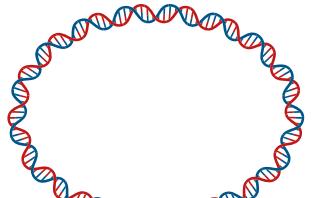


Genome Announcement: *Proteus mirabilis*

Accession#ERS21332210 (ENA)
INS0004948 (INDA)

1. Genome Sequencing



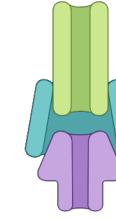
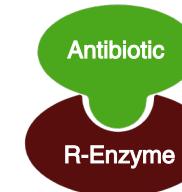
BRIC-THSTI
presenting the
complete genome
sequence of
Proteus mirabilis
isolated from Indian
wastewater from
the urban region.

2. Analysis



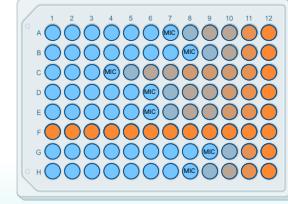
Through this genomic analysis, we gain valuable insights into environmental adaptability, antibiotic resistance, virulence factors and metabolic capabilities.

3. Insights



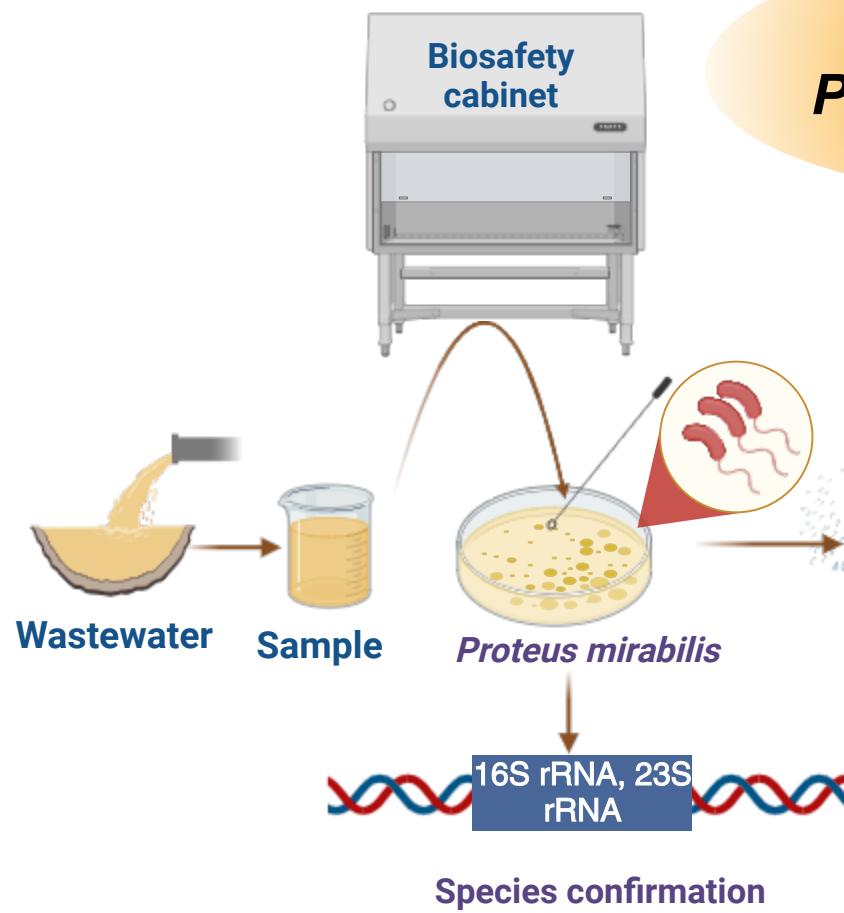
Proteus mirabilis has genes for urease, hemolysin and other toxins which contribute to tissue damage and infection involved in UTI.

4. Translation



Understanding this genomic feature is possible to target urease and flagella could lead to novel treatment options for *P. mirabilis*.

***Proteus mirabilis*: "An Alkalator" alkalizing acidic environment for biological adaptation**



Genomics of *Proteus mirabilis*

GENOMICS

Genome size: 4.06mb
GC percent: 38.5%
CDS: 3663
rRNA=10, tRNA=82

Important Functions

AMR genes: *tet(C)*,
tet(J), *floR*, *dfr*, *sul*,
ant(3")-Ila, *aph(3")-Ib*,
aph(3'), *aph(6)-Id*,
aadA, *ereA*, *InuF*, *cat*