



Government of India
Ministry of Science & Technology
Department of Biotechnology

संवर्धन वाचक



— ONE DAY — ONE GENOME

Neisseria brasiliensis



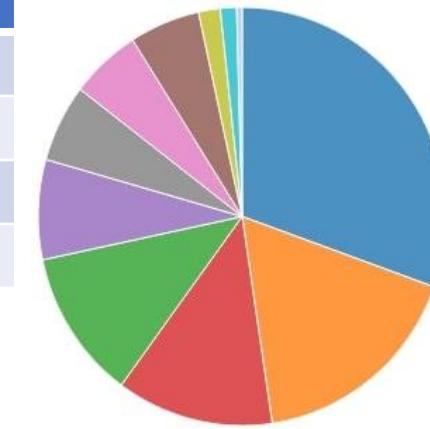
Its notable feature is its potential to
form biofilms over chronic wounds

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	118
GC Content	49.22
Contig L50	14
Genome length	2,587,839 bp
Contig N50	55,562

Table 2: Annotated Genome Features

CDS	2,765
tRNA	56
Repeat Regions	32
rRNA	3

Subsystem Analysis

Subsystem (Subsystems, Genes)

- METABOLISM (71, 474)
- PROTEIN PROCESSING (40, 203)
- STRESS RESPONSE, DEFENSE, VIRULENCE (29, 97)
- ENERGY (27, 172)
- DNA PROCESSING (18, 83)
- MEMBRANE TRANSPORT (14, 52)
- RNA PROCESSING (13, 54)
- CELLULAR PROCESSES (13, 81)
- CELL ENVELOPE (4, 27)
- MISCELLANEOUS (3, 11)
- REGULATION AND CELL SIGNALING (1, 5)

Table 3: Antimicrobial Resistance Genes

AMR Mechanism	Genes
Antibiotic inactivating enzyme	AAC(3)-II, III, IV, VI, VIII, IX, X, ANT(6)-I, APH(3')-III/APH(3')-IV/APH(3')-VI/APH(3')-VII, APH(6)-Ic/APH(6)-Id, CARB/RTG family, Mph(E)/Mph(G) 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
Antibiotic target protection protein	Msr(E)
Gene conferring resistance via absence	gidB
Protein altering cell wall charge conferring antibiotic resistance	PgsA

Genome Assembly