

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	44
GC Content	53.11
Contig L50	3
Genome length	2,793,428 bp
Contig N50	413,177

Table 2: Annotated Genome Features

CDS	2,619
tRNA	52
Repeat Regions	76
rRNA	2

Subsystem Analysis

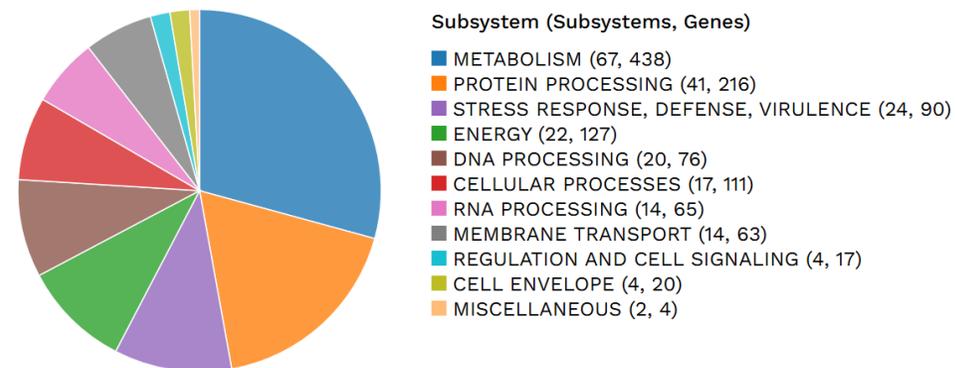


Table 3: Antimicrobial Resistance Genes

AMR Mechanism	Genes
Antibiotic target in susceptible species	Alr, Ddl, dxr, EF-G, EF-Tu, folA, Dfr, folP, gyrA, gyrB, Iso-tRNA, kasA, MurA, rho, rpoB, rpoC, S10p, S12p
Efflux pump conferring antibiotic resistance	MacA, MacB, TolC/OpmH
Protein altering cell wall charge conferring antibiotic resistance	GdpD, PgsA
Regulator modulating expression of antibiotic resistance genes	OxyR
Antibiotic target replacement protein	fabV

Genome Assembly

