependent and independent programmed cell death/apoptosis pathway using human cancer cell lines.
08/2007-08/2009 Research Associate, Winship Cancer Institute of Emory University, GA. Investigate the mechanism of drug actions using in vitro cell culture, in vivo animal models, and patient samples.

Industry Experience

- 1993 Rhone Poulenc Rorer, Inc. One month internship
1994-1995 North Bengal Pharmaceuticals Ltd. Bangladesh. Quality Control Officer
1995- 1996 Beximco Pharmaceuticals Ltd. Bangladesh. Supervise manufacturing, including formulation, in-process quality control, and quality assurance of solid dosage forms.

Academic and Professional Appointments

- 1996- 2004 Faculty, Department of Pharmacy, Rajshahi University, Bangladesh
2004- 2007 Postdoc, Department of Genetics, Case Western Reserve University, OH
2007- 2008 Research Associate, Winship Cancer Institute of Emory University, GA
2009-2010 Instructor, Winship Cancer Institute of Emory University, GA
2011- 2017 Assistant Professor, Winship Cancer Institute of Emory University, GA
2017- 2023 Assistant Professor, Marshall University School of Pharmacy, WV
2023- Associate Professor (tenured), Marshall University School of Pharmacy, WV
2018- Adjunct Assistant Professor, Marshall University JCE School of Medicine, WV

Honors, Special Recognition, and Awards

- 2022 Teacher of the Year, Marshall University School of Pharmacy
2022 Dean's Award of Excellence in Research, Marshall University School of Pharmacy
2020 Distinguished Researcher Award, Association of Pharmacy Professionals
2013 Rising Star, Department of Hematology and Medical Oncology, Emory University
2012 Robbins Scholar Award, Winship Cancer Institute
1998 Japanese Govt. Monbusho Scholarship

Editorial Board Member and Journal Reviewer (a Few selected Journals)

Cancers Oncology Reports, Frontiers in Cell and Developmental Biology, Aging, Cancer Research, Cancer Letters, Cancer, Molecular Cancer Therapeutics, Molecular Carcinogenesis, Carcinogenesis, Cell Cycle, Frontiers in Oncology, Mutation Research, BMC Cancer, Cancer Research Frontier, PLOS One, Toxicology and Applied Pharmacology,

Grant Review Panel

NIH CDP Study Section, Winship Invests Pilot Grant, American University of Beirut Pilot Grant

Invited Lectures (Representative list- total 18)

1. Synergistic Antitumor Effects of the Combination of Resveratrol and EGCG. MSPS Seminar Series, Marshall University School of Pharmacy, January 2022
2. Mechanism of Resistance to Targeted Therapy in Head and Neck Cancer. Department of Clinical Oncology, Marshall University John C. Edwards School of Medicine, February 2020
3. Toward Personalized Treatment of Head and Neck Cancer: Current Status and Future Perspectives. Guest Speaker, Dhaka University Bangladesh, June 2016
4. Co-targeting EGFR and PI3K in Head and Neck Cancer: Mechanisms of Synergy and Resistance. Third AABPS Convention, Philadelphia, PA. 2015
5. Keynote Speaker, Seminar on “Cancer Prevention: Future Perspective with Natural Compound.” Southeast University, Dhaka, Bangladesh, 2014

Grant Supports

Pending

1. R01DE033045 (PI-Amin)
Title: Dual targeting of JAK-STAT3 and NRF2 pathways for chemoprevention of head and neck cancer by FLLL12
Agency: NIDCR
2. R15DE032063 (PI: Amin)
Title: Targeting oncogenic pathways for chemoprevention of head and neck cancer by FLLL12
Agency: NIDCR/NCI

Active

1. WV INBRE Center for Natural Products (PI: Amin); Agency: NIGMS
Title: Increasing the efficacy of actinomycin D with resveratrol in aerodigestive tract cancers (\$60K for 2 years)
2. Faculty Research Support Grant (PI: Amin); Agency: School of Pharmacy
Title: Chemoprevention of HNC using a combination of EGCG and luteolin (\$25K)

Completed

1. WV INBRE Center for Natural Products (PI: Amin); Agency: NIGMS
Title: Chemoprevention of head and neck cancer by the combination of EGCG and resveratrol (\$60K for 2 years)
2. WV INBRE Cancer Biology (co-PI: Amin); Agency: NIGMS
Title: Exploring the role of GPR68 in head and neck carcinogenesis and treatment (\$60K)

- for 2 years)
3. WV INBRE Cancer Biology (PI: Amin); Agency: NIGMS
Title: Genetic profiling of HNC cell lines resistant to apoptosis induced by EGFR and PI3K co-targeting (\$30K for 1 year)
 4. WV INBRE Center for Natural Products (PI: Amin); Agency: NIGMS
Title: Microbial extracts for the treatment of tobacco-associated malignancies (\$30K for 1 year)
 5. School of Medicine and School of Pharmacy Collaborative Grant (Co-PI)
Title: Chemoprevention of lung cancer using a combination of EGCG and luteolin (\$50K for 1 year)
 6. R03CA159369: 03/01/2012-2/28/2014 (PI: Amin); Agency: NCI
Title: Mechanism of chemopreventive synergism from the combination of EGCG and Erlotinib (\$100K direct)
 7. R03CA171663: 03/01/2013-02/28/2015 (PI: Amin); Agency: NCI
Title: Targeting both intrinsic and extrinsic apoptosis by FLLL-12 in lung cancer (\$100K direct)
 8. SPORE in Head and Neck, Career Development Award (PI: Amin); Agency: NCI
Title: Chemoprevention of Squamous Cell Carcinoma of the Head and Neck by Dietary Polyphenols EGCG and Luteolin (\$60K direct)
 9. Robbins Scholar Award (00023544): 03/01/2012-2/28/2014 (PI: Amin); Agency: Emory
Title: Combination of natural compounds EGCG and luteolin for prevention of HNC (\$60K for 1 year)

Representative Publications (Total: 44 Research, 12 Review, 4 Book Chapters, and 52 Abstracts)

1. Shore D, Griggs N, Graffeo V, **Amin AR**, Zha X, McAleer J. GPR68 limits the severity of chemical-induced oral epithelial dysplasia. *Scientific Reports*, 2023; 13:353
2. Adeluola AA, Bosomtwe N, Long TE, **Amin AR**. Context-dependent activation of p53 target genes and induction of apoptosis by actinomycin D in aerodigestive tract cancers. *Apoptosis*, 2022; 27: 342-353
3. **Amin AR**, Wang D, Nannapaneni S, Lamichhane R, et. al. Combination of resveratrol and green tea epigallocatechin gallate induces synergistic apoptosis and inhibits tumor growth *in vivo* in head and neck cancer models. *Oncology Reports*, 2021; 45:87.
4. Journigan VB, Feng Z, Rahman S, Wang Y, **Amin AR**, et al. Structure-based design of novel biphenyl amide antagonists of human Transient Receptor Potential Cation Channel Subfamily M Member 8 channels (TRPM8) with potential implications in the treatment of sensory neuropathies. *ACS Chemical Neuroscience*, 2020; 11:268-290.
5. Anisuzzaman ASM, Haque A, et. al. *In vitro* and *in vivo* synergistic anti-tumor activity of the combination of BKM120 and erlotinib in head and neck cancer: Mechanism of apoptosis and resistance. *Molecular Cancer Therapeutics*, 2017; 16:729-738.
6. Wang D, Qian G, Zhang H, et. al. HER3 targeting sensitizes HNSCC to cetuximab by reducing HER3 activity and HER2/HER3 dimerization - evidence from cell line and patient derived xenograft models. *Clinical Cancer Research*, 2017; 23:677-686.

