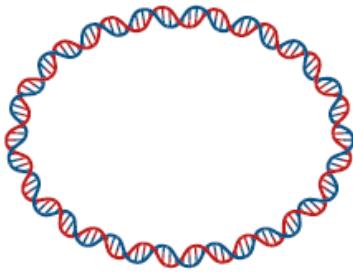


Genome Announcement: *Enterobacter hormaechei*

Accession# SRR23106264(NCBI)
INS0000621(INDA)

1. Genome Sequencing



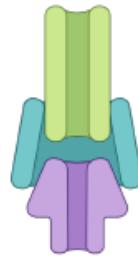
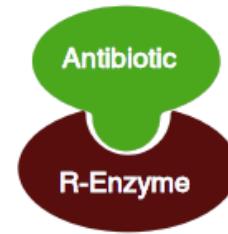
BRIC-THSTI presenting the whole genome sequence of *Enterobacter hormaechei* isolated from the neonatal blood sample

2. Analysis



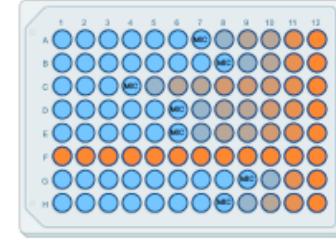
This genomic analysis provides insights into the molecular basis of virulence factors, antimicrobial resistance mechanisms, and fitness traits.

3. Insights

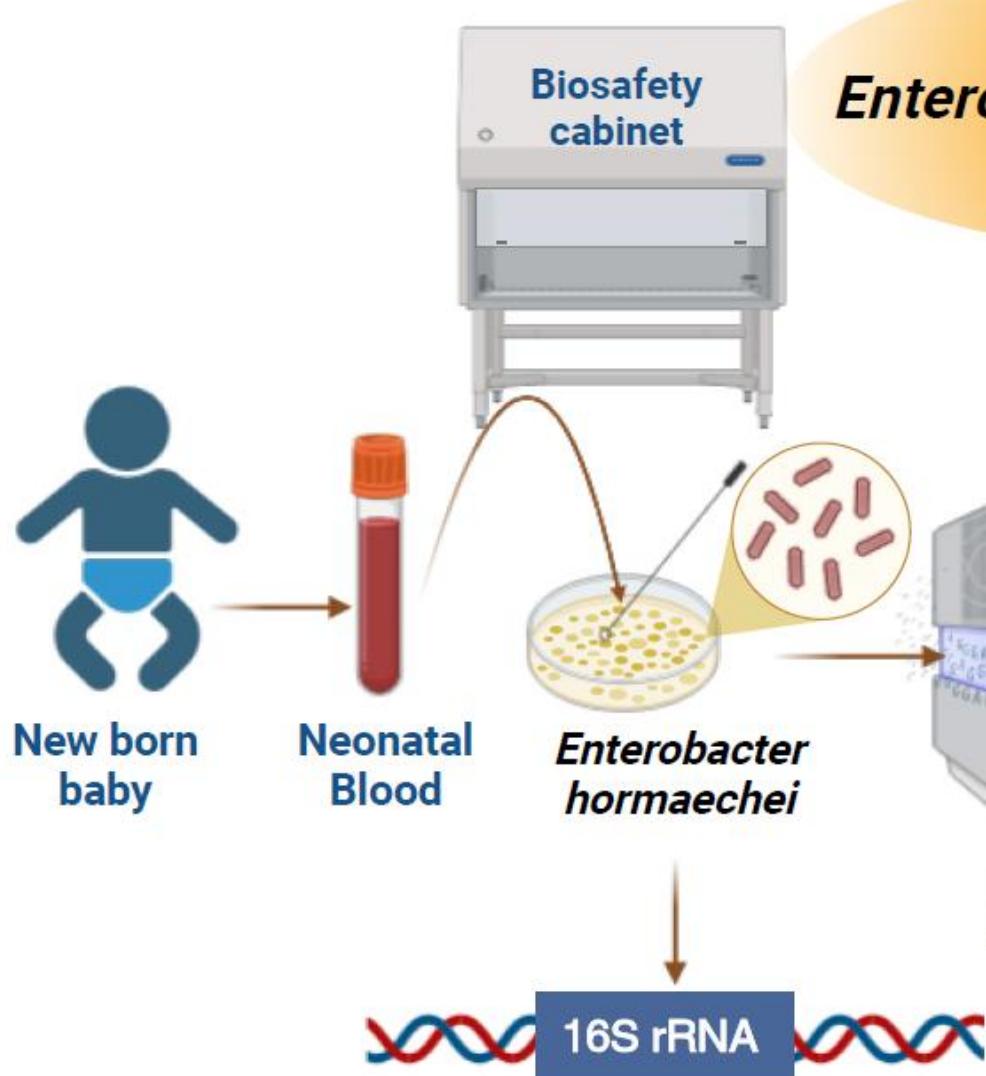


Diverse AMR genes and other factors in *E. hormaechei* confer resistance to nearly all antibiotics commonly used in clinical practice.

4. Translation



This genomic analysis helps improve prognostic outcomes and supports the fight against antibiotic resistance, ultimately promoting better health and treatment strategies.



Genomics of *Enterobacter hormaechei* SRR23106264

GENOMICS

Genome size: 3.68 mb
GC percent: 55.4
CDS: 3569
Stable RNAs: 64
MGEs: Present

AMR genes

vanG, aac(6')-Iaa, bacA, arnT, pmrF, uhpT, PBP3, glpT, soxS, soxR, acrAB-tolC, marR, Efflux pumps,