**Leveraging Vet-LIRN AMR data from USA to identify potential drug targets in imipenem-resistant *E. col*i isolates using Interactive GIS dashboards, genomic analysis, subtractive genomics, and druggability assessment**

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**Abstract**

**Background**  
Antimicrobial Resistance (AMR) is a major global health challenge, particularly in Africa, where antibiotic misuse worsens resistance. This study aims to identify potential drug targets in imipenem-resistant E. coli isolates from the Vet-LIRN database through a four-phase approach integrating GIS analysis, genomic data analysis, subtractive genomics, and druggability assessments.

**Methods**  
Phase I involved a literature review and the creation of interactive Geographical Information System (GIS) dashboards to examine resistance patterns for Ampicillin, Minocycline, and Imipenem across North America and Africa, using data from the ATLAS and Vet-LIRN databases. Phase II focused on genomic analysis of resistant and susceptible E. coli isolates to identify non-synonymous mutations linked to imipenem resistance. Phase III applied subtractive genomics to identify essential bacterial proteins unique to E. coli and absent in humans and dogs. Phase IV assessed the druggability of these proteins by analyzing their physicochemical properties and interactions with drugs in the DrugBank database.

**Results**  
GIS analysis revealed significant geographical variations in resistance, with Africa showing higher resistance to Ampicillin (80%) compared to North America (55%). Genomic analysis identified 337 proteins in the imipenem-resistant E. coli isolates, with 68 considered potential drug targets. Of these, 29 proteins were homologous to DrugBank proteins that interacted with over 1,000 drugs. The cell wall/membrane protein group matched with 80 drugs, metabolic enzymes group with 166 drugs, transport-related proteins group with 700 drugs, regulatory proteins group with 1 drug, and DNA methylation/epigenetic proteins group with several drugs, respectively.

**Conclusions**  
This study demonstrates that integrating GIS, genomics analysis, subtractive genomics, and druggability assessments enhances AMR research and provides a framework for identifying novel drug targets. The 29 proteins matched proteins in DrugBank that interacting with over 1,000 drugs offer potential for drug repurposing, particularly against imipenem-resistant E. coli and other multidrug-resistant pathogens.

**Keywords**  
Antimicrobial Resistance (AMR), Imipenem-resistant E. coli, drug targets, GIS Analysis, Vet-LIRN, Genomics, subtractive genomics, DrugBank, Druggability.