7. Anisuzzaman ASM, Haque A, et. al. Preclinical *in vitro*, *in vivo* and pharmacokinetic evaluations of FLLL12 for the prevention and treatment of head and neck cancers. *Cancer Prevention Research*, 2016; 9:63-73.
8. Haque A, Rahman MA, Fuchs JR, Chen ZG, Khuri FR, Shin DM, **Amin AR**. FLLL12 induces apoptosis in lung cancer cells through a p53/p73-independent but death receptor 5-dependent pathway. *Cancer Letters*, 2015; 363:166-75.
9. Haque A, Rahman MA, Chen ZG, Saba NF, Khuri FR, Shin DM, **Amin AR**. Combination of Erlotinib and EGCG Induces Apoptosis of Head and Neck Cancers through Post-transcriptional Regulation of Bim and Bcl-2. *Apoptosis*, 2015; 20:986-95.
10. **Amin AR**, Haque A, Rahman MA, Chen ZG, Khuri FR, Shin DM. Curcumin induces apoptosis of upper aerodigestive tract cancer cells by targeting multiple pathways. *PLoS One*, 2015; 10: e0124218.
11. Jiang N, Wang D, Hu Z et. al. Combination of Anti-HER3 Antibody MM-121/SAR256212 and Cetuximab Inhibits Tumor Growth in Preclinical Models of Head and Neck Squamous Cell Carcinoma. *Molecular Cancer Therapeutics*, 2014; 13:1826-36.
12. Wang X, Beitler JJ et al. Honokiol Enhances Paclitaxel Efficacy in Multi-Drug Resistant Human Cancer Model through the Induction of Apoptosis. *PLoS One*. 2014; 9:e86369.
13. Majumdar D, Jung KH, Zhang HZ, et. al. Luteolin nanoparticle in chemoprevention- *in vitro* and *in vivo* anticancer activity. *Cancer Prevention Research*, 2014; 7:65-73.
14. Shin DM, Zhang HZ, Saba NF et. al. Chemoprevention of Head and Neck Cancer by Simultaneous Blocking of Epidermal Growth Factor Receptor and Cyclooxygenase-2 Signaling Pathways: Preclinical and Clinical Studies. *Clinical Cancer Research*, 2013; 19:1244-56.
15. **Amin AR**, Thakur VS, Gupta K et. al. N-(phosphonacetyl)-L-aspartate induces TAp73-dependent apoptosis by modulating multiple Bcl-2 proteins: Potential for cancer therapy. *Oncogene*, 2013; 32:920-9. *Corresponding author
16. Rahman MA, **Amin AR** et. al. Systemic Delivery of siRNA-Nanoparticles Targeting RRM2 Suppresses Head and Neck Tumor Growth. *Journal of Controlled Release*, 2012; 159:384-92.
17. **Amin AR**, Wang D, Zhang HZ, et al. Enhanced Anti-tumor Activity by the Combination of the Natural Compounds (-)- Epigallocatechin-3-gallate and Luteolin: Potential role of p53. *Journal of Biological Chemistry*, 2010; 285:34557-65.
18. **Amin AR**, Thakur VS, Gupta K et. al. Restoration of p53 functions protects cells from Concanavalin A-induced apoptosis. *Molecular Cancer Therapeutics*, 2010; 9:471-9.
19. Hastak K, Paul RK, Agarwal MK, Thakur VS, **Amin AR et al**. DNA Synthesis from Unbalanced Nucleotide Pools Causes Limited DNA Damage that Triggers ATR-CHK1-Dependent p53 Activation. *PNAS*, 2008; 105:6314-9.
20. **Amin AR**, Thakur VS, Paul RK, et. al. SHP-2 tyrosine phosphatase inhibits p73-dependent apoptosis and expression of a subset of p53-target genes induced by the green tea polyphenol EGCG. *PNAS*, 2007; 104:5419-5424.

Publication Link My NCBI:

<https://www.ncbi.nlm.nih.gov/sites/myncbi/a.r.m..amin.1/bibliography/47921469/public/?sort=date&direction=ascending>

PS-2

CRISPR-Cas Genome Editing for Sustainable Development in the Life Sciences

*Professor and Founding Director, Institute of Biotechnology and Genetic Engineering (IBGE), Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur, Bangladesh
e-mail: tofazzalislam@bsmrau.edu.bd*

The Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-CRISPR-associated (Cas)-mediated genome editing is a transformative new technology, which revolutionized basic and applied biology. Over the last decade of tremendous improvement in the methodologies, the CRISPR-Cas toolbox is now beneficial for crop improvement, curing genetic diseases, and engineering desirable genetic traits. Live-cell imaging, high-throughput functional genomic screens, domestication of wild crops, creating biodiversity and point-of-care diagnostic are also being done with the versatile CRISPR-Cas toolbox. The diversity, modularity, and efficacy of CRISPR-Cas systems are driving a biotechnological revolution. On the other hand, the global climate change, heavy reliance on synthetic chemical inputs and degradation of soil, causing environmental pollution and affecting animal and human health. Climate change poses serious threat to plant health and sustainable higher productivity in the crop field. To address these challenges, we aimed to use some frontier sciences such as genomics, CRISPR-Cas genome editing, and nanotechnology in the farmers' field for better nutrition and protection of plants from biotic and abiotic stresses. For example, we rapidly determined the genetic identity and origin of the first epidemic outbreak of a devastating wheat blast disease in 2016 using field pathogenomics, open data sharing and international collaboration approaches. That discovery helped right policy decision to tackle any future epidemics which saved huge economic losses caused by wheat blast. By discovering genome-specific primers and using CRISPR-Cas technology, we developed a point-of-care diagnostic method for the detection of wheat blast fungus in the lab, field and plant quarantine. To control wheat blast disease, we developed novel daylight-driven rechargeable TiO₂ nanocatalyst, which are effective in controlling wheat blast in the field. Furthermore, we edited some disease susceptibility genes in wheat genome by CRISPR-Cas technology for the development of a durable blast resistance variety. Large-scale application of these frontier technologies would significantly reduce (up to 50%) the reliance on synthetic agrochemicals, improve the farm productivity and profitability. This lecture illustrates and discusses the progress of our interdisciplinary research utilizing genomics and CRISPR-Cas genome editing along with open science practices and international collaboration for promoting sustainable crop production and food security issues in Bangladesh and elsewhere.



Brief Resume of Professor Dr. Md. Tofazzal Islam

Professor Tofazzal Islam is an internationally reputed researcher in the field of molecular host-microbe interactions and agrobiotechnology. He did PhD at Hokkaido University in applied Biosciences. Dr. Islam conducted postdoctoral research at Hokkaido University, University of Goettingen, University of Nottingham and West Virginia University under the fellowship programs of JSPS, Alexander von Humboldt, Commonwealth and Fulbright, respectively.

Prof. Tofazzal discovered a large number (>50) of bioactive secondary metabolites from the host and non-host organisms, and elucidated the mode of actions of some of these natural products. He has been leading a large group of national and international researchers for the mitigation of worrisome wheat blast disease caused by *Magnaporthe oryzae Triticum* since its first epidemic outbreak in Bangladesh in 2016 using genomics, genome editing and other advanced molecular approaches. His team developed a rapid, convenient and highly sensitive method for the diagnosis of wheat blast fungus in collaboration with researchers in China, USA and KSA using CRISPR-Cas12a technology. Recently, his team sequenced the whole genome of a year-round fruiting jackfruit which opens opportunity for molecular breeding and agroprocessing of this national fruit for food and nutritional security.

He is the Editor-in-Chief of two series books, *Bacilli and Agrobiotechnology*, and *CRISPR-Cas Methods* that publish by Springer Nature. He serves as an Academic Editor of *PLOS ONE*, Editor of *Scientific Reports*, Associate Editor of *Frontiers in Microbiology* and Member of Editorial Advisory Board of *CABI Reviews*.

Prof. Islam is an elected Fellow of Bangladesh Academy of Sciences (FBAS), American Phytopathological Society (FAPS), Bangladesh Academy of Agriculture (FBAA) and The World Academy of Sciences (FTWAS). He received many awards and medals including a Gold Medal of Bangladesh Academy of Sciences, Commonwealth Innovation Award, Islamic Development Bank Innovation Award, and the GNOBB Award.

He published more than 300 articles in the international journals and book series with >7,000 citations (*h*-index 46). He is the highest cited researcher in Bangladesh in the field of Genetics and Molecular Biology. His research team utilizes frontier technologies to mitigate new challenges in agriculture such as wheat blast.

O1

Association of *NOS3* rs1799983 polymorphism with increased risk of Chronic Kidney Disease in Bangladeshi patients

Author: Dr. Mohammed Mafizul Islam, Umma Habiba Rahman, Md. Neamat Ullah, Dr. Shipan Das Gupta

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Background: Chronic kidney disease (CKD) is a complex, pathophysiologic condition that is irreversible and frequently results in a terminal state when the patient needs renal replacement treatment. There are currently known mutations in several hundred genes that could potentially cause kidney-related single-gene disorders and one of these genes are *NOS3*. Numerous analyses have demonstrated a connection between the single-nucleotide polymorphism (SNP) rs1799983 (Glu298Asp) in the *NOS3* and the pathophysiology of CKD. There have been no such studies conducted on the population of Bangladesh. The aim of this study is to investigate the association between CKD and the *NOS3* rs1799983 polymorphism in the Noakhali region of Bangladesh.

Method: This study compared the genotype distributions of 110 CKD patients with 40 controls. Genotyping was performed by the polymerase chain reaction-restriction fragment length polymorphism technique (PCR-RFLP).

Result and Discussion: When the genotype frequencies were compared between both groups, it was found that a total of 13.64% of the CKD patients and 32.5% of the controls carried the TT genotype, whereas these values were 55.46% and 52.5% in the case of the TG genotype and 30.90% and 15% in the case of the GG genotype. The genotype frequencies of rs1799983 of the *NOS3* are consistent with Hardy-Weinberg equilibrium ($p > 0.05$) in both CKD patients and controls. The patient carrying the TG genotype had 2.52 times more risk (OR = 2.52, $p = 0.042$) in comparison to the TT genotype for the development of CKD, and the result is statistically significant ($p < 0.05$), whereas the patient carrying the GG genotype had 4.91 times more risk (OR = 4.91, $p = 0.0063$) for the development of CKD in comparison with controls carrying the TT genotype, and the result is statistically significant ($p < 0.05$). In terms of the dominant model, patients with the TG+GG genotype were 3.049 times more likely (OR = 3.049, $p = 0.0108$) to develop CKD than controls with the TT genotype, and the difference was statistically significant ($p < 0.05$). In the recessive model, patients with the GG genotype had 2.54 times more risk (OR = 2.54, $p = 0.057$) of developing CKD than patients with the TT+TG genotype, but the difference was not statistically significant ($p > 0.05$). Patients with the G allele were 2.019 times more likely (OR = 2.019, $p = 0.008$) to develop CKD than patients with the T allele, and this difference was also statistically significant ($p < 0.05$).

