

Comparative Analysis of Extended Spectrum β -Lactamase (ESBL) Producing *Enterobacteriaceae* Isolated from Local and Broiler Chicken Samples in Dhaka City:

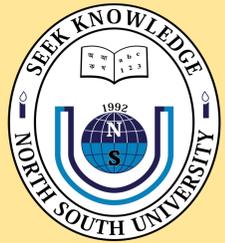
A Study in Antibiotic Resistance

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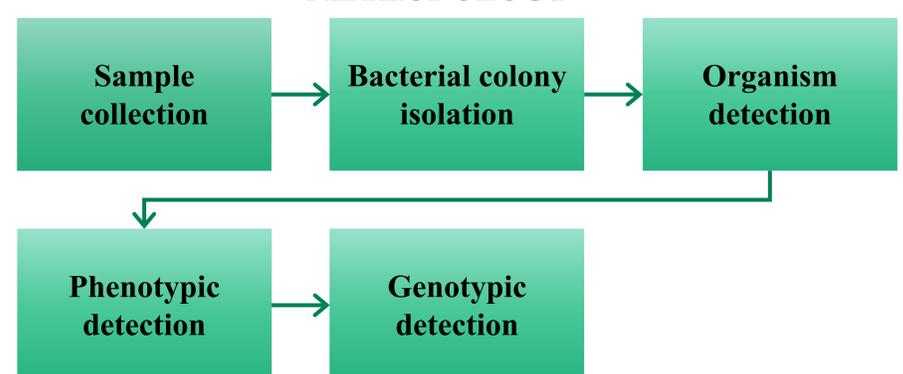
ABSTRACT

Enterobacteriaceae family, a diverse group known to cause infections in both healthcare and community settings. ESBL-producing bacteria pose a significant challenge as they exhibit resistance to commonly prescribed antibiotics. To better understand this resistance mechanism, we focused on isolating and comparing ESBL-producing bacteria from local and broiler chicken samples, as contamination through various sources exacerbates the spread of ESBL infections. Tissue samples including leg, wing, breast, thigh, neck, liver, gizzard, and kidney were collected from a Dhaka-based slaughterhouse. Microbiological analysis utilizing MacConkey agar revealed 16 strains from local chicken and 10 strains from broiler chicken samples. After organism detection test 75% & 80% *Klebsiella* spp. Followed by 25% & 20% *E. coli* were detected from Local chicken and Broiler chicken respectively. Further phenotypic and genotypic characterizations were conducted, and the double disk synergy test confirmed ESBL production using Ceftazidime & Cefotaxime (CAZ/CTX \pm clavulanic acid). The results indicated that 50% of local chicken strains (8 out of 16) and 40% of broiler chicken strains (4 out of 10) were ESBL producers. Subsequent genetic analysis was done by ESBL-producing genes (*bla*CTX-M, *bla*TEM & *bla*OXA). Polymerase Chain Reaction (PCR) followed by gel electrophoresis result revealed that all of the genes were present in broiler chicken, while the couple of genes were present in local chicken except *bla*OXA. These findings underscore the potential influence of ESBL genes within the food chain on future treatment options for Gram-negative *Enterobacteriaceae* infections. Addressing antibiotic resistance is critical, necessitating the development of strategies to reduce antibiotic usage.

- Antibiotic Resistance is an alarming issue.
- Commonly prescribed antibiotics do not work in case of ESBL infection. [1]
- ESBL producing bacteria have already been identified in water and clinical samples in Bangladesh. [2]

- ✓ Identification of ESBL producing Gram-negative bacteria Isolated from chicken samples.
- ✓ Conduct the phenotypic screening of β -lactamase producing bacteria by double disk diffusion test.
- ✓ Detect the prevalence of *bla*CTX-M, *bla*TEM and *bla*OXA genes in ESBL producing bacteria.

