One Day One Genome

Paenibacillus peoriae (IBSD35) Genome accession number PTJM00000000

Natural killer of AMR pathogen !

Paenibacillus peoriae (IBSD35) is an endophytic bacteria, isolated from a traditional medicinal plant (*Millettia pachycarpa*) of Ukhrul, Manipur, India.

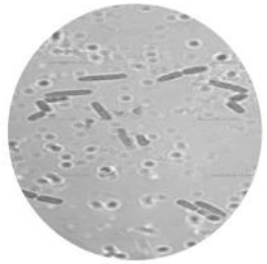
It produce Anti Microbial Peptides (AMP) Peoraerin IBSD35 with high broad spectrum antimicrobial activity against pathogenic bacteria.

Peoraerin IBSD35 can be used to counter AMR because very low or no resistance developed against it.

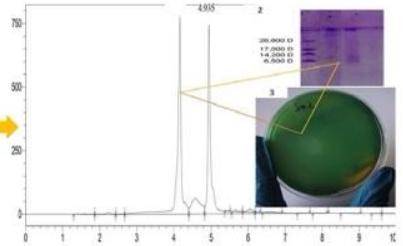
Organism name	Genome Accession number	Culture type	Isolated from	Pathogenicity	Genome Size	No. of Genes	Pathogenic genes	Importance
Paenibacillus peoriae (IBSD35)	PTJM00000000	Gram positive, rod shaped, motile facultatively anaerobic	Stem of medicinal plant (*Millettia pachycarpa*)	Non pathogenic	5.86 million base pair	5,466	BceA, BceB, YkkCD, GdpD, MprF, PgsA	Can produce novel AMPs with antimicrobial property

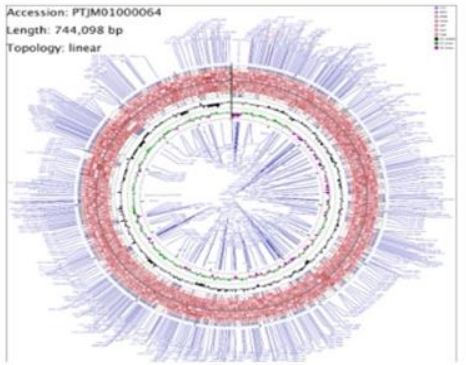
Genome sequencing and proteomic analysis of antimicrobial peptide from *Paenibacillus peoriae*, an endophytic bacterium isolated from traditionally used medicinal plant *Millettia pachyacarpa* Bentham

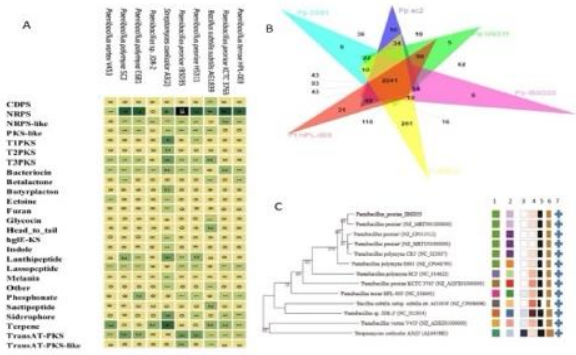
Millettia pachycarpa Bentham



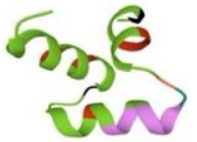
Paenibacillus peoriae IBSD35



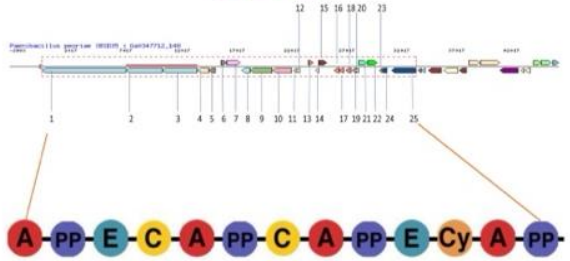




Heatmap of the biosynthetic of the selected genome.



Peoriaerin



NRPS BGC in *P. peoriae* IBSD35

This findings highlighted that the less explored ecological niches provide new sources of an unprecedented opportunity to find novel microbes and metabolites to counter AMR to our already exhausted sources of bio-molecules.

Scan for archived data from NCBI

Quality of Genome Assembly and Annotation:

***Paenibacillus peoriae* (IBSD35)**

Reference genome accession number: PTJM00000000

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	65
GC Content	45.56
Plasmids	0
Contig L50	6
Genome Length	5,862,582 bp

Table 2. Annotated Genome Features	
CDS	5,466
tRNA	85
Repeat Regions	55
rRNA	3
Partial CDS	0