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When I was pursuing my undergraduate degree in Molecular Biology at the University of Dhaka, I witnessed the suffering of people around me who were infected by drug-resistant bacteria. This experience motivated me to contemplate the actual scenario of antibiotic-resistant infectious bacteria in the environment and to find ways to mitigate their spread to vulnerable populations, particularly in resource-limited settings.

After my MS, I seized the opportunity to join the Laboratory of Food Safety and One Health, icddr,b. Here, I am working on transmission dynamics of multi-drug resistant intestinal and extra-intestinal pathogens in both community and hospital-acquired infections, for example, gastrointestinal tract infections, urinary tract infections, septicemia and meningitis. So far, I have worked on several research projects with the collaboration of Stanford University, University of Maryland and Washington State University, and worked on projects funded by NIH, USAID and SIDA.

During my research, I learned that whole-genome sequencing helps understand bacterial transmission by comparing genomes to trace clonal lineage between humans and environments. I have gained expertise in next generation sequencing and bioinformatics analysis to determine transmission. Using this knowledge, we published an article in Frontiers in Microbiology showing intestinal colonization with extended-spectrum β-lactamase-producing Escherichia coli among children is linked to the colonization status of mothers and exposure to the contaminated household environments. We have also published in the Journal of Global Antimicrobial Resistance showing that hospital environments in Bangladesh are contaminated with highly virulent carbapenem-resistant Pseudomonas aeruginosa, which might be a potential source of hospital-acquired infections.

Besides my research work, I have received training in various aspects of microbiology, bioinformatics, and statistics, including identification, antimicrobial susceptibility testing, and whole-genome sequencing of bacterial pathogens. Additionally, I completed a course on quantitative risk assessment from JIFSAN, USA, and an introduction to bioinformatics/genomic data analysis from Washington University.

My research aims to contribute to the global fight against infectious diseases, particularly in resource-poor settings. Through my work, I hope to make a positive impact on the lives of those most affected by these diseases and to advance our understanding of their transmission and control.

Project

Identifying the genetic relatedness of Carbapenem-resistant A. baumanni (CRAB) isolated from pregnant mothers, newborns and hospital environments in Bangladesh

Carbapenem-resistant Acinetobacter baumannii (CRAB) is a significant contributor to nosocomial infections and an urgent public health threat. The route of transmission from hospital environments to incoming patients in low-resource settings is poorly understood. Very few studies used whole genome sequencing (WGS) approach to evaluate CRAB transmission from potential hospital environments to humans. In our recently completed study among 32 pregnant women admitted for elective delivery to a tertiary care hospital in Bangladesh during February-March 2020, we found no CRAB in vaginal and rectal swabs in pregnant mothers on presentation whereas a significantly high percentage (60%, n=19 each for vaginal and rectal swabs) of samples from mothers was contaminated with CRAB after delivery. Alarmingly, 41% (n=13) of rectal samples of their newborns had CRAB colonization and 34% (n=17 out of 50) of frequently touched environmental samples had CRAB contamination. This preliminary result indicates high possibility of CRAB acquisition from hospital environments to mothers and their newborns. However, genetic relatedness among CRAB from mothers, newborns and environmental sources is largely missing in this setting. In such cases, WGS will be an important tool to determine clonality among isolates by whole-genome MLST and core-genome SNP (single nucleotide polymorphism) analysis. For this, we will use a molecular typing tool such as ERIC-PCR (Enterobacterial Repetitive Intergenic Consensus-PCR) to type all the CRAB isolates that were collected from vaginal and rectal swabs of the mother, rectal swabs of the newborn, and hospital environments. After initial similarity analysis by ERIC-PCR, whole genome sequencing approach will be employed on about 30 – 40 CRAB isolates to examine in-depth genetic relatedness, phylogenetic relationship and clone analysis. The study findings will be helpful to understand the potential CRAB-contaminated environments, identify predominant clones circulating in the hospitals, and implement effective infection prevention and control strategies to ensure public health safety.