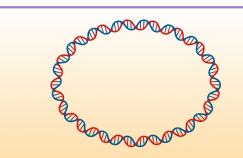


Genome Announcement: Proteus vulgaris

Accession#SAMEA116288359 (NCBI) INS0005069 (IBDC)



1. Genome Sequencing



BRIC-THSTI

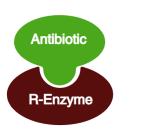
presenting the complete genome sequence of **Proteus vulgaris** isolated from North Indian wastewater.

2. Analysis



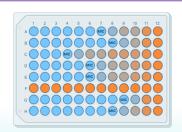
The genomic analysis reveals a multidrugresistant profile conferring resistance to aminoglycosides, βlactams, rifampin, tetracyclines, fluoroquinolones, trimethoprim, and sulfonamides.

3. Insights



Proteus vulgaris
reveals a robust
arsenal of resistance
mechanism including
genes against βlactams,
aminoglycosides,
tetracyclines,
sulfonamides,
fluoroquinolones, and
rifampin.

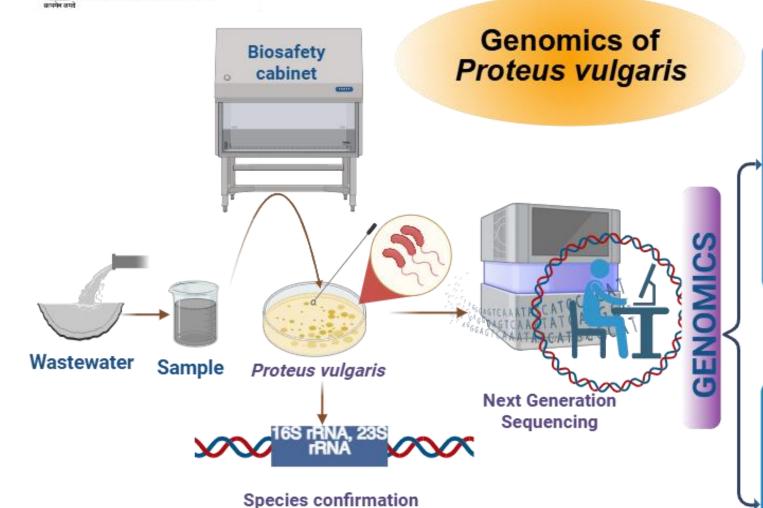
4. Translation



The translational approach enables the development of targeted therapies, informs infection control measures, and supports rapid diagnostic tools for managing multidrugresistant infections

Proteus vulgaris: A resilient rebel armed with genes to outsmart antibiotics.





Genome size: 3.99Mb

GC percent: 39%

CDS: 3557

rRNA=08, tRNA=76

AMR genes: ant(3")lia, blaDHA, blaOXA, arr, tet(B), qnrD1, dfr, sul

Important Functions

Genome characteristics