

Genome size: 3.95Mb

GC percent: 59%

CDS: 3702

rRNA= 5, tRNA=75

Important Functions

characteristics

Genome

AMR gene: mphE, msrE, dfr

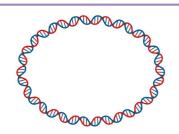


Genome Announcement: Aeromonas simiae

BRIC Othsti

Accession#SAMEA116290030 (NCBI) INS0005208 (IBDC)

1. Genome Sequencing



BRIC-THSTI

presenting the complete genome sequence of **Aeromonas simiae** isolated from Indian wastewater.

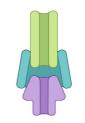
2. Analysis



Genomic analysis
helps to find a public
health concern due
to its multi-drug
resistant genotype
against macrolide
and trimethoprim
warranting a careful
monitoring.

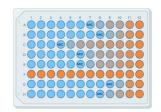
3. Insights





The genomic analysis of Aeromonas simiae reveals a high-risk MDR genotype, driven by mobile ARGs like mphE, msrE, and dfr facilitating the cross-resistance.

4. Translation



These genomic insights underscore the urgency of rational antibiotic use in clinics and aquaculture and monitoring the genomic surveillance to track emerging MDR strains.

Aeromonas simiae: Underscores its dual threat to human health and ecosystems