METHODOLOGY



RESULTS

Organism detection test result of local chicken sample

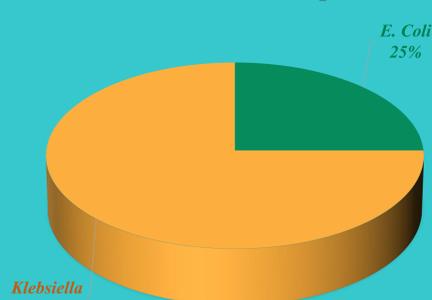


Figure 1: Organism Detection Test of Local Chicken Sample

Organism detection test result of broiler chicken sample

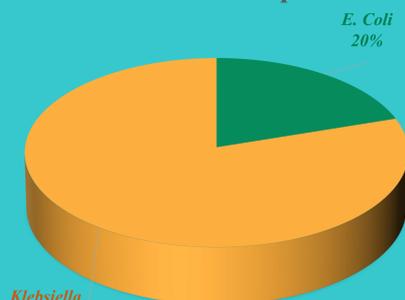


Figure 2: Organism Detection Test of Broiler Chicken Sample

Double disk diffusion test result of local chicken sample

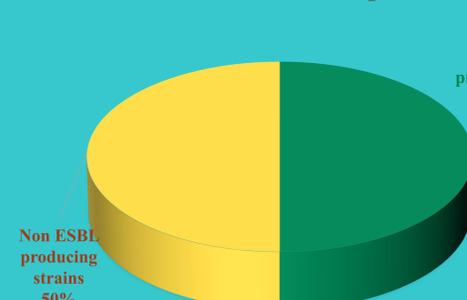


Figure 3: Double Disk Diffusion ESBL detection Test of Local Chicken Sample

Double disk diffusion test result of broiler chicken sample

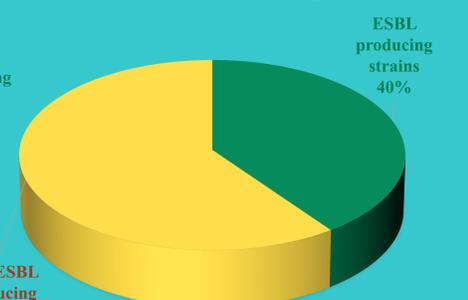
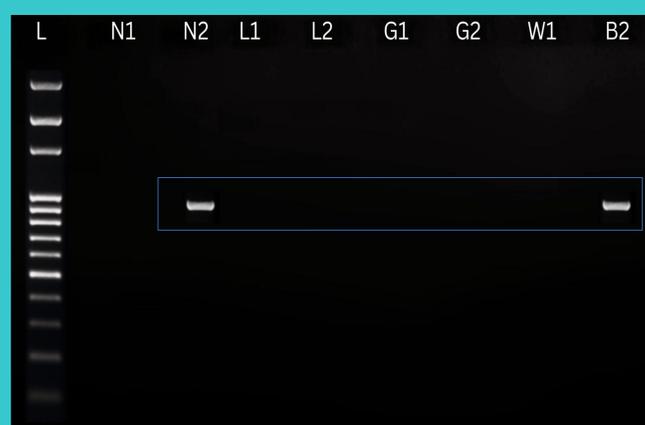


Figure 4: Double Disk Diffusion ESBL detection Test of Broiler Chicken Sample

a. *bla*CTX-M (593bp)



b. *bla*TEM (964bp)



c. *bla*OXA (813bp)

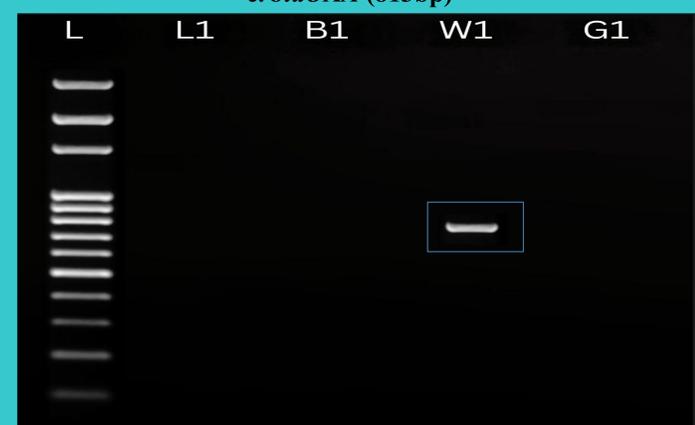


Figure 5 (a –c): Gel electrophoresis results of amplified PCR products

DISCUSSION

- ❑ The results of gel electrophoresis show that ESBL-producing genes are present in strains isolated from both the local and broiler chicken.
- ❑ The presence of ESBL genes in the food chain may influence future treatment options for many Gram-negative *Enterobacteriaceae* infections.

CONCLUSION

- ❑ The emergence of antibiotic resistance in humans emphasizes the significance of establishing strategies to decrease antibiotic use.
- ❑ This, in turn, will improve the national antimicrobial resistance surveillance system, allowing for the development of local antibiotic therapy guidelines.

FUTURE WORK

- ❑ Large number of samples with more number of primers will be used for genotypic detection of ESBL.
- ❑ 16S rRNA sequencing analysis and phylogenetic tree construction.
- ❑ Whole genome sequencing will be performed to unveil genes that are critical for those bacteria to survive in chicken.

REFERENCES

1. Singh, T. et al. (2019) "Transcriptome analysis of beta-lactamase genes in diarrheagenic escherichia coli,". Available at: <https://doi.org/10.1038/s41598-019-40279->
2. Beta-lactam pharmacology (2020) betalactam_pharm Available at: https://tmedweb.tulane.edu/pharmwiki/doku.php/betalactam_pharm.