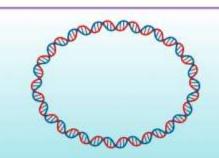


Genome Announcement: Citrobacter sp.

Accession#SAMEA116293624(NCBI) INS0005125 (IBDC)



1. Genome Sequencing



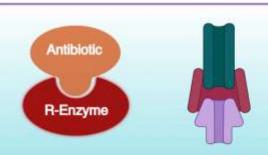
presenting the whole genome sequence of Citrobacter sp. from the Indian sewage water source.

2. Analysis



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

3. Insights



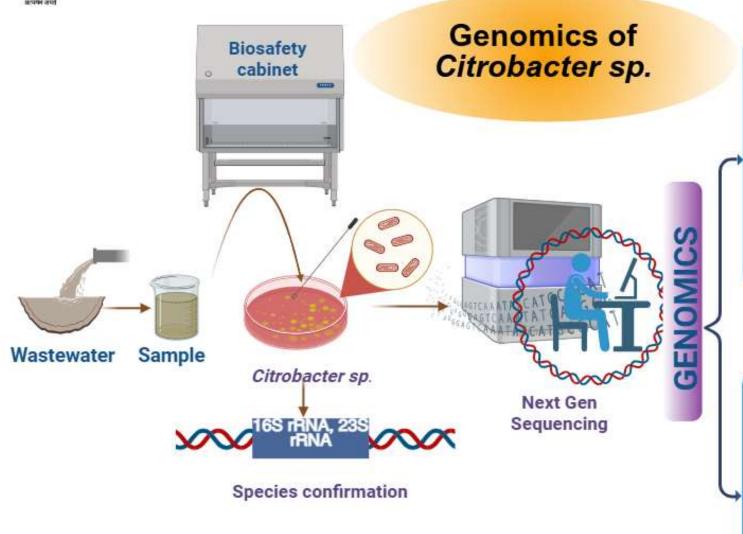
Genomic insights of Citrobacter sp. reveals the presence of key ARGs like bacA, SED-2, and efflux pump genes like emrB, mdtB highlighting its potential role in multidrug resistance.

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.





Genome size: 4.7Mb

GC percent: 51%

CDS: 4419

rRNA= 10, tRNA=79

Important Functions

AMR genes: marA, msbA, H-NS, CRP, emrB, bacA, SED-2, mdtB