**blaTEM Phylogenetic Analysis Project**

**Overview**

This project investigates the evolutionary relationships of the blaTEM beta-lactamase gene across multiple multidrug-resistant bacteria. blaTEM is responsible for resistance to beta-lactam antibiotics and spreads through horizontal gene transfer.

**Research Question**

* How has blaTEM diversified across different bacterial pathogens?
* What are the phylogenetic relationships between blaTEM variants from Gram-negative and Gram-positive bacteria?

**Methods Summary**

* Collected blaTEM sequences from public databases (NCBI)
* Performed Multiple Sequence Alignment (MEGA X)
* Built a Phylogenetic Tree using Neighbor-Joining method
* Interpreted the tree to identify evolutionary patterns

**Findings**

* Some blaTEM variants from unrelated bacteria clustered together, suggesting horizontal gene transfer.
* Klebsiella pneumoniae formed a separate branch, indicating divergence.

**Tools Used**

* MEGA X
* UniProt databases