भारत सरकार
GOVERNMENT OF INDIA
विज्ञान और प्रौद्योगिकी मंत्रालय
MINISTRY OF SCIENCE AND TECHNOLOGY
जैवप्रौद्योगिकी विभाग
DEPARTMENT OF
BIOTECHNOLOGY
सत्यमेव जयते

Genome Announcement: *Klebsiella quasipneumoniae*

Accession#ERS21335039 (ENA)
INS0005094 (INDA)

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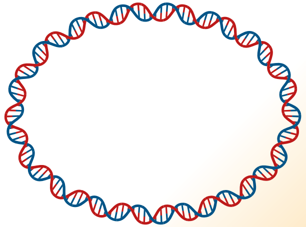
1. Genome Sequencing

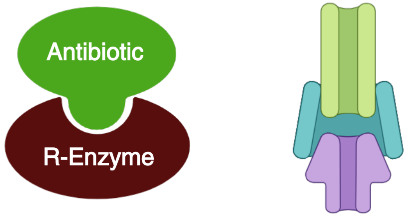


BRIC-THSTI presenting the whole genome sequence of ***Klebsiella quasipneumoniae*** isolated from the urban wastewater sourse in India.

2. Analysis

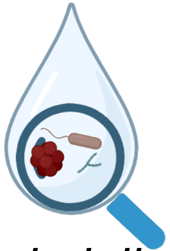
This genomic analysis reveals metabolic versatility, AMR genes, virulence factors and environmental stress, adoptation mechanism

3. Insights



Genomic insights mentions the presence of multiple ARGs and virulence factors like capsule production, genes for biofilm production.

4. Translation



Klebsiella quasipneumoniae genomic feature is key to accessing its pahtogenicity in clinical settings through the development of alternative therapies.

Klebsiella quasipneumoniae: **The hidden invader in wastewater and healthcare**

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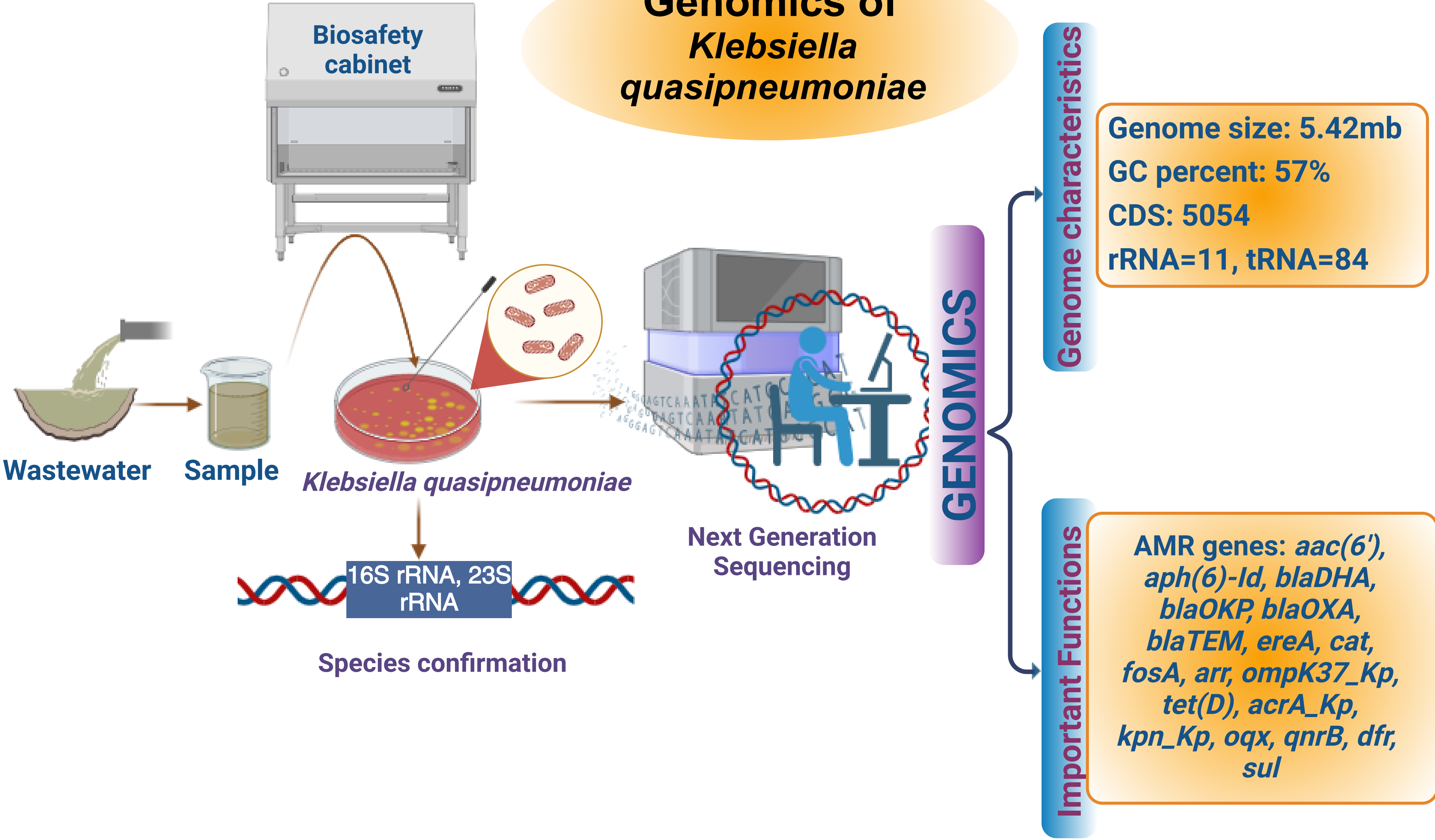
Genomics of *Klebsiella quasipneumoniae*



Biosafety cabinet

Wastewater

Sample

Klebsiella quasipneumoniae

16S rRNA, 23S rRNA

Species confirmation

Next Generation Sequencing

GENOMICS

Genome characteristics

Genome size: 5.42mb
GC percent: 57%
CDS: 5054
rRNA=11, tRNA=84

Important Functions

AMR genes: *aac(6'), aph(6)-Id, blaDHA, blaOKP, blaOXA, blaTEM, ereA, cat, fosA, arr, ompK37_Kp, tet(D), acrA_Kp, kpn_Kp, oqx, qnrB, dfr, sul*