Conclusion: Our results indicate that the rs1799983 SNP of the *NOS3* is associated with an increased risk of CKD in the Bangladeshi population. As we have identified the genetic basis of CKD among Bangladeshi patients, we hope that it will be helpful for the treatment selection of CKD patients and the future meta-analysis of these markers.

Key Words: CKD; ESRD; *NOS3*; SNP; PCR-RFLP; Endothelial dysfunction

O2

Track 1: Pharmacology and Biomedical Sciences

Assessment of the Association of *CYP1A1* Gene Polymorphisms with the Susceptibility of Cervical Cancer: A Case-Control Study and Meta-Analysis

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Abstract

Background: Cervical cancer (CC) is Bangladesh's second most common type of female malignancy. Polymorphisms in the *CYP1A1* gene have been reported to be associated with CC in different populations.

Methods: A total of 185 CC patients and 220 healthy controls were recruited, and the PCR-RFLP (Polymerase chain reaction-restriction fragment length polymorphism) technique was applied for genotyping. RevMan 5.3 and Metagenyo web tool were used for performing the meta-analysis.

Results: The rs4646903 polymorphism was significantly linked with CC in all association models, namely, additive 1, 2, dominant, recessive, overdominant and allele models (OR=2.41, 4.75, 2.67, 3.61, 2.13, 2.44, respectively). On the contrary, rs1048943 showed no association ($p>0.05$) with CC. Haplotype analysis revealed AT and AC haplotypes significantly decreased (OR=0.45) and increased (OR=4.86) CC risk, respectively, and SNPs are in strong linkage disequilibrium ($D'=0.912$, $r^2=0.448$). Again, rs4646903 carriers with a contraception history and >5 years of taking contraceptives showed an enhanced risk of CC (OR=2.39, OR=3.05). Besides, rs1048943 carriers aged >40 years (OR=0.44), conceived first child aged ≤ 18 years (OR=3.45), and history of contraceptives (OR=2.18) were significantly linked with CC. Our meta-analysis found that codominant 1 (COD 1), codominant 2 (COD 2), codominant 3 (COD 3), dominant model (DM), recessive model (RM) and allele model (AM) in Caucasians and overdominant model (OD) in the overall population are associated with an elevated risk of CC.

Conclusion: Our case-control study and meta-analysis summarize that *CYP1A1* rs4646903 and rs104893 polymorphisms are correlated with CC risk.

Keywords: Cervical cancer; *CYP1A1*; rs4646903; rs104893; PCR-RFLP

Track: The Fourth Industrial Revolution (4IR) in life sciences

Identifying risk factors of preeclampsia among pregnant women in Bangladesh: A machine learning perspective

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Background: Preeclampsia (PE) is a form of pregnancy hypertension condition that is harmful to the mother and the developing fetus. Early prediction of preeclampsia is challenging because of poorly understood causes, various risk factors, and likely multiple pathogenic phenotypes of preeclampsia. Moreover, the prevalence of preeclampsia is not well-documented, and the associated data are scarce in Bangladesh. Therefore, we aim to provide a machine learning model to identify patients with PE and also to analyze the socioeconomic and health factors associated with it.

Method: The data used to perform this study were collected from Noakhali Sadar Hospital at Noakhali during October 2022-May 2023 consisting of 168 mothers with preeclampsia and 168 mothers without preeclampsia. In this study, five machine learning models were applied, including logistic regression, k-nearest neighborhood, decision tree, random forest, and support vector machine, and their performance was compared using the criteria of accuracy, sensitivity, and specificity.

Results: Underlying condition (e.g., diabetes, kidney disease, hypertension), age, blood pressure, and the number of pregnancies are the most important risk factors for diagnosing preeclampsia. The accuracy of the models were as follows: logistic regression (0.914), k-nearest neighborhood (0.921), decision tree (0.938), random forest (0.946) and support vector machine (0.971).

Conclusion: Support vector machine was the most effective at predicting preeclampsia out of all the machine learning techniques used in this study. As a result, this model can be considered as a screening tool to diagnose this disorder.

Keywords: Decision Tree; Logistic Regression; Preeclampsia; Random Forest; Support Vector Machine.

Track 2: Approaches in Biotechnology, Molecular Biology and Microbiology

Title: Combating multidrug resistant pathogens: Development of antibiotic resistance breakers and the way forward**Author Name: Md. Murad Hossain****Presentation Type: Oral Presentation**

Affiliation: Department of Biotechnology and Genetic Engineering, Noakhali Science and Technology University, Noakhali-3814

Background: One of the foremost challenges to global health is the development of antibiotic resistance (AR) among pathogen. Consequently, effective antibiotics are decreasing with every passing year, which is predisposing us toward a future with no antibiotics of use. Therefore, development of effective antibiotic resistance breakers (ARBs) and other novel antimicrobial therapies could be promising to combat against multidrug-resistant (MDR) pathogens.

Methods: Multidrug-resistant bacteria were identified from collected samples through biochemical tests and were confirmed by 16S rRNA sequencing and species-specific PCR screening. To search for novel ARBs, molecular docking of different chemicals from ZINC-15 database and application of medicinal plant extracts were performed. Finally, antibiotic combination therapy was adjudged to evaluate their efficacy to re-sensitize MDR pathogens.

Results: Biochemical and molecular tests confirmed the presence of MDR *Escherichia coli*, *Klebsiella*, *Pseudomonas*, *Citrobacter sp.* *Staphylococcus aureus* bacteria containing bla_{TEM-1}, bla_{CMY}, bla_{TEM}, and bla_{SHV}, tetA, tetB AR genes. *In silico* study identified several compounds from ZINC-15 database as potential ARBs. Ethanolic extract of *Kalanchoe pinnata* leaf extract along with penicillin showed concentration-dependent inhibition of *K. pneumoniae*, suggesting the presence of promising ARB molecules(s) in *K. pinnata*. Antibiotic combinations, through synergistic effect, have shown different zones of inhibition that indicate re-sensitization of resistant antibiotics.

Conclusion: Several compounds from chemical database as well as bioactive compounds from medicinal plants could serve as effective ARB(s) against MDR pathogens. Moreover, antibiotic combinations showed potential to re-sensitize MDR *E. coli* and *K. pneumoniae*. Further researches with novel strategies would be instrumental to re-sensitize existing antibiotics.

Keywords: Antibiotic resistance; Antibiotic resistance breaker; Antibiotic combination therapy; Molecular docking, Multidrug-resistant pathogens.

Track 3: Food safety and security

Genetic differentiations in sparid fishes inferred from mtDNA control region analysis

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Background: Marine fishes were also traditionally thought to be highly connected with long-distance dispersal potential and presence of few barriers to gene flow in the sea resulted in little or no genetic differentiation among populations. However, recent advancement in molecular techniques has identified significant genetic differentiation among populations in marine taxa. The sparid fishes of the genus of *Acanthopagrus* are commercially and ecologically important fishes distributed widely in shallow coastal waters and estuaries of the Indo-West Pacific Ocean.

Method: This study, therefore, investigated the genetic variability, population structure of different sea bream species (*A. datnia*, *A. sivicolus* and *A. pacificus*) using mitochondrial DNA (mtDNA) control region sequence analysis.

Result: Genetic diversity was high in all studied fish species. Low levels of nucleotide diversity were detected in *A. sivicolus* (0.007 to 0.010) and *A. pacificus* (0.008 to 0.026) populations whereas medium levels of nucleotide diversity were observed in *A. datnia* (0.018 to 0.025) populations. Significant genetic differentiations were observed among populations of *A. sivicolus* ($F_{ST} = 0.073$, $P < 0.05$) and *A. pacificus* ($F_{ST} = 0.1546$, $P < 0.05$) populations whereas non-significant genetic differentiations were found among *A. datnia* populations. The high level of genetic structuring in *A. sivicolus* and *A. pacificus* populations might be the result of different physical features of the ocean e.g. different oceanic currents in north-west Pacific Ocean and biological attributes of fish such as self-recruitment.

Conclusion: These findings would be very much helpful for developing sustainable management and conservation strategies of marine resources.

Keywords: Genetic subdivision; Gene flow, Genetic diversity; Oceanic currents; Self-recruitment

O6

Track 1: Pharmacology and Biomedical Sciences/ Track 3: Food Safety and Security

Phytochemical screening, Antioxidant activity and detection of bioactive compounds present in water, methanol and ethanol extracts of Japanese Peach Fruit and their antibacterial study

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Background: In Bangladesh many varieties of fruits like mango, pineapple, lichi, guava, jack fruit etc are producing in a large scale and contributing in the poverty reduction and household food security of rural peoples. A sweet nutritionally rich foreign fruits, Peach (*Prunus persica* L.) fruit may also contribute in the poverty reduction and household food security as well as to improve the immunity to prevent different types of diseases. Even though several works have been done on nutritional and medicinal values of Peach fruit in abroad but as far we know there is no reports for the cultivation and medicinal uses of this fruit in Bangladesh.

Methods: Phytochemical screening were carried out by standard methods, the antioxidant activities were determined by DPPH method, Compounds were detected by TLC and analyzed by Spectrophotometer. Antibacterial activities were carried out by disc diffusion method.

