



Government of India
Ministry of Science & Technology
Department of Biotechnology



INSTITUTE OF
LIFE SCIENCES

ONE DAY ONE GENOME

Vibrio fortis

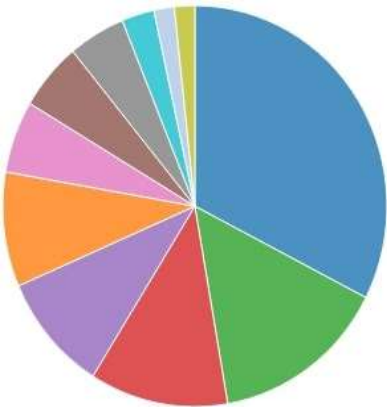
HIGHLIGHTS THE IMPORTANCE OF
MONITORING EMERGING PATHOGENS
AND THEIR ADAPTIVE MECHANISMS IN
THE FACE OF CLIMATE CHANGE

Quality of Genome Assembly and Annotation:

Results from indigenously developed **BHARAT** analysis pipeline: (**B**acterial **H**ybrid genome **A**ssembly and **R**apid **A**nnnotation **T**oolset)

Table 1: Assembly Details	
Contigs	11
GC Content	45.06
Contig L50	2
Genome length	5,439,955 bp
Contig N50	1,195,239

Table 2: Annotated Genome Features	
CDS	5,076
tRNA	138
Repeat Regions	0
rRNA	44



Subsystem Analysis

- Subsystem (Subsystems, Genes)
- METABOLISM (95, 839)
 - PROTEIN PROCESSING (43, 244)
 - STRESS RESPONSE, DEFENSE, VIRULENCE (34, 191)
 - MEMBRANE TRANSPORT (28, 170)
 - ENERGY (27, 260)
 - DNA PROCESSING (17, 88)
 - CELLULAR PROCESSES (16, 151)
 - RNA PROCESSING (14, 86)
 - MISCELLANEOUS (8, 21)
 - REGULATION AND CELL SIGNALING (5, 18)
 - CELL ENVELOPE (5, 32)

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	MdtL, MexEF-OprN, Tet(35), TolC/OpmH
Antibiotic inactivation enzyme	CatB family
Gene conferring resistance via absence	gidB
Protein altering cell wall charge conferring antibiotic resistance	GdpD, PgsA
Regulator modulating expression of antibiotic resistance genes	OxyR

Genome Assembly

