

Quality of Genome Assembly and Annotation:

Results from indigenously developed **BHARAT** analysis pipeline: (**Bacterial Hybrid genome Assembly and Rapid Annotation Toolset**)

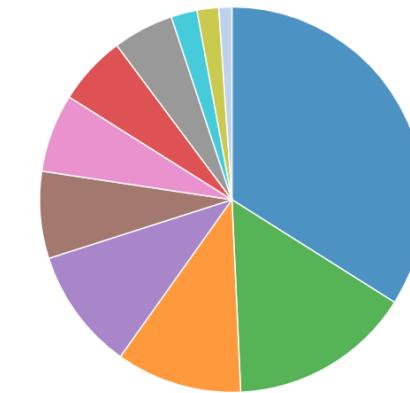
Table 1: Assembly Details

Contigs	36
GC Content	46.23
Contig L50	5
Genome length	4,189,249 bp
Contig N50	290,274

Table 2: Annotated Genome Features

CDS	3,970
tRNA	55
Repeat Regions	7
rRNA	0

Subsystem Analysis



Subsystem (Subsystems, Genes)
METABOLISM (93, 680)
PROTEIN PROCESSING (42, 227)
ENERGY (29, 228)
STRESS RESPONSE, DEFENSE, VIRULENCE (28, 121)
DNA PROCESSING (20, 104)
MEMBRANE TRANSPORT (18, 99)
CELLULAR PROCESSES (16, 135)
RNA PROCESSING (14, 74)
MISCELLANEOUS (6, 18)
CELL ENVELOPE (5, 30)
REGULATION AND CELL SIGNALING (3, 16)

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	MexEF-OprN, TolC/OpmH
Regulator modulating expression of antibiotic resistance genes	OxyR
Antibiotic target replacement protein	fabV
Protein altering cell wall charge conferring antibiotic resistance	GdpD, PgsA

Genome Assembly