Results: Water, Methanol and Ethanol extracts of Japanese Peach Fruit showed the presence of Alkaloids, Tannins, Saponin, Flavonoids, Cardiac Glycosides, Carbohydrates, Proteins and Amino Acids. All extracts showed strong antioxidant activity. The result also showed that the white color compound present in the water and methanol extracts of this Fruit may be Vitamin C. The other two purple-blueish and white color compounds that were present in methanol and ethanol extracts and another white compound in water extract may be important unknown phytochemical compounds. In spectral analysis, two same compounds were detected in all three extracts. On the other hand, a single compound was found in both ethanol and methanol extracts. In the antibacterial study, we only found strong activity against *Salmonella typhi* by Ethanol extract, but we found less activity against this bacterium by water and methanol extracts. Unknown

phytochemical compounds present in different extracts were detected by UV light will be identified and characterized in further study.

Conclusion: From this overall results it can be concluded that Japanese Peach Fruit will be useful as an additive in food and pharmaceutical industries to prevent oxidative damage and also to prevent and fight against infection caused by *Salmonella typhi* and COVID-19 worldwide and other infectious diseases by increasing our body immunity in the long term by including this fruit in our diet chart and it will also will be useful as a raw material in the pharmaceutical and food industries to prepare drugs and food products.

O7

An *In Silico* Approach to Identify the Conserved Virulent Proteins of *Campylobacter* species Explores Potential siRNA Candidates as a Novel Therapeutic Strategy against Campylobacteriosis

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Background

Campylobacter is a major zoonotic disease which account for leading global cause of gastroenteritis in humans and fourth reason of deaths due to diarrheal disease among under five years children. The emergence of multi-drug resistant (MDR) *Campylobacter* isolates in both human and poultry, and lack of availability of vaccines have led to develop a new therapeutic strategies against campylobacter infections. For this reason, developing small interfering RNA (siRNA) candidates to stop the spread of such infectious agents is a new strategy for providing novel treatment candidates to stop the rapid rise of anti-microbial resistance (AMR).

Methodology and Results

In this study, a total of 281 conserved sequences retrieved from 26 different virulent genes of *Campylobacter sp.* Primarily, 302 siRNA candidates were selected after validation by the Sidirect and i-score designer which are also known as first generation and second generation algorithm. 83 siRNA have been optimized based on the score of i-score, dG value and % of GC content. The IM score predicted 48 siRNA as a non-immunogenic candidates from 83 siRNAs where only 13 siRNA candidates passed the acceptable 3D structure validation score. After evaluation of the positive ΔG value, target site accessibility and thermodynamic score, we found 8 siRNAs (siRNA 3, siRNA 8, siRNA 24, siRNA 51, siRNA 54, siRNA 73, siRNA 74, siRNA 75) using the following tools, Sfold filtration, SMEpred, siRNA efficacy and siRNAPred validity Score (Binary). Finally, 4 different siRNA candidates selected by OligoWalk, are expected to impede the expression of *campylobacter* virulence genes, namely cadF (siRNA3), cdtC (siRNA8), flaA (siRNA73 and siRNA 74).

Conclusion

However, this computational investigation needs further experimental validation in the laboratory to use those siRNAs as a therapeutic alternatives for the treatment of campylobacteriosis and prevent antibiotic resistance.

KeyWords: siRNA; *Campylobacter*; AMR

P1

Track 1: Pharmacology and Biomedical Sciences

Influence of *Clerodendrum infortunatum* leaf extract on Anti-inflammatory and Anti-obesity gene expression in high-sugar diet-induced obese mice

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Background: Obesity is becoming an alarming state throughout the world and finding a new way to combat obesity is warranted. The present study aimed to investigate the role of *Clerodendrum infortunatum* leaves in reducing the risk of adiposity and adipocyte inflammation in high-sugar diet-induced obese mice.

Method: *Clerodendrum infortunatum* leaves were collected and prepared with the methanolic extract. Twenty adult mice were divided into four groups, five for each; normal diet, high-sugar diet, and high-sugar with two different treatment groups. After the induction of obesity by a high-sugar diet, mice were treated with 200 and 400 mg/kg of *C. infortunatum* leaf extract (CILE). Changes in body weight, organ weight, Lee index, fat accumulation, liver, and lipid functions were monitored. Alteration in the expression of IL-6, COX-2, GLUT4, TNF α , MCP-1, UCP-1, ICAM-1, VCAM-1, and P-selectin at the transcript level was also studied.

Results: Our data showed a significant reduction in body weight and fat accumulation followed by significant changes in liver and lipid function levels by the extract. Expression in inflammatory genes (IL-6, COX-2, TNF α) and adhesion molecules (VCAM-1 & P-selectin) have found a significant decrease in the extract group. Of interest, an in-silico study was done with the major component of *C. infortunatum* with PPAR γ and COX-2 and has shown the highest binding affinity with β -sitosterol and oleanolic acid.

Conclusion: Taking it all together, it could be predicted that *C. Infortunatum* leaf extract have strong activity against inflammation and obesity in high-sugar diet-induced obese mice.

Keywords: *Clerodendrum infortunatum*; inflammation; obesity; COX-2; IL-6

P2

Track 1: Pharmacology & Biomedical Sciences

Title: Pharmacovigilance in the Fourth Industrial Revolution: Enhancing Drug Safety and Surveillance

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Abstract

Background: The fourth industrial revolution, characterized by the integration of advanced technologies such as artificial intelligence, big data analytics, and machine learning, has brought about transformative changes across various sectors, including healthcare. This poster presentation will shed light on the significant advancements in pharmacovigilance practices in the context of the Fourth Industrial Revolution. It has been targeted to clarify the impact of the fourth industrial revolution on pharmacovigilance practices and highlight the opportunities and challenges that arise in this rapidly evolving landscape.

Method: This study will discuss the key technological advancements that have revolutionized pharmacovigilance, including:

Big Data Analytics: The availability of vast amounts of structured and unstructured healthcare data has enabled the development of sophisticated analytics tools, allowing for enhanced signal detection, risk assessment, and safety monitoring.

Artificial Intelligence (AI) and Machine Learning (ML): AI and ML algorithms have the potential to improve the accuracy and efficiency of adverse event reporting, signal detection, and risk prediction.

Real-World Data (RWD) and Real-World Evidence (RWE): The integration of RWD from various sources, such as electronic health records, social media, and wearable devices, provides a more comprehensive understanding of drug safety and effectiveness in real-world settings.

Results: The emergence of novel therapies, such as gene editing, targeted therapies, and artificial intelligence-driven drug discovery, presents unique challenges for pharmacovigilance and allows more proactive monitoring and detection of adverse drug reactions (ADRs).

Conclusion: The fourth industrial revolution presents significant potential for advancing pharmacovigilance practices, enabling more proactive and efficient identification of drug safety issues.

P3

Track 1 : Pharmacology and Biomedical Sciences

Inhibition of mPGES-1 with trans-Ferulic acid and catechin derivatives from *Zingiber capitatum* Roxb rhizome reduces pyrexia via downregulating PGE₂

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Background: Microsomal prostaglandin E synthase-1 (mPGES-1) is a potential drug target involved in pyrexia and inflammatory disorders. The present study aimed to uncover the antipyretic potential of *Z. capitatum* rhizome (ZCR) and identify the phenolic components involved in downregulating PGE₂ via inhibiting mPGES-1.

Method : Phenolic profiles of *Z. capitatum* rhizome were discerned by HPLC-DAD analysis. *In vivo* antipyretic potential was assessed in mice by yeast-induced pyrexia. Also, molecular docking and molecular dynamics (MD) simulation of the discovered components was explored against the antipyretic enzyme mPGES-1.

Results: The results demonstrated that ZCR significantly reduced ($P < 0.001$) the increased body temperature of mice since 1 hr at both doses (200 and 400 mg/kg dose), which was more pronounced than the control. Eight polyphenolic components were detected and quantified by HPLC-DAD analysis. including (-) epicatechin, catechin hydrate, trans-ferulic acid, catechol, myricetin, rosmarinic acid, kaempferol, and rutin hydrate. The molecular docking study showed higher docking scores of identified polyphenolic compounds (ranges from - 4.4 to - 6.2 kcal/mol) than the cofactor glutathione (-4.0 kcal/mol), thus inactivating microsomal prostaglandin E synthase-1 (mPGES-1). Moreover, RMSF, RMSD, Rg, hydrogen bonds, and binding energy analysis performed during MD simulation of some major compounds in the extract revealed that (-) epicatechin, catechin hydrate, and trans-ferulic acid bind to the mPGES-1 active site in a stable manner in comparison to glutathione.

Conclusion: It can be concluded that the polyphenols in *Z. capitatum* rhizome alleviate pyrexia in mice by reducing mPGES-1 activity via downregulating PGE₂ synthesis.

Keywords: *Zingiber capitatum*; mPGES-1; pyrexia; Molecular dynamics simulation

Antidiabetic Potential of Whole Plant Extract of *Fimbristylis aestivalis*: Chemical Profiling, *in-vitro*, *in-vivo* and *in-silico* Approach

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Abstract

Background: T2DM is the most widespread form of diabetes, accounting for nearly 90% of cases. Due to harmful side effects, poor efficacy, and expensiveness of synthetic anti-diabetic drugs, scientists increasingly realize the need for natural-origin antidiabetic drugs. The current study evaluates the phytochemical profile and inhibitory activity of this whole plant extract (FAWE) through *in-vitro*, *in-vivo*, and computer simulations.

