**Methods: blaTEM Phylogenetic Analysis**

**Sequence Collection**

* Databases: NCBI GenBank
* Genes Collected: blaTEM gene from 7 multidrug-resistant bacteria (E. coli, K. pneumoniae, P. aeruginosa, etc.)
* Format: FASTA nucleotide sequences

**Multiple Sequence Alignment**

* Software: MEGA X
* Method: ClustalW algorithm
* Parameters: Default settings

**Phylogenetic Tree Construction**

* Software: MEGA X
* Method: Neighbor-Joining Tree
* Bootstrap Replications: 1000
* Output: Newick format (.nwk) and tree image (.png)

**Interpretation**

* Analyzed clustering patterns
* Investigated possible horizontal gene transfer events