RES-250

Analysis of Fluoroquinolone Resistance in ESBL-Producing *E. coli*: Genetic Determinants and Prevalence in Clinical Samples from Toyama University Hospital

Asmaa Abushwaish[1], Yoshitomo Morinaga[1], Hitoshi Kawasuji, Mika Morita, Makito Kaneda, Hiroshi Yamada[1].
[1] Department of Microbiology, Faculty of Medicine, Academic Assembly, University of Toyama.

Background

Antimicrobial Resistance :ESBL-producing *E. coli* cause serious resistance to β-lactams and fluoroquinolones in hospitals.

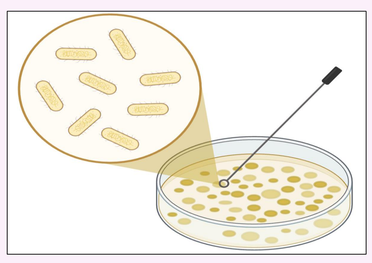
Genetic Focus:

- CTX-M enzymes are the most widespread ESBLs.
- Key drivers: plasmid-mediated quinolone resistance (PMQR) genes & chromosomal mutations.

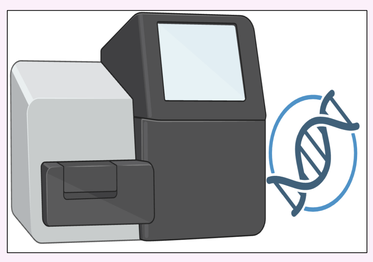
Study Goal :

- Characterize CTX-M groups, PMQR, and chromosomal mutations.
- Assess links to patient characteristics using PCR & WGS.

Methods

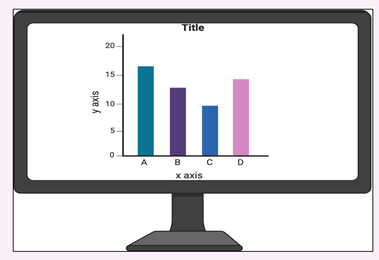


Sample Collection
- 41 ESBL-producing *E. coli* isolates
- Sept 2023 – Apr 2024
- Sources: urine, blood, others



Sequencing Analysis
- PCR and WGS
- CTX-M, PMQR and Chromosomal Mutation

Patient Characteristics
- Demographics
- Prior antibiotic use
- Hospitalization Hx.



Statistical Analysis
- PCR vs WGS concordance
- Mutation co-occurrence
- Patient associations

Results

Figure 1. Distribution of CTX-M Groups Among Clinical Isolates

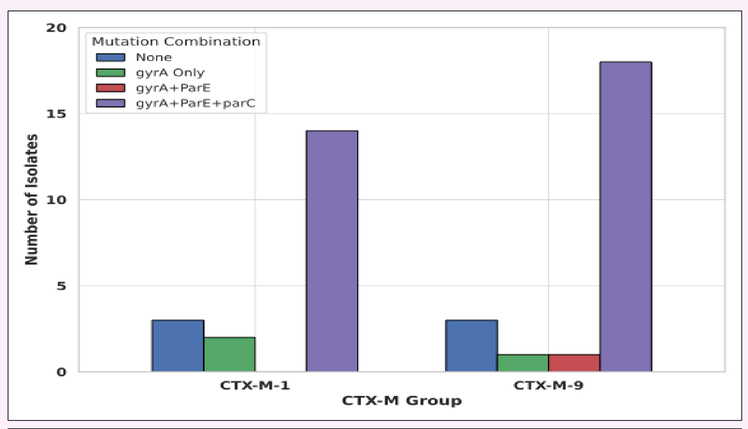


Figure 2. Distribution of Gene Mutation Combinations Among CTX-M Groups

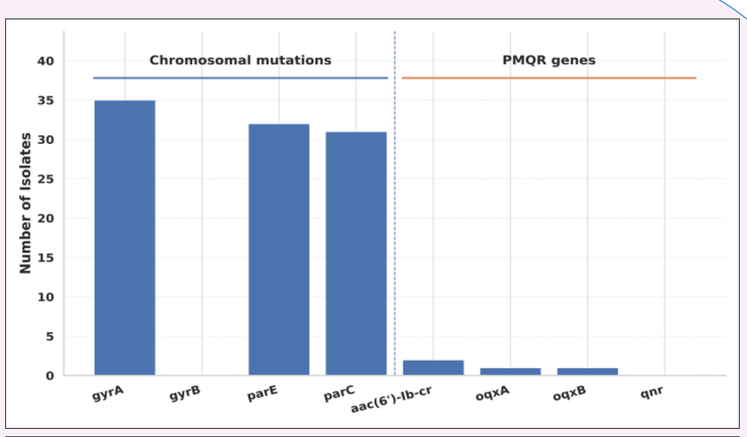


Figure 3. Distribution of Chromosomal Mutations and PMQR Genes Among ESBL E. coli Isolates