Methodology: FAWE was evaluated for *in-vitro* α -glucosidase inhibitory activities while the *in-vivo* antidiabetic potential was investigated on alloxan-induced diabetic mice. The plant extract was also studied by GC-MS to detect the compounds. In addition, *in-silico* analysis was performed aiming to identify the compound(s) responsible for the antidiabetic activity.

Result: The study found that FAWE showed 60% inhibition of α -glucosidase with an IC₅₀ value of 0.631 mg/ml. It reduced blood glucose levels and restored body weight in diabetic mice with statistical significance ($P < 0.01$). Twenty days after treatment, the standard glibenclamide reduced glucose levels by 49.3%, while FAWE at 200 mg/kg and 400 mg/kg reduced it by 39.34% and 43.16%, respectively. The GC-MS analysis of FAWE showed a diverse phytochemical composition with 104 detected compounds. The *in-silico* study validated the *in-vitro* and *in-vivo* results, where 61 compounds (including standard inhibitors) from the plant were tested against four target receptors (PPAR- γ , α -amylase, α -glucosidase, and glycogen phosphorylase). Twenty compounds from the docked candidates revealed higher binding scores with reference standards, Acarbose & Voglibose, highlighting the anti-diabetic potential of the tested Extract.

Conclusion: FAWE can therefore be considered an ideal antidiabetic drug candidate for further investigations and its associated complications.

P5

Track 2: Approaches in Biotechnology, Molecular Biology, and Microbiology

Title: Association of the single nucleotide polymorphism rs2241766 in *ADIPOQ* gene with type 2 diabetes mellitus

Authors name: Rumaisa Saifee, Md. Anamul Haque, Fatema-Tuz-Johura, Md. Sad Salabi Sawrab, Md. Murad Hossain*

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Abstract:

Background: Type 2 diabetes mellitus (T2DM) is a global health concern affecting millions of people worldwide. In Bangladesh, the prevalence of T2DM has been increasing rapidly over the past few decades. Adiponectin plays an important role in the development of T2DM and obesity. Lower levels of adiponectin are associated with insulin resistance and an increased risk of developing T2DM. Several single nucleotide polymorphisms (SNPs) in the adiponectin gene (*ADIPOQ*) have been reported to be associated with the development of T2DM. In this study, we investigated the association of *ADIPOQ* polymorphism rs2241766 (+45 T>G) with T2DM in the population of Noakhali, Bangladesh.

Method: This study includes 215 diabetic patients and 61 healthy controls. Blood samples from healthy controls and patients were used to measure biochemical parameters and extract DNA. PCR-RFLP (Polymerase Chain Reaction-Restriction Fragment Length Polymorphism) was used for genotyping.

Results: Significant differences in biochemical parameters were observed (p-value < 0.05), except for DBP, TG, and HDL (p-value > 0.05). Mean values of age, BMI, SBP, LDL, and total cholesterol seemed to be significantly higher in T2DM patients. The genotypes are tested for the Hardy-Weinberg equilibrium (HWE) and genotype frequencies for patient samples followed by HWE ($\chi^2 = 3.172$, p = 0.204) where p > 0.05. This study revealed a significant association of *ADIPOQ* polymorphism rs2241766 with T2DM.

Conclusion: SNP rs2241766 in the adiponectin gene is significantly associated with T2DM in the population of Noakhali, Bangladesh. This study could be used as a reference for future studies.

Keywords: T2DM; *ADIPOQ*; adiponectin; rs2241766; single nucleotide polymorphism.

P6

Track 2: Approaches in Biotechnology, Molecular Biology, and Microbiology.

Title: Re-sensitizing multidrug-resistant *E. coli* and *K. pneumoniae* through investigation of antibiotic resistance breakers from traditional medicinal plants and antibiotic combination therapy

Authors Name: Md Salahuddin, Shahana Akter, Nilufa Yeasmin, Md. Murad Hossain*

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Background: Antibiotic resistance (AR) among microbes is a global health issue with resistance detected to most antibiotics. Development of effective antibiotic resistance breakers (ARBs) or antibiotic combination therapy could overcome this challenge. Leaf extract of *M. spicata* and *O. tenuiflorum* was previously reported to show anti-microbial activities. This study aims to identify potential ARB compound(s) from *M. spicata* and *O. tenuiflorum* that may synergistically contribute to topple AR of pathogenic organisms with a special focus on re-sensitizing multidrug-resistant pathogens *E. coli* and *K. pneumoniae*. Antibiotic combination therapy, through its synergistic effects, was also hypothesized to be able to overturn the resistant pattern of *E. coli* and *K. pneumoniae*.

Method: Multidrug-resistant *K. pneumoniae* and *E. coli* bacteria were identified through a series of biochemical tests and were confirmed by species-specific PCR. AR profiling of the isolates was performed using the disc diffusion method. The aqueous and ethanolic extract of *M. spicata* and *O. tenuiflorum* leaves were screened out for their ARB ability via well diffusion method. Ampicillin, ciprofloxacin, azithromycin and amoxicillin antibiotics were used for the combination therapy and all types of combinations were created for the assay.

Result: No plant extract showed antimicrobial as well as ARB activity against drug-resistant *E. coli* and *K. pneumoniae*. Antibiotic combinations have shown different zones of inhibition that indicate re-sensitization of resistant antibiotics.

Conclusion: Although studied plant extracts can't exert ARB ability, however, antibiotic combinations can re-sensitize multidrug-resistant *E. coli* and *K. pneumoniae*.

Keywords: Antibiotic resistance breakers; Medicinal plants; Antibiotic combination therapy, Multidrug-resistant pathogens.

P7

Track 2: Approaches in Biotechnology, Molecular Biology and Microbiology

Identification and molecular characterization of microbial community with heavy metal tolerance patterns of some bacteria in textile effluents from Chattogram municipal area, Bangladesh

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Background: Textile effluents contain varying amount of heavy metals and metalloids that are harmful for human health and also have negative impact on the environment. Microbial communities have the potential to tolerate various metals present on textile wastewater. Thus, the study was carried out to identify metal tolerant bacteria and find out the resistance strain for effective bioremediation of heavy metal pollution.

Method: A series of biological and biochemical tests were performed for identification of potential bacterial isolates. The 16S rRNA sequencing was also done for species level identification of bacterial isolates. Salt tolerance pattern of selected bacterial isolates were observed and measured by using Spectrophotometer. Antibiotic resistance pattern of metal tolerant bacteria was also performed by using Disk Diffusion Assay and further validated by molecular screening.

Results: From biochemical and sequencing data analysis, a total of 27 isolates were characterized. In tolerance pattern study, effective salt resistance was found for 12 different bacterial strains which showed high tolerance to chromium and lead salts at various salt concentrations. The *Staphylococcus* spp., *Exiguobacterium* spp., and *Enterobacter* spp. were found as the most effective salt remover strains. Also, these isolates showed some degree of resistance to all applied antibiotics.

Conclusion: These findings suggest that the bacteria reside in industrial effluents contain resistance mechanisms for heavy metals and common antibiotics. So, these isolates could be efficiently utilized in the development of alternative and eco-friendly method for effective removal of heavy metals from contaminated sites.

Keywords: Textile effluent; 16S rRNA sequencing; Metal resistance; Disk Diffusion Assay

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Track 2: Approaches in Biotechnology, Molecular Biology and Microbiology

Assessment of bacterial load in a street food (Fuchka) in Noakhali with their characterization and study on antibiotic-resistant pattern

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Background:

Concerns about food safety are raised by the rising popularity of street food like Fuchka, which is made with less structured safety standards at tiny and roadside stalls. These foods are often contaminated with different kind of bacteria, of which coliform are the primary concern. Coliform is not only hazardous to human health but also the recent trend of antibiotic resistance making it a major public health issue.

Method:

A total of 4 samples of Fuchka, its dressing and salad were collected from the street vendor at Noakhali Science and Technology University campus. Bacteria were isolated and identified by appropriate biochemical methods after the bacterial loads were assessed as total viable count (TVC). Furthermore, antibiogram was performed using the Kirby–Bauer disk diffusion approach. Finally, in order to confirm the presence of ESBL-producing antibiotic resistance genes in the isolates, PCR (polymerase chain reaction) was done.

Result:

A total of 15 isolates were found containing 73.33% of gram-negative bacteria (*E. coli*, *Salmonella* spp., *Proteus* sp., *Enterobacter* sp., *Acinetobacter* sp., *Pseudomonas* spp., *Vibrio* sp., *Citrobacter* spp.) and 26.67% gram-positive bacteria (*Staphylococcus* spp., *Micrococcus* sp.). All the isolates were resistant to the Cefoxitin antibiotic, 64.29% to both Aztreonam and Tetracycline. About 66.67% of the bacteria are multidrug resistant.

Conclusion:

Such an alarming escalation of antibiotic resistance bacteria make us think twice before eating street food. Therefore, it is necessary to undergo national surveillance to promote public awareness and the proper implementation of safety regulations in order to solve this grave problem.

Keywords: Street food, Bacterial community, Antibiotic resistance

P9

Track 2: Approaches in Biotechnology, Molecular Biology, and Microbiology.

**Micro RNAs expression analysis shows key affirmation of ESR1
(Estrogen Receptor 1) as a novel prognostic and therapeutic
biomarker for cervical and liver cancers.**

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Background: MicroRNAs play very important role in carcinogenesis, tumor growth, and metastasis; as a result, they aid in the development of several cancers, such as cervical and liver cancers. This work intends to find prognostic biomarkers responsible for those cancers through an integrated bioinformatics approach.

