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Whole-genome sequence of *Microbacterium enclense* GM-13, isolated from field-grown bean in Sinaloa

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Abstract

Objectives The genus *Microbacterium* contains bacteria ubiquitously distributed in various environments and includes plant-associated bacteria able to colonize the tissue of agricultural crop plants. The objective of this work was to complete the genome sequence of *Microbacterium enclense* GM-13 isolated from a field-grown bean in Sinaloa.

Data description Here, we report the complete genome sequence of *Microbacterium enclense* GM-13, isolated from a conventionally grown bean (*Phaseolus vulgaris*) from a field in Culiacán, Sinaloa, Mexico. The nucleotide sequence of this genome was deposited into NCBI GenBank under the accession PRJNA1168145. In this report, we introduce the entire genomic sequence of *Microbacterium enclense* GM-13, which is 3,172,320 bp long, with 71.74% G + C content and 3,076 CDSs. The *Microbacterium enclense* GM-13 genome is essential for understanding the genetics of