

# One Day One Genome

## Bacillus sp.

*Demonstrate biotherapeutic and probiotic potential*

### Isolation

From stool of patient after six months  
of anti-TB antibiotic treatment

### Genomics

Whole genome sequencing (WGS) to investigate the  
impact of prolonged antibiotic exposure on gut  
microbiota

### Insights

Resistance to two different classes of  
antibiotics



**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**

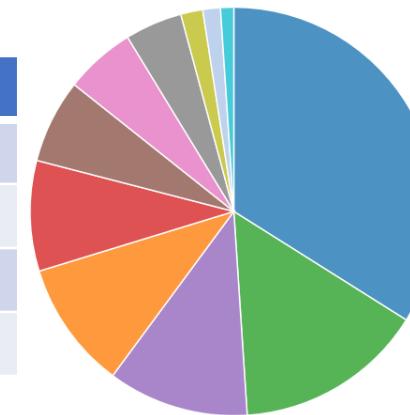
Contigs	24
GC Content	43.57
Contig L50	2
Genome length	4,179,687 bp
Contig N50	1,082,378

**Table 2: Annotated Genome Features**

CDS	4,369
tRNA	71
Repeat Regions	0
rRNA	3

**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, inhA, fabI, Iso-tRNA, kasA, MurA, rho, rpoB, rpoC, S10p, S12p
Efflux pump conferring antibiotic resistance	BceA, BceB, EbrA, EbrB, Lmr(B), YkkCD
Protein altering cell wall charge conferring antibiotic resistance	GdpD, MprF, PgsA
Regulator modulating expression of antibiotic resistance genes	BceR, BceS, LiaF, LiaR, LiaS
Antibiotic target protection protein	BcrC
Antibiotic target modifying enzyme	RlmA(II)

**Subsystem Analysis**

Subsystem (Subsystems, Genes)
METABOLISM (97, 776)
PROTEIN PROCESSING (43, 222)
STRESS RESPONSE, DEFENSE, VIRULENCE (32, 126)
CELLULAR PROCESSES (29, 258)
ENERGY (25, 213)
DNA PROCESSING (19, 103)
MEMBRANE TRANSPORT (16, 77)
RNA PROCESSING (13, 55)
CELL ENVELOPE (5, 26)
MISCELLANEOUS (4, 11)
REGULATION AND CELL SIGNALING (3, 11)

**Genome Assembly**