Method: Data were collected from GEO Database for both cervical and liver cancer. Volcano plots were created individually. And common miRNA(s) were identified. Genes associated with those miRNAs and DEG genes for cervical (CESC) and liver (LIHC) cancer were collected. After thorough analysis, one gene was identified as a down-regulated gene that activates or inhibits some crucial pathways and contributes to the onset and development of these two malignancies. This gene may also serve as a therapeutic target. After that Fifteen approved medicines were recognized as activators or inhibitors of the identified gene and might be a potential target to regulate the expression of the gene in CESC and LIHC. Among them, one showed strong evidence to be used for increasing the expression of genes. As the identified gene was downregulated this medicine can be used to increase the expression of the gene.

Result: Reduced expression of ESR1 is linked to a poor prognosis for CESC and LIHC, and it serves as a therapeutic target. Estradiol showed strong evidence to be used for increasing the expression of ESR1.

Conclusion: This research proposes ESR1 as a prognostic and therapeutic biomarker for cervical and liver carcinoma that may aid the primary screening and treatment of malignant lesions.

Keywords: Biomarker, Bioinformatics, Cancer, CESC, LIHC, ESR1, Estradiol, microRNA,

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Track 2: Approaches in Biotechnology, Molecular Biology and Microbiology

Phenotypic and Genotypic Detection of Multi-drug Resistant Gram-negative Bacteria from Gut and Rectal swab of Poultry Chickens in Noakhali

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Abstract

Background

Multidrug resistance (MDR) in bacteria has become a grave concern in Bangladesh due to overuse and misuse of antibiotics. To identify the current situation of MDR bacteria in poultry chicks, we aimed to isolate and identify MDR gram-negative bacterial strains carrying antimicrobial resistance (AMR) genes (ESBL, carbapenem, tetracycline, and sulfonamide resistant genes) from Noakhali region of Bangladesh.

Method

Identification of MDR gram negative bacterial isolates was done by biochemical tests, 16s rRNA sequencing, and targeted gene specific PCR screening (for *Klebsiella pneumonia* and *Aeromonas species*), respectively. MDR pattern of the isolates were evaluated according to CLSI guideline against seventeen different antibiotics. Presence of AMR genes (ESBL, carbapenem, tetracycline, and sulfonamide resistant genes) were confirmed by amplification of targeted gene sequences.

Result

Escherichia coli, *Klebsiella pneumonia*, *Proteus penneri*, and *Enterobacter hormaechei* were the common isolates found in both broiler and layer poultry showing average MAR index of 0.66, 0.76, 0.8, 0.84 in broiler and 0.81, 0.76, 0.84, 0.41 in layer, respectively. *Providencia stuartii* and *Salmonella enterica* isolates were found only in broiler chicken samples with average MAR index of 0.82 and 0.84, respectively. Additionally, *Morganella morganii*, *Aeromonas spp*,

Wohlfahrtimonas chitiniclastica, and, *Pseudomonas spp.* were isolated from layer poultry chickens having MAR index of 0.73, 0.73, 0.91, and 0.76 respectively. One strain of *P. stuartii* from broiler and one *Aeromonas spp.* from layer showed resistant to all used drugs and considered as pan-drug resistant. All the isolates showed MAR index of > 0.2 and, thereby, considered as MDR. Furthermore, AMR gene screening confirmed the presence of *blaTEM*, *blaSHV*, *tetA*, *sul1*, *tetB*, and *sul2* genes in many of the bacterial isolates.

Conclusion

Our findings suggest that both broiler and layer chickens are at a high risk of developing MDR bacteria and AMR genes. Strict regulations, robust monitoring procedures, food safety training are urgently warranted to lessen the impact on those involved in the industry, consumers, and other animals.

Keywords: Poultry; Gram-negative bacteria; 16s rRNA sequencing; MDR; AMRgene.

Exploration of endophytic fungi from *Allium cepa* along with its in-vitro antioxidant, antimicrobial and cytotoxic potential

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Abstract

Background: Endophytic fungi have drawn an intense attraction to drug discovery as endophytes undergo a mutualism; they can mimic the chemical potentials of the host. Therefore, the renowned pharmacological resource *Allium cepa* (onion) were taken under investigation as a first approach in Bangladesh to isolate its fungi and determine their in-vitro antioxidant, antimicrobial, and cytotoxic properties.

Methods: The principal steps, including sample collection, surface sterilization, cultivation, preliminary selection, and purification, were followed to isolate fungi. Morphological characters, light microscopic (40X) spores, and DNA sequencing identified the fungal strains, and then, small-scale cultivation of the fungi followed solvent extraction. Antioxidant, antimicrobial, and cytotoxic activities of the extract were determined by 1,1-diphenyl-2-picrylhydrazyl (DPPH) free radical scavenging activity, disc diffusion method, and brine shrimp lethality bioassay, respectively.

Results: Several cultivations of fleshy scales of onion isolated a fungus as *Fusarium oxysporum* (OR062575), which mainly resides at plant roots. The 50% free radical inhibition concentration (IC₅₀) 45.956 µg/ml was around 40% of ascorbic acid's potential. Gram-negative bacteria *E. coli* and Gram-positive *Enterococcus sp.* exhibited excellent susceptibility to the fungal metabolites by 18 mm and 15 mm zone of inhibition at 80 µg/disc, respectively. In the cytotoxic evaluation, this extract was toxic to brine shrimp, with a logarithmic value of LC₅₀ 0.44 µg/ml, and compared to reference vincristine sulfate, the potential was also roughly 75%.

Conclusion: Onion bulbs have physical barriers against microfungus penetration that require repeated cultivation to isolate a single fungus. However, bioactivity tests were prospective of having pharmacologically valuable molecules in the fungal metabolite.

Keywords: *Allium cepa*; Endophyte; *Fusarium*; Antioxidant; Antimicrobial

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Track 3: Food safety and security

Title: Prevalence and characteristics of microplastics in surface water of urban river, Bangladesh

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Background

Microplastic (MPs) (<5mm) are ubiquitous, man-made particles distributed in aquatic environments, and their ecological risk have become a worldwide concern. Bangladesh is one of the countries with the highest plastic input into the freshwater environment yet very less is known about their pollution load and their ecological risk of MPs contamination. Hence, this study aimed to provide quantification and diversity of MPs in surface water from an urban freshwater river Buriganga, Bangladesh.

Method

Surface water sample was collected from five sampling station of Buriganga river, Dhaka. To extract MPs, at first sample were dried in oven. After that wet peroxide oxidation (WPO) was done and samples were kept in density separator for overnight. Then the supernatant was collected through filter paper to observe in microscope.

Results

Results demonstrate that MPs ranged in the sampling locations from 350.00 ± 64.79 to 660 ± 122.52 items/m³ water, with an average of 486.8 ± 84.44 items/m³. Fibers were the dominant type of MPs that occurred in this study, followed by sheet > fragment > foams. In this study, colored particles were the major microplastic type, accounting for 56.71% of total microplastics in number. most of the MPs were irregular in shape.

Conclusion

The present study clearly indicates the anthropogenic impact on gradual accumulation of MPa in freshwater river. This study can be used as baseline data for the management of the river and aware the policy maker to control plastic pollution considering its ecological risk.

Keywords: Microplastics; River pollution, Bangladesh

P13

Track 3: Food safety and security

Title: Morphological variation among different eel fish species in Bangladesh

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Abstract

The present study was carried out to estimate the morphological characteristics, length-length and length-weight relationships and condition factor for different eel fish species caught from various river of Bangladesh. A total of 132 specimens of five eel fish species *Monopterusuchia* (21 from the Brahmaputra River, 17 from Feni River and 11 from Meghna River), *Anguilla bengalensis* (10 from Feni River), *Ophisternon bengalense* (25 from Kakshiyali River), *Gymnothorax tile* (6 from Meghna Estuary) and *Pisodonophis boro* (18 from Meghna Estuary, 23 from Kakshiyali River) samples were collected from the month of September to November, 2022. The mean values of total length were (58.50±5.48 to 67.60±6.47, 55.16±13.88, 35.66±3.60, 43.62±6.96 & 42.10±9.39 to 44.28 ±7.85 respectively), and body weight were (221.76±60.50 to 402.60±156.8, 373.78±301.66, 38.19±12.1, 74.81±36.11 & 17.48±3.17 to 48.56±54.57 respectively) for *Monopterusuchia*, *Anguilla bengalensis*, *Ophisternon bengalense*, *Gymnothorax tile* and *Pisodonophis boro* respectively. The length-length relationships were highly correlated for all species. The regression coefficient 'b' obtained from LWRs were recorded as 2.75 to 3.73, 3.56, 2.92, 3.27 and 3.19 to 3.38 respectively (W-TL), with significantly positive correlation ($r=0.89$ to 0.96 , 0.99 , 0.91 , 0.95 and 0.95 to 0.96 respectively, $p<0.01$) for *Monopterusuchia*, *Anguilla bengalensis*, *Ophisternon bengalense*, *Gymnothorax tile* and *Pisodonophis boro* respectively. LWRs indicated positive allometric growth for all except *Monopterusuchia* from Brahmaputra & Meghna River and *Ophisternon bengalense* (negative allometric growth) in the sampling area. The analysis of all LWRs and LLRs were significant ($p < 0.01$). However, this is the first ever attempt to document the morphological characteristics comparison among the species. These results will be useful for future researchers, policy planners and fishery managers to take decision and to impose adequate regulations for sustainable fishery management.

