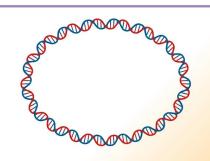


Genome Announcement: Vagococcus fluvialis



Accession#ERS27068111 (ENA) #INRR022998 (IBDC)

1. Genome Sequencing



BRIC-THSTI

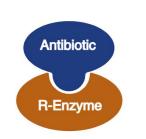
presenting the whole genome sequence of Vagococcus fluvialis isolated from the Indian urban wastewater.

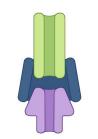
2. Analysis



The genomic features of Vagococcus fluvialis from waste water serves as the reservoir and mixing pot of AMR genes with more pathogenic bacteria or opportunistic infection.

3. Insights





The specific detection of **ErmB** and **SAT-4** provides insight into the exact mechanisms of this bacterium uses to evade antibiotic action.

4. Translation



Genomic surveillance of Vagococcus fluvialis in wastewater facilitates the monitoring of antibiotic-resistant strains across both hospital and community settings

Vagococcus fluvialis: A lesser-known bug with well-known resistance





Genomics of Vagococcus fluvialis

Next Generation

Sequencing

Wastewater Sample Vagococcus fluvialis

Species confirmation

characteristics Genome

Genome size: 2.6Mb

GC percent: 32.5%

CDS: 2666

Total RNA: 25

Important Functions

AMR genes: ErmB, SAT-4