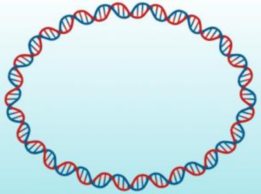
Genome Announcement: *Citrobacter freundii*

Accession#SAMEA116290602(NCBI)
INS0005018 (IBDC)

1. Genome Sequencing

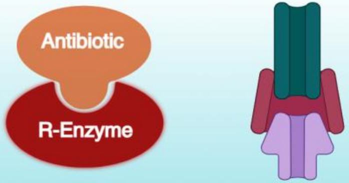


BRIC-THSTI presenting the whole genome sequence of *Citrobacter freundii* from the Eastern Indian sewage water source.

2. Analysis

This genomic analysis explore the prevalence of the bacterial species, alongwith the dynamics of ARGsand their association with MGEs in sewage sample.

3. Insights



Genomic insights of *Citrobacter freundii* reveals the presence of key ARGs like ***h-ns, qnrB,*** various ***aph*** genes and multiple ***bla*** genes highlighting its potential role in multi-drug resistance.

4. Translation

It helps in the surveillance of multi drug resistance dissemination to alarm an early warning system for AMR that will guide a targeted intervention.

Citrobacter freundii: A Rising Reservoir of Resistance

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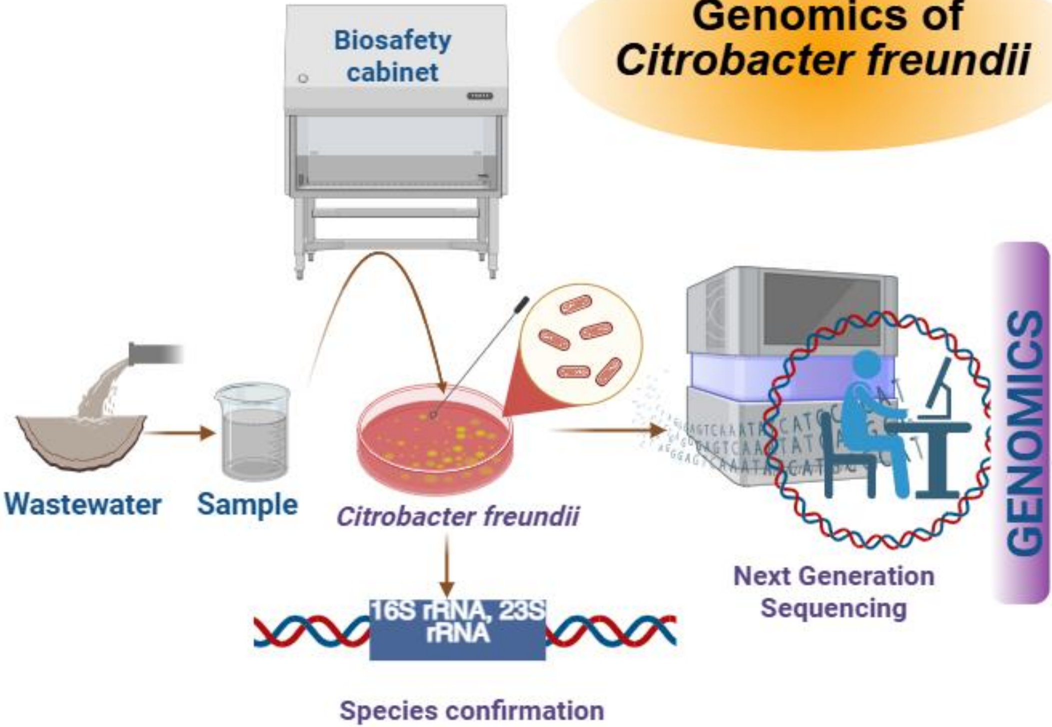
Genomics of *Citrobacter freundii*



Genome characteristics

Genome size: 2.62Mb
GC percent: 51.7%
CDS: 4519
rRNA=11 , tRNA=80

Important Functions

AMR genes: *aph(3")-Ib, aph(6)-Id, blaCMY, blaTEM, tet(A), h-ns, qnrB*