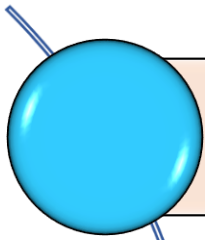
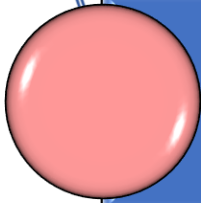


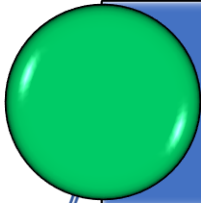
One Day  
One  
Genome



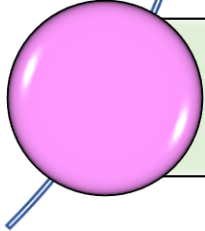
*Lysinibacillus xylanilyticus* t26 (Genome accession: [NZ\\_PHQY01000000](#))



*Lysinibacillus xylanilyticus* t26, isolated from the rhizosphere of *Capsicum chinense* (King Chilli), produces defensive enzymes and growth-promoting factors, offering an eco-friendly alternative to agrochemicals for crop disease management



The strain harbors key biosynthetic gene clusters for the production of siderophores, bacteriocins, and lantibiotics, making it a promising biocontrol agent against soil-borne fungal diseases, with significant potential in sustainable agriculture



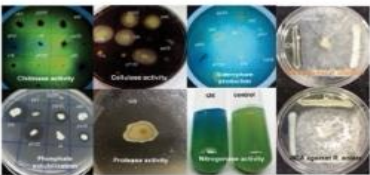
*Microbes from North East: Empowering Agriculture in India!*

Accession number	Organism name	Culture type	Pathogenicity	Genome Size	No. of Genes	Important genes	Importance
<a href="#">NZ_PHQY010000</a>	<i>Lysinibacillus xylanilyticus</i> t26	Gram-positive, rod-shaped, and facultative anaerobic bacterium	Beneficial	5.6 million bp	6,302	Type III polyketides, non-ribosomal peptides, terpenes, and lantibiotics including cerecidin, bacteriocins, siderophores, and thiopeptides	The genome provides valuable information that can be leveraged for developing eco-friendly biocontrol agents, promoting sustainable agriculture, and enhancing soil fertility

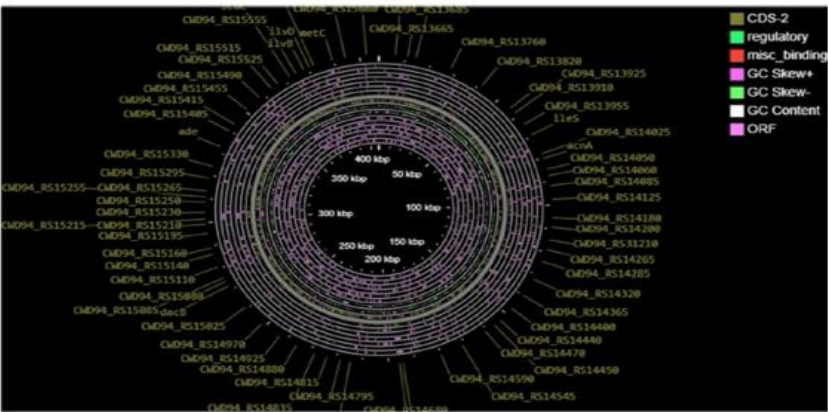
Draft genome sequence and functional analysis of *Lysinibacillus xylanilyticus* t26, a PGPR bacterium isolated from *Capsicum chinense* rhizosphere



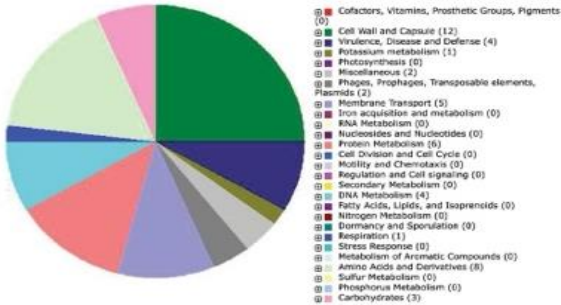
*Capsicum chinense*



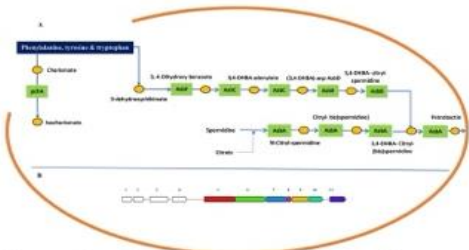
*In vitro* multiple plant growth promotion and biocontrol activity of t26 includes chitinase, cellulase, siderophore, BCAs, phosphate solubilization, protease, and nitrogenase activity of the rhizobacteria



Circular genome map of *L. xylanilyticus* t26



Functional traits identified from the whole genome sequence of t26 that were found connected with the KEEG pathway database.



Biosynthesis pathway of siderophore (petrobactin) from *L. lysinibacillus* t26 predicted from KEEG Pathway analysis



Biosynthetic gene clusters of siderophore which is 33% similar to petrobactin.

This study for genome analysis highlights the current gap in our understanding of complex plant biomass metabolism in rhizosphere bacteria. PGPR exhibiting may be used in the development of new, eco-friendly, and effective bio-formulations as an alternative to synthetic fungicides.

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

Quality of Genome Assembly and Annotation:

*Lysinibacillus xylanilyticus* t26  
Reference genome accession number: [NZ PHQY01000000](#)

Table 1. Assembly Details	
Contigs	769
GC Content	36.77
Plasmids	0
Contig L50	25
Genome Length	5,686,836 bp

Table 2. Annotated Genome Features	
CDS	6,302
tRNA	133
rRNA	51
Partial CDS	0