Keywords: Eel fish; morphological characteristics; allometric growth; sustainable fishery management

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Track 3: Food Safety and Security

**Determination of Antioxidant Activity in Some Fresh Fruits
Commonly Consumed at Noakhali, Bangladesh.**

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ABSTRACT

Introduction: According to epidemiological research, increased fruits and vegetables intake are linked to a decreased risk of developing chronic degenerative illnesses. Our unhealthy diet and lifestyle currently cause a large amount of abnormal production of free radicals. By eliminating the free radical intermediates, antioxidants stop the chain reactions and more oxidative processes. The Present study was taken to determine the antioxidant activity in 15 common fruits that are consumed at Noakhali regions in Bangladesh. By estimating antioxidant activity of these fruits, we can have a clear idea about their antioxidant activity.

Methods: Antioxidant content and activity were estimated by DPPH (2, 2-diphenyl-1-picrylhydrazyl) method and the absorbance was measured at 517 nm by Spectrophotometer.

Results: The different fruits extract showed variable antioxidant properties. The lowest IC50 value indicates the most potent ability of samples to act as DPPH scavengers. The IC50 value of the fruit samples ranges from 79.78 to 55.76 µg/mL (Olive > Mandarin orange > Apple > Pomelo > Guava > Trifoliolate orange > Pineapple > Grapes > Hog palm > Orange > Amla > Eureka Lemon > Carambola > Mandarin > Meyer lemon). The IC50 values of different fruits sample are compared with the IC50 value of standard ascorbic acid. Among the sample, Meyer Lemon (55.76 µg/mL) showed highest scavenging activity, while Olive (79.78 µg/mL) showed the lowest scavenging activity.

Conclusion: Compared with standard Ascorbic acid, our fruit samples give medium range of scavenging activity, which is good in various fruits.

Keywords: Antioxidant; DPPH; IC50 value.

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Track 3: Food Safety and Security

Determination of Harmful Algal Bloom and Their Subsequent Effects on the Food System Security in Noakhali, Bangladesh.

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Abstract:

In last few decades, harmful algal blooms (HABs) have grown such an incredible way and are warning to public health. Water infested with algal bloom are not safe for consumption and drinking. Because of different problems, economic damaging to the fishing industry, harmful for hydrophyte ecosystem, fish fatality and other living organisms, harmful algal blooms are playing a detrimental role in several coastal region. The present study was therefore conducted to understand the long-term effect of HABs on the food security in the South Western Coastal Region of Bangladesh. Plankton samples were collected by using a plankton net, which mesh size is 25µm and preserved at 5-7% formalin at the sampling site. A light binocular microscope was used at magnifications of 16*10 and 16*40 to determine the profusion of plankton. During the experiment, environmental parameters such as temperature, pH, TDS, and free CO₂ were measured, and their relation with the diatom was demonstrated. The study revealed the presence of several toxic species such as, *Chlorogonium*, *Navicula*, *Alexandrium*, *Botryococcus*, *Oocystis*, etc. that produce blooms. The study also focuses on some conservative measures and actions to halt the HABs in the studied area.

Keyword: Plankton, Food Security, HABs, Bloom

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Track 3: Food Safety and Security

Accumulation and human health risk assessment of micro and mesoplastics in some coastal and marine water fishes from Bangladesh

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Coastal and marine waterbodies provide substantial ecosystem goods and services to living organisms, at the same time, they are the ultimate reservoir of different contaminants including plastic particles. In this study, we aimed to assess micro and mesoplastic contamination (occurrence, morphological features and polymer types) and associated human health risks in some coastal and marine water fishes (*Harpadon nehereu*, *Liza subviridis*, *Rhinomugil corsula*, *Polynemus paradise*, *Lepturacanthus savala* and *Lutjenus sanguineus*) with stereomicroscopic and fourier-transform infrared spectroscopy (FTIR). The average abundance of micro and mesoplastics were 2.82 items/g and 0.12 items/g, respectively. Microplastics found in fish samples were predominantly constituted by transparent and violet fibres (70–100%) with sizes <0.5 mm suggesting there is a greater exposure risk. Mesoplastics were found in only gut content with a lower abundance compared to microplastics. Polyester, polyethylene (PE) and polyethylene terephthalate (PET) were identified as the prevalent polymers detected. These findings are consistent with those of other studies conducted around the world. Nevertheless, additional investigation is needed to precisely determine the possible exposure risk for the people who consume these fish and the impact of plastic contamination on Bangladeshi fishery activities.

Keywords: Microplastics; mesoplastics; coastal fishes; marine water fishes; human health.

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Track 3: Food Safety and Security

Title: Quantification and characterization of microplastics from five major estuaries of Bangladesh

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** Corresponding author*

Background:

There is growing concern across the globe over the existence of microplastics (MPs), their occurrence and their effects on the aquatic environment. However, knowledge about the exposure of MPs in the marine environment of Bangladesh is limited. This study was a first attempt to describe MPs in surficial water and sediment from five major river estuaries.

Method:

The samples were collected from Meghna, Karnaphuli, Matamuhuri, Bakkhali and Naf river estuary along Bangladesh coast. A total of 90 surface sediment and water samples were collected from the intertidal zone, and MPs were extracted using the density separation method. FTIR spectroscopy was used for qualitative and quantitative identification.

Results:

Among the five estuaries, the lowest abundance (150.00 ± 65.62 items/m³) of MPs in surface water was found in Meghna river and the highest (350.00 ± 69.22 items/m³) in Karnaphuli river. However, in terms of surface sediment, the Meghna River had the lowest value (30.56 ± 9.34 items/kg), and the Matamuhuri River had the highest value (118.33 ± 26.81 items/kg). One-way Analyses of variance (ANOVA) showed a significant ($p < 0.01$) difference among the five rivers. Most of the identified MPs were fibers and transparent in both water and sediment samples and < 0.5 mm in size. PE, PET, PS, PP, Nylon, EVA, and ABS polymers were identified from the both the water and sediment samples.

Conclusion:

This investigation provided preliminary information on MPs pollution in the marine ecosystem that the policymakers can use to take appropriate management approaches.

Keywords: Microplastics; water pollution; estuaries; Bangladesh

Presentation type: Poster presentation

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Track 3: Food Safety and Security

Morphological and physico-biochemical characterization of diversified Tomato (*Solanum lycopersicum*) genotypes in Bangladesh

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Abstract:

Background: Tomato is considered a fruit and most popular vegetables, coming in third after potato and sweet potato in terms of worldwide production. The study aimed to investigate diversity of the exotic tomato genotypes (V1-V17) to identify the most suitable varieties by morphological and biochemical traits in the research field of the Department of Agriculture, NSTU.

Methods: Tomato seeds were grown on coco peat. Then, twenty-eight days old seedlings were transplanted in the research field in Randomized Complete Block Design (RCBD) with three replications. Proper care and intercultural practices were done in a timely till harvesting.

Results: Significant variations for all the characters except TSS and pH were revealed in the study. The variations with similar features were grouped in a Euclidean Dendrogram while in the principal component analysis the first eight PCA components explained 99.95 % of total variances among the genotypes, with the first principal component accounting for 35.25 %. The highest plant height (240.7 cm), V15 required minimum time (29.67 DAT) for first flowering, TSS maximum value (5.63) was recorded V5, the highest amount of vitamin C was recorded at (11.72 mg/100 g) in V8, the maximum amount of β -carotene was also recorded (0.37 mg/100 mL) in V1. The highest lycopene (8.91 mg/100 mL) was recorded in V11, the maximum fruit diameter (10.23 cm) was observed in V8, the highest fruit length (10.13 cm) was observed in variety V8, the maximum fruit width (10.03 cm) was revealed in variety V8. The maximum number of fruits/plants (34.75) was recorded in V12, the highest single fruit weight (294.3 g) was found in variety V8, the maximum amount of fruits/plant (4615 g) was recorded in V7, the largest amount of fruits (153.8 t/ha) was also revealed in variety V7.

Conclusion: Finally, V7, V8, and V9 are promising varieties in terms of yield attributing features, and biochemical traits such as lycopene, β -carotene, and vitamin C and could be utilized in the future breeding program.

Keywords: Tomato; Genotypes; Morphophysical; Biochemical; Traits

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Track 3: Food Safety and Security

Accumulation and characterization of microplastics in some commercially important marine fishes from the Bay of Bengal

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Abstract

Background: Microplastics (MPs) are emerging environmental pollutants that have gained tremendous scientific interest in recent years. In marine environments, microplastics are a threat to marine organisms, as they are often the same size range as prey are mistaken as food. This study investigated the presence and characteristics of microplastics in commercial fish species from the Bay of Bengal, off the coast of Bangladesh. Gill, gastrointestinal tract (GIT) and muscle of commonly consumed marine fishes (e.g., *Thunnus obesus*, *Pampus chinensis*, *Acanthopagrus datnia*) were analyzed to determine the presence of MPs.

Method: MPs were extracted from fish sample by using alkali digestion protocol, density separation method and identification was carried out using stereomicroscope with imaging facility. Fourier-transform infrared spectroscopy (FTIR) analysis were also done.

