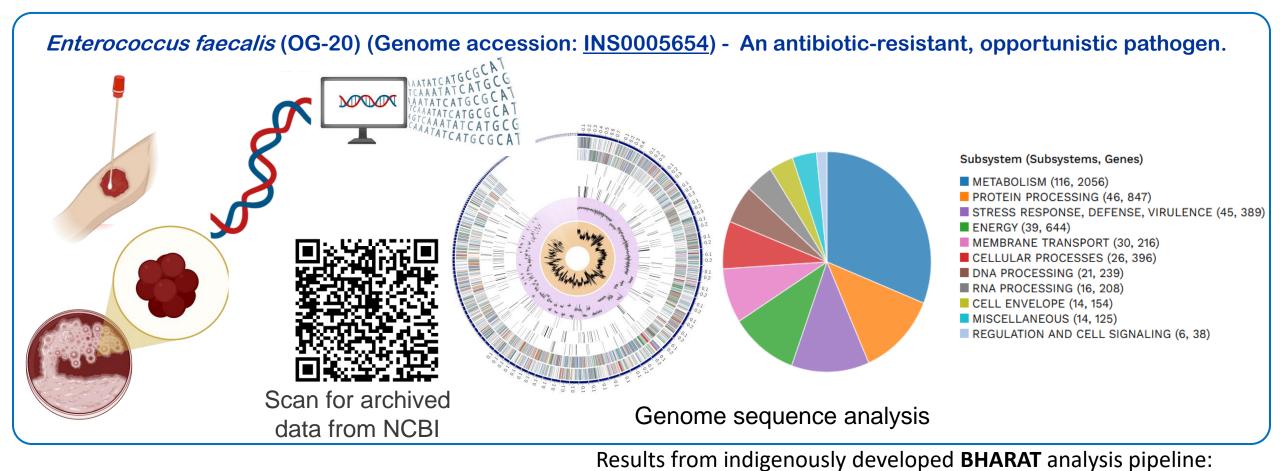
One Day One Genome

Enterococcus faecalis (OG-20) (accession number: INS0005654)

- BRIC-NIBMG sequenced *Enterococcus faecalis* (OG-20) genome, a resilient bacterium, to combat its antibiotic resistance and develop effective treatments for wound infections
- This discovery will aid in understanding its stress-evading mechanisms and develop targeted therapies

Fighting Infections with Strong Gut Feelings!

| Accession number | Organism name | Culture type | Pathogenicity | Genome Size | No. of Genes | Pathogenic genes | Importance |
|---------------------|-------------------------------------|--|---------------------------|-------------------|-----------------|---|--|
| <u>INS0005654</u> | Enterococcus faecalis (OG-20) | Anaerobic, Gram +ve, Coagulase negative | Opportunistic pathogen | 2.6 million bp | 2,579 | Resistance and virulence genes were detected, including those for tetracycline, aminoglycosides, beta-lactams, chloramphenicol and sulfonamides | Genome of E. faecalis is crucial for understanding its antibiotic resistance mechanisms and pathogenic potential |



Quality of Genome Assembly and Annotation:

Enterococcus faecalis (OG-20) Genome accession number: INS0005654

| Table 1. Assembly Details | | Table 2. Annotated Genome Features | | | | | |
|---------------------------|--------------|------------------------------------|-------|--|--|--|--|
| Contigs | 219 | CDS | 2,579 | | | | |
| GC Content | 40.90 | tRNA | 243 | | | | |
| Plasmids | 0 | Repeat Regions | 16 | | | | |
| Contig L50 | 18 | rRNA | 13 | | | | |
| Genome Length | 2,648,649 bp | Partial CDS | 0 | | | | |
| Contig N50 | 195,930 | | | | | | |

(Bacterial Hybrid genome Assembly and Rapid Annotation Toolset)