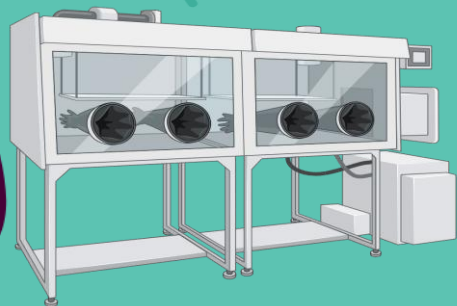




Morganella morganii (NIBMG_HMR_15)

Facultative Pathogenic Bacteria of Wounds and Skin Lesions

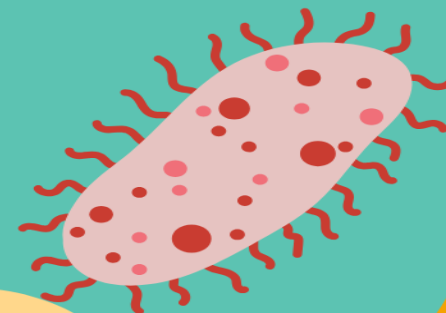


Isolated from
Chronic Wounds

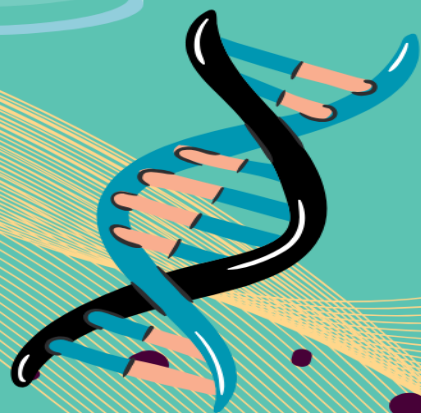
- ❖ Antibiotic Resistant
- ❖ Biofilm Producer



- ❖ Produces Toxin
- ❖ Damage Tissue



Genome Sequencing will Facilitate
Personalized Treatment Solutions



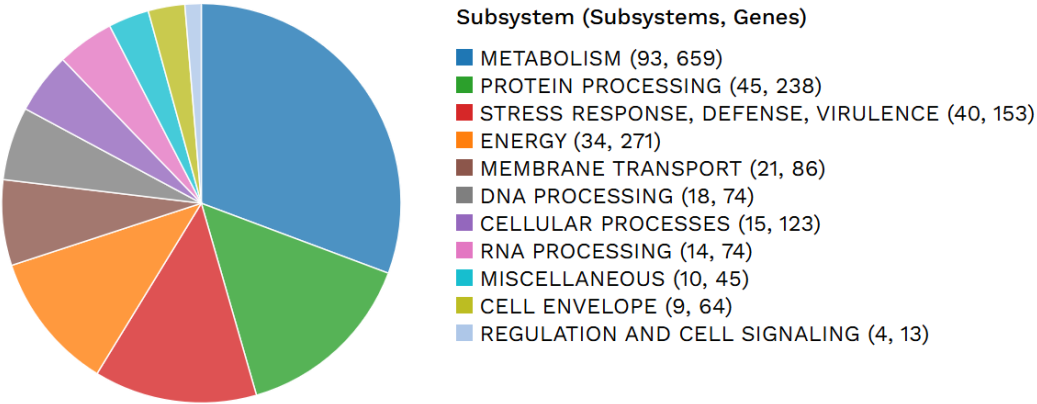
Quality of Genome Assembly and Annotation:
Results from indigenously developed **BHARAT** analysis pipeline:
(**B**acterial **H**ybrid genome **A**ssembly and **R**apid **A**nnotation **T**oolset)

Table 1: Assembly Details	
Contigs	36
GC Content	51.04
Contig L50	3
Genome length	3,831,496 bp
Contig N50	522,746

Table 2: Annotated Genome Features	
CDS	3,830
tRNA	75
rRNA	4
Repeat Regions	0

Table 3: Antimicrobial Resistance Genes	
AMR Mechanism	Genes
Antibiotic inactivation enzyme	CatA1/CatA4 family, CatA2 family, CatB family, DHA/MOR family, Mph(A) family, Mph(E)/Mph(G) family, OXA-1 family
Antibiotic target in susceptible species	Alr, Ddl, dxr, EF-G, EF-Tu, folA, Dfr, folP, gyrA, gyrB, inhA, fabI, Iso-tRNA, kasA, MurA, rho, rpoB, rpoC, S10p, S12p
Efflux pump conferring antibiotic resistance	AcrAB-TolC, EmrAB-TolC, MacA, MacB, MdtABC-TolC, QacE, Tet(A), TolC/OpmH
Protein altering cell wall charge conferring antibiotic resistance	GdpD, PgsA
Regulator modulating expression of antibiotic resistance genes	AcrAB-TolC, EmrAB-TolC, H-NS, OxyR

Subsystem Analysis



Genome Assembly