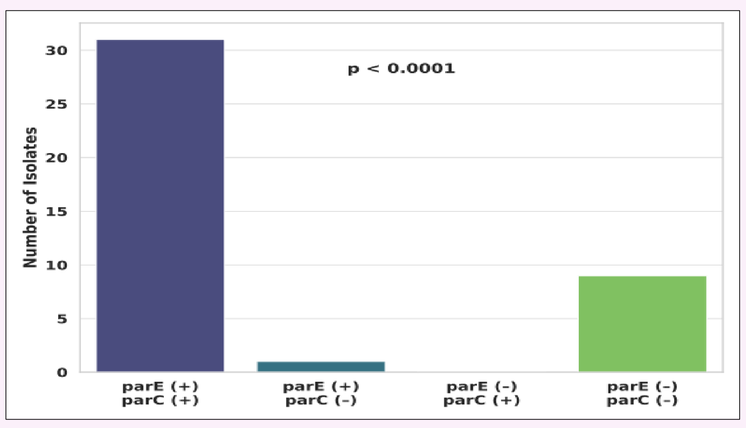


Figure 4. Association Between parC and parE Mutations

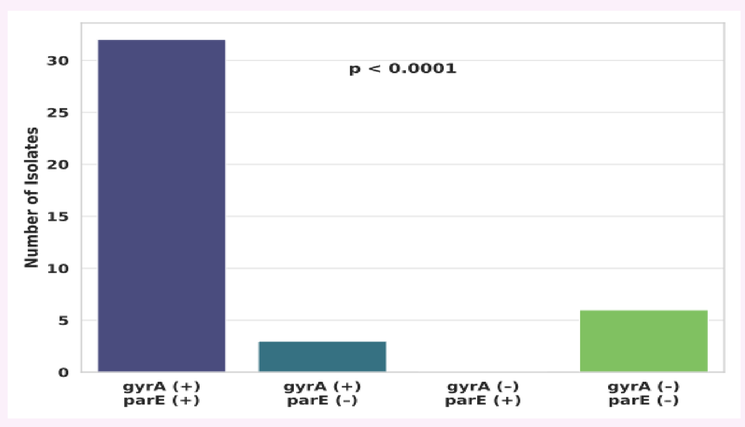


Figure 5. Association Between gyrA and parE Mutations

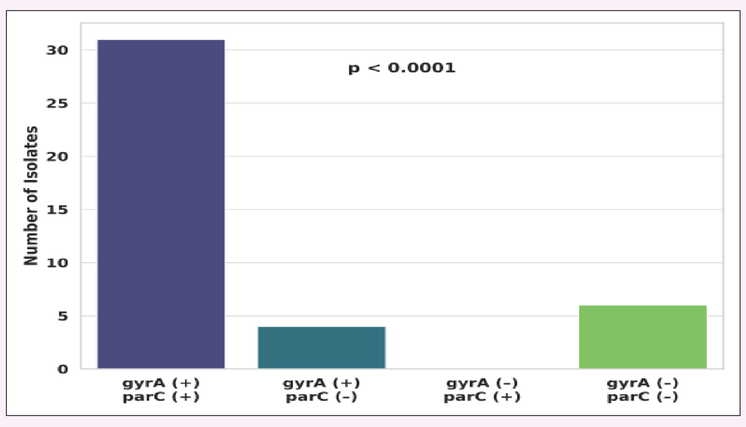


Figure 6. Association Between gyrA and parC Mutations

Characteristic	CTX-M-1 (n=19)	CTX-M-9 (n=22)	Total (n=41)	p-value
Sex (Male)	8 (42.1%)	13 (56.5%)	21	0.54
Antibiotic use (1 mo)	11 (57.9%)	10 (43.5%)	21	0.54
Antibiotic use (3 mo)	7 (36.9%)	4 (17.4%)	11	0.18
Hospitalization (1 mo)	4 (21.1%)	4 (17.4%)	8	1.00

Table 1. Clinical and Demographic Profiles of Patients With CTX-M-1 and CTX-M-9 Isolates

Conclusion

- **WGS outperformed PCR** for CTX-M detection, especially in the CTX-M-1 group ($p < 0.0001$).
- **High prevalence of QRDR mutations**: *gyrA* (87.5%), *parC* (75.6%), *parE* (78.0%).
- **Significant co-occurrence** of *parE–parC, gyrA–parC* and *gyrA–parE* mutations ($p < 0.0001$).
- **PMQR genes were rare** but detected alongside CTX-M variants.
- **No demographic associations**, indicating silent transmission.