Genomic insights of *Escherichia coli* (*ExPEC*) isolates from periprosthetic joint infections and their clinical implications

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INTRODUCTION

Escherichia coli is an infrequent cause of PJI, highly associated with treatment failure in hip and knee arthroplasty. Genomic data on PJI-associated *E. coli* remain limited, constraining understanding of their pathogenic potential and resistance profiles. This study employed whole-genome sequencing (WGS) to characterize PJI-*E. coli* isolates, focusing on antimicrobial resistance (AMR) determinants, virulence profiles, and their association with treatment outcome.

METHODS

Fifty-one E.coli strains (40 monomicrobial ; 11 polymicrobial) from 21 cases and 18 patients (female= 8; male= 10) who underwent hip (n=12) and knee (n=6) septic revision between 2021-2025 were analysed. All cases fulfilled the EBJIS “infection confirmed“ criteria and were characterized as acute (2/21), late acute (4/21) and chronic (17/21). Treatment failure occured in 11/21 (52.4%) cases (persistence: 72.7%; reinfection: 27.3%). For WGS genomic DNA was extracted with MagMAX Microbiome Ultra kit (ThemoFisher Scientific, USA) and sequenced with the Rapid Barcoding kit (Oxford Nanopore Technologies, UK).

RESULTS

Predominace of ST127, ST69 and ST131 was observed, while phylogroup B2 accounted for 84.3% (43/51) of the isolates, suggesting enrichment of extraintestinal pathogenic *E.coli* (ExPEC)-assocated lineages. Frequently detected AMR genes included *TEM-1* (29.4%), *tet(A)* (23.5%), *aadA* (19.6%), *sul1/sul2* (17.6-15.7%), *APH(3”)-Ib* (15.7%), and *dfrA17* (15.7%), reflecting multidrug resistance (Fig.1). Core biofilm-associated genes (*csg-C* and type 1 fimbriae) were detected in all isolates, while pilus genes (*yagZ*/*ecpA*) were present in 90% of *E. coli* strains. Notably, *fimB* (OR=6; 95% CI= 1.18-45.4; p=0.001; q=0.06) and *gsp* gene cluster (*gspC-gspK*) (p=0.004 for all *gspC-gspK* genes; q=0.06) were strongly associated with treatment failure.

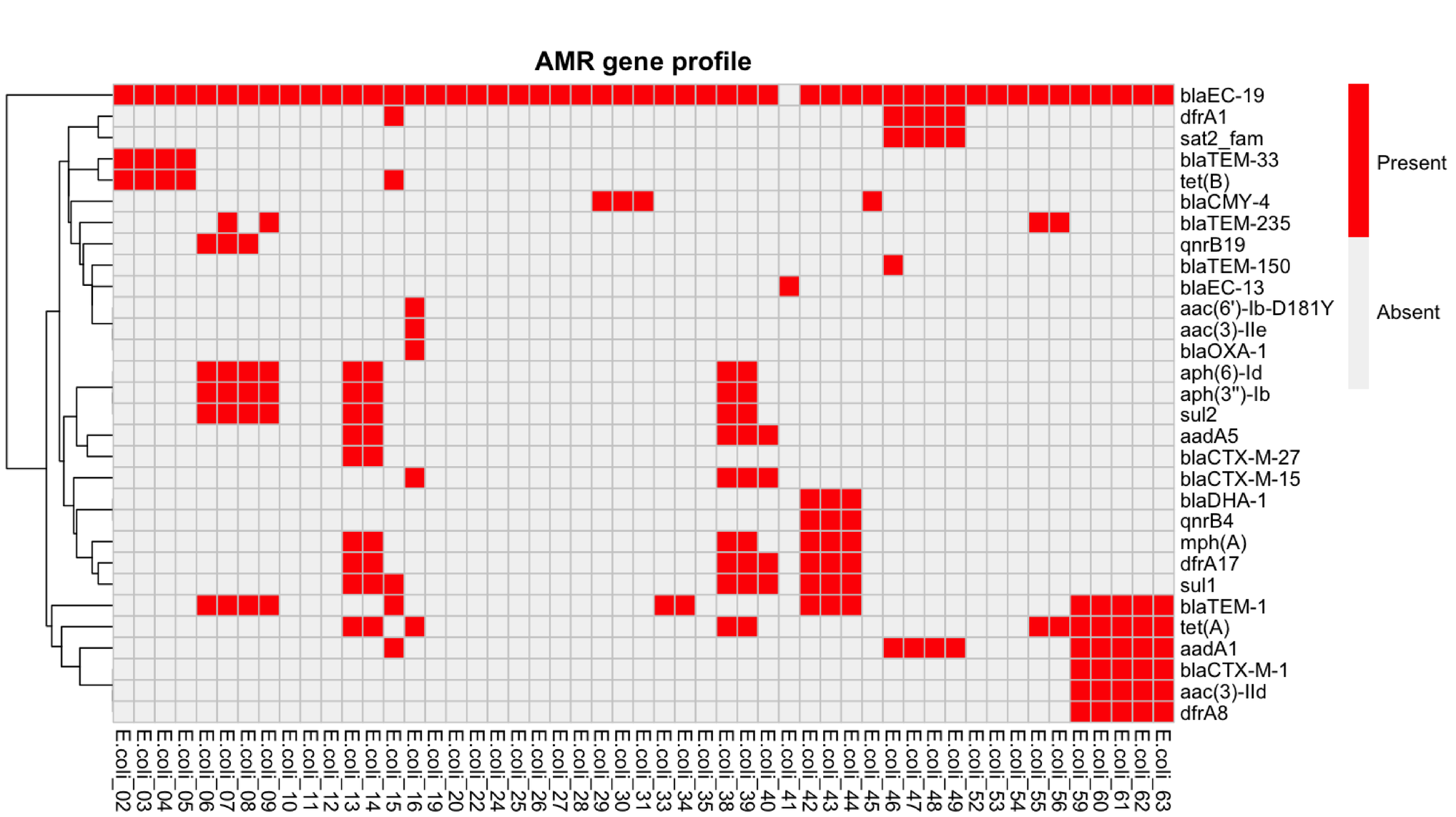

Figure 1: Distribution of acquired AMR genes in *Escherichia coli* isolates associated with hip and knee periprosthetic joint infection (PJI).

CONCLUSION

Genomic characterization of PJI-associated *E. coli* revealed predominance of emerging *ExPEC* lineages with multidrug resistance, extensive virulence, and strong biofilm capacity. These features likely contribute to treatment failure and highlight the need for alternative management strategies addressing virulence and AMR in implant-associated infections.

REFERENCES

1. Meléndez-Carmona, M. Á., Martín-Higuera, M. C., Recio, R., Benavent, E., Gómez-Junyent, J., Mancheño-Losa, M., Hernández-Jiménez, P., Chaves, F., & Lora-Tamayo, J. (2026). Genomic profile of extraintestinal pathogenic *Escherichia coli* isolates from prosthetic joint infections: The search for molecular fingerprints. *Virulence*, *17*(1), 2613491.

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