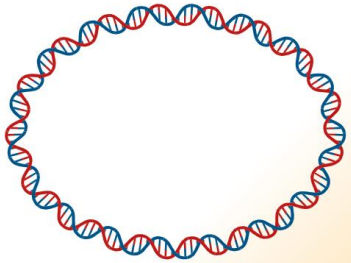
Genome Announcement: *Enterococcus avium*

Accession#ERS27068119 (ENA)
INRR023000 (IBDC)

1. Genome Sequencing

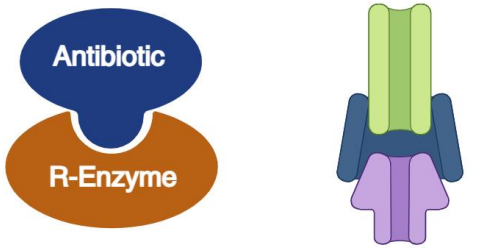


BRIC-THSTI presenting the whole genome sequence of ***Enterococcus avium*** isolated from the Indian urban wastewater.

2. Analysis

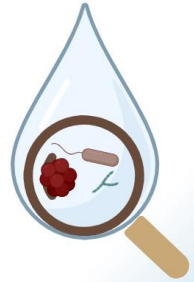
This genomic analysis describes a normal and commensal gut flora acquires antibiotic resistance with mobile genetic element posing a clinical and public health threat.

3. Insights



Enterococcus avium carries multiple drug resistance genes and CRISPR systems for viral defense, with horizontal gene transfer aiding the spread of resistance.

4. Translation



Understanding specific resistance mechanisms, such as efflux pumps and ribosome protection, enables targeted strategies like novel antibiotics and improved wastewater treatment

***Enterococcus avium*: From the gut to the sewer, with a stash of genes that makes resistance surer.**

भारत सरकार विज्ञान और प्रौद्योगिकी मंत्रालय
GOVERNMENT OF INDIA MINISTRY OF SCIENCE AND TECHNOLOGY

जैवप्रौद्योगिकी विभाग
DEPARTMENT OF
BIOTECHNOLOGY

BRIC thsti

Genomics of *Enterococcus avium*

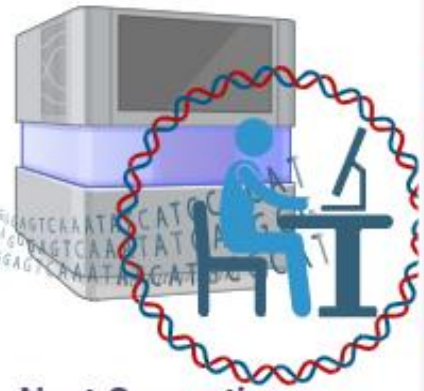
Anaerobic Chamber

Wastewater

Sample

Enterococcus avium

Species confirmation



Next Generation Sequencing

GENOMICS

Genome characteristics

Genome size: 4.5Mb
GC percent: 38.8%
CDS: 4469
Total RNA=17

Important Functions

AMR genes: *APH(3')-IIIa, ErmB, SAT-4, aad(6), tetM*
Plasmid: repUS43_1_CDS12738 (DOp1)