



## #One day One Genome initiative

**BRIC-IBSD has identified thermophilic *Bacillus velezensis* MRC 5958 from hot spring of Meghalaya, India having cellulase activity**

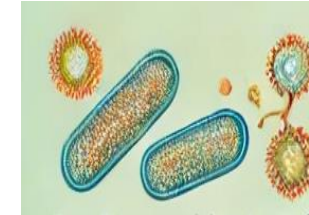


Source Shillong, Meghalaya

Bakra Natural Hot Springs



### Isolation & Characterisation



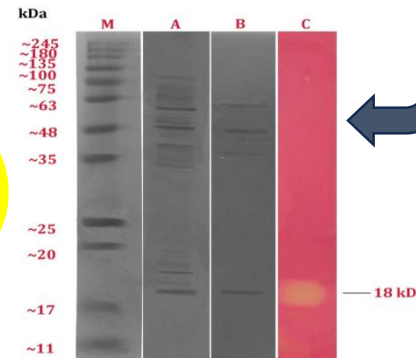
### Thermophilic Cellulase Production



*Bacillus velezensis* MRC 5958,  
Accession Number: PTTN01000000

- Bacteria from hot springs are naturally adapted to high temperatures
- Thrive in extreme environments, displaying resilience to harsh pH, salinity, and oxidative stress.
- Hot spring bacteria often harbour unique biosynthetic gene clusters

Genome Size: 4.46 Mb  
Encodes cellulase gene cluster of 1500 bp



### Importance:

- Capable of fermentation at high temperature for industrial applications
- Capability to produce thermostable lignocellulosic enzymes for lignocellulosic biomass conversion
- Potential for waste management, ethanol production, and cellulase



*Bacillus velezensis* PTTN00000000

Quality of Genome Assembly and Annotation:

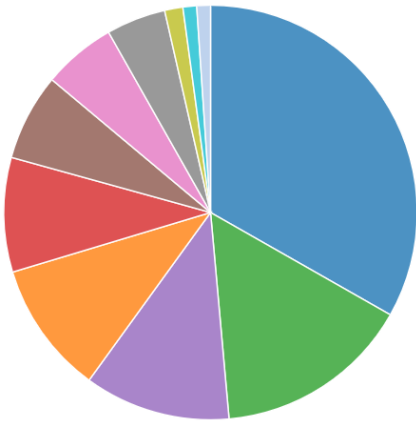
Results from indigenously developed **BHARAT** analysis pipeline:  
(**B**acterial **H**ybrid genome **A**ssembly and **R**apid **A**nnotation **T**oolset)

Table 1: Assembly Details	
Contigs	100
GC Content	45.69
Contig L50	8
Genome length	4,518,411 bp
Contig N50	158,259

Table 2: Annotated Genome Features	
CDS	4,867
tRNA	85
rRNA	7
Repeat Regions	0

Table 3: Antimicrobial Resistance Genes	
AMR Mechanism	Genes
Antibiotic inactivation enzyme	ANT(6)-I, BclI family, FosB, TEM 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 replacement protein	fabL
Efflux pump conferring antibiotic resistance	BceA, BceB, EbrA, EbrB, Lmr(B), Tet(L), YkkCD
Gene conferring resistance via absence	gidB
Protein altering cell wall charge conferring antibiotic resistance	GdpD, MprF, PgsA
Regulator modulating expression of antibiotic resistance genes	BceR, BceS, LiaF, LiaR, LiaS

Subsystem Analysis



Subsystem (Subsystems, Genes)	
METABOLISM	(93, 748)
PROTEIN PROCESSING	(43, 222)
STRESS RESPONSE, DEFENSE, VIRULENCE	(32, 132)
CELLULAR PROCESSES	(29, 244)
ENERGY	(25, 214)
DNA PROCESSING	(19, 95)
MEMBRANE TRANSPORT	(16, 73)
RNA PROCESSING	(13, 53)
CELL ENVELOPE	(4, 15)
MISCELLANEOUS	(3, 10)
REGULATION AND CELL SIGNALING	(3, 10)

Genome Assembly

