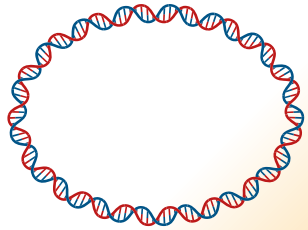


## 1. Genome Sequencing



### BRIC-THSTI

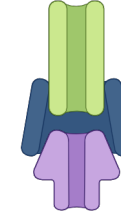
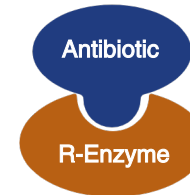
presenting the whole genome sequence of *Enterococcus faecium* isolated from the India urban wastewater.

## 2. Analysis



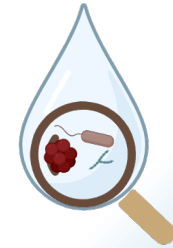
This genomic analysis reveals information related to resistance mechanism, genetic adaptability and potential pathogenicity.

## 3. Insights



The insights of the *Enterococcus faecium* showing multi drug resistance including aminoglycosides,  $\beta$ -lactam, macrolide, tetracyclin.

## 4. Translation

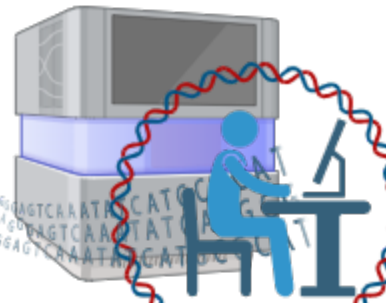


Genomic surveillance of *E. faecium* in wastewater can track the spread of antibiotic resistance strains in hospital and community settings

***Enterococcus faecium*: 'An Exploiter' bridging the gut and organic decay**

# Genomics of *Enterococcus faecium*

## Anaerobic Chamber



Species confirmation

## Genome characteristics

Genome size: 2.95mb  
GC percent: 38%  
CDS: 2822  
Plasmid: repU (*tetM*)  
rRNA=8, tRNA=64

## GENOMICS

## Important Functions

AMR genes: *aac(6')*  
*aph(3')* *erm*, *mcrC*  
*tetM* *van*