Results: A total 977 MPs were detected from all examined fish sample. Fibers were the dominant type of MPs occurred in this study, followed by sheet and then fragments. Most of the microplastics in this study were filamentous. The predominant MPs were found to be < 0.5mm in size. The most abundant color of MPs were violet and red.

Conclusion: The consumption of microplastics containing fish is a route of exposure to human and has implications on human health and food safety. The findings of this study raised concern that microplastics in marine fish could be a threat to public health via the food chain and help to assess future eco-toxicological risk and food safety for human well-being.

Keywords: Food safety; Ecotoxicology; Microplastics; Food chain; and Marine fish

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Track 3: Food Safety and Security

Evaluation and performance analysis of some inbreed and hybrid cotton varieties in coastal areas

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Cotton is a fiber producing crop that grows in a boll, or protective case, around the seeds of the cotton plants. The fiber is almost pure cellulose, and can contain minor percentages of waxes, fats, pectins, and water. The textile sector is the important source of growth in Bangladesh's rapidly developing economy. The basic raw material of textile sector is cotton. Bangladesh is the 2nd Raw cotton consumer and highest raw cotton importer country. The present study was carried out near by the field at Noakhali Science and Technology University, Noakhali during August 2022 to April 2023 to investigate the potentiality of cotton cultivation in coastal areas. Six cotton varieties were used to evaluate in this experiment. The seeds of these varieties were collected from Cotton Development Board (CDB), Bangladesh. The experiment was laid out following Randomized Complete Block Design (RCBD) with three replications. Different growth and yield parameters such as plant height, ball per plant, ball diameter, weight of cotton per ball, weight of cotton per plant, weight of cotton per plot etc were collected at suitable time. Data were analyzed using the statistical tools. The maximum plant height (177.5cm) was observed in Rupali-1. Number of branch (20.1), number of ball per plant (29.7), weight of cotton per ball (5.6gm), weight of cotton per plant (166.5gm), weight of cotton per plot (7646.7 gm) were found higher in Rupali-1 among the evaluated varieties. Eventhough, it needs to do multilocation and multiseason trails in futher studies, on the basis of this experiment, Rupali-1 can be used to cultivate in coastal areas.

Keywords: Cotton; coastal area; performance; growth; yield

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Track 3: Food Safety and Security

**GENE EFFECTS FOR THE TRAITS CONTRIBUTING TO
YIELD IN PUMPKIN (*Cucurbita moschata* Duch. Ex. Poir)**

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The Gene action for yield contributing characters was studied through analysis of components of generation means in pumpkin. The components (A, B and C) of scaling test and χ^2 value of joint scaling test were significant for yield contributing characters in CM-1 X BARI MISTIKUMRA-1 and CM-8 X CM-1. It indicated simple additive-dominance model was inadequate to explain the inheritance. In CM-5 X CM-14 and CM-8 X CM-20, some characters including number of male flower and female flowers per plant respectively fitted well to three-parameter model. So, the model was extended to six-parameter model or to epistasis. In cross CM-1 X BARI MISTIKUMRA-1, days to male flower open, number of female flowers and number of fruits per plant were controlled by additive, dominance gene actions and non-allelic gene interactions (additive x additive, additive x dominance, dominance x dominance). The yield contributing traits, single fruit weight, yield per plant, fruit length, fruit dia showed additive-dominance gene action. In CM-5 X CM-14, number of female flowers per plant was controlled by all types of gene actions, indicated complex controlled of the characters. Fruit length was controlled by additive-dominance gene effect and additive x additive gene action. Other characters flesh thickness, number of male flower per plant, fruit diameter, single fruit weight and yield per plant showed epistasis. In CM-8 X CM-1, single fruit weight was controlled by additive-dominance effect and other all epistatic gene interactions. In CM-8 X CM-20, fruits per plant and yield per plant were controlled by mainly additive-dominance gene action.

Key words: Gene actions; traits; pumpkin

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Track 3: Food Safety and Security

poster presentation

Impact of Tobacco Farming on the Micro Algal Community and Food Security in Chakaria, Bangladesh

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The Diversity and abundance of phytoplankton communities were studied in the coastal waters of the Matamuhuri river in the Chakaria region, Cox's Bazar, Bangladesh. The study was conducted during the month of June-July in 2022. Three areas along with six stations near the river were selected for research where tobacco farming occurs, a moderate region, and where tobacco farming does not occur. Throughout the investigation, a total of 26 genera of phytoplankton were recorded. In addition, an analysis of water quality revealed that NH₃, salinity, rainfall, transparency, TDS, and TSS were the key factors that promote the community composition of plankton populations. The study observed Chlorophyceae, Bacillariophyceae, Cyanophyceae, and Euglenophyceae, four major phytoplankton groups. Furthermore, this study demonstrates the potential impact of tobacco production on the river's plankton community. However, the study also found that the highest number (98125±1125) ind/l. of plankton species was in the moderate region and the lowest number (40125±1125) ind/l was in the non-tobacco-farming area. The phytoplankton population in the Matamuhuri river is adversely impacted by excessive inputs of fertilizers, suspended particles, and freshwater nutrient enrichment. Therefore, the main purpose of this study is to assess the distribution of phytoplankton community in the Matamuhuri river, Chakaria region as well as its impact on the food security of the particular region.

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Track 1: Pharmacology and Biomedical Sciences

The linkage between IL-6 rs1800797 Polymorphism and breast cancer susceptibility in Bangladeshi women

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Background: Breast cancer (BC) is currently one of the most commonly diagnosed malignancies in women. The IL-6 rs1800797 has been used to investigate the association of risk for different cancers in different populations worldwide. We aimed to investigate the association of the rs1800797 polymorphism to the susceptibility of BC in Bangladeshi women.

Methods: The present case-control study recruited a total of 220 BC patients and 216 healthy volunteers. Then, DNA was extracted from the blood samples and tetra-primer amplification refractory mutation system polymerase chain reaction (T-ARMS-PCR) and gel electrophoresis were used for genotyping.

Results: For BC patients, additive model 1 (AG vs. GG: OR=2.16, 95%CI=1.06-4.43, p-value=0.035), additive model 2 (AA vs. GG: OR=2.91, 95%CI=0.55-15.42, p-value=0.209), the dominant model (AG+AA vs. GG: OR=2.26, 95%CI=1.15-4.23, p-value = 0.018) and the over-dominant model (AG vs. GG+AA: OR=2.08, 95%CI=1.02-4.24, p-value=0.044) showed significantly increased risk.

The recessive model also showed 2.52-fold increased risk in the BC patients against the control population (AA vs. GG+AG: OR=2.52, 95%CI=0.48-13.30, p-value = 0.275). This result was not statistically significant. The allele frequency analysis showed that mutant allele A carriers among the BC patients had a significantly higher risk than the wild-type G allele carriers (A vs. G: OR=2.15, 95%CI=1.18-3.92, p-value=0.012).

Conclusion: Our results indicated that IL-6 rs1800797 polymorphism is associated with a significantly higher risk of BC in Bangladeshi women. Further studies with a larger sample should be conducted to consolidate and re-evaluate our findings.

Keywords: Breast cancer; IL-6, T-ARMS-PCR; Polymorphism; rs1800797

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Track 2: Approaches in Biotechnology, Molecular Biology and Microbiology

Title: Bioactive molecule(s) of *Kalanchoe pinnata* synergistically act to re-sensitize multidrug-resistant *Klebsiella pneumoniae*

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Background: Global health is threatened by antibiotic resistance as effective antibiotics are decreasing with each passing year. Therefore, the development of effective antibiotic resistance breakers (ARBs) could be promising to overcome this challenge. This study aimed to re-sensitize multi-drug resistant (MDR) *K. pneumoniae* by targeting β -lactamase enzyme and to identify bioactive molecules in *Kalanchoe pinnata* leaves with potential as antibiotic resistance breakers (ARBs).

Methods: Chicken guts for microbial samples were collected from poultry farms in Noakhali Sadar Upazila. Resistant *Klebsiella pneumoniae* bacterial species were identified through biochemical tests and were confirmed by 16S rRNA sequencing and species-specific PCR screening. Ethanolic and aqueous extracts of *Kalanchoe pinnata* leaf combined with penicillin were evaluated for their presence of antibiotic resistance breakers (ARBs) against MDR *K. pneumoniae*. Molecular docking was performed to identify bioactive compounds from *Kalanchoe pinnata* with ARB potential.

Results: Biochemical and molecular tests of sample confirmed the presence of MDR *Klebsiella pneumoniae*. Antibiotic-resistant gene screening identified blaTEM, blaSHV, and blaCTX genes responsible for beta-lactamase resistance in *K. pneumoniae*. Ethanolic extract of *Kalanchoe pinnata* along with penicillin showed concentration-dependent inhibition, while aqueous extract showed no inhibition, indicating the presence of potential ARB molecule(s) in ethanolic extract. Moreover, molecular docking identified several compounds present in *Kalanchoe pinnata* with promising ARB potential (Daigremontianin, Kaempferol, Luteolin, Rutin, Friedelin, alpha-amyrin, Quercetin-3-O-arabinoside, 5-7-4'-Trihydroxy-3-8-dimethoxy).

Conclusion: Bioactive compound of *K. pinnata* could be a potential ARB as it can synergistically act to re-sensitize MDR *K. pneumoniae*.

Keywords: Antibiotic resistance; Antibiotic resistance breaker; *Kalanchoe pinnata*; *Klebsiella pneumoniae*; Molecular docking