

# Diversity of Lactamase Genes in Sequenced Bacteria Genomes and Plasmids

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Resistance to antimicrobials is a serious threat to public health.  $\beta$ -lactam based antimicrobials are one of the most widely used antibiotics for controlling several life threatening infections. Resistance to these antibiotics is primarily due to secretion of an enzyme called lactamase, which renders the antibiotic ineffective by cleaving the lactam ring. Studying the diversity of lactamases will help us in developing better antimicrobial resistance diagnostic probes, identify new regulatory networks controlling the expression of lactamase genes thus identifying novel targets for controlling the resistance to antimicrobials. Availability of sequenced bacterial genomes provided an excellent opportunity to screen genes coding for lactamase.

We studied the diversity of lactamase genes and proteins in sequenced bacterial genomes and plasmids. From genomic and plasmid DNA sequences of 1471 bacterial strains, genes encoding for lactamase were found in 705 strains. We found a total of 19,832 genes encoding for lactamase which is far more than any of the reported number of genes encoding for lactamase. We found that the enzyme is present across diverse taxonomic lineages. The collected data was organised in a database for further analysis. The database is available at <http://bmi.icmr.org.in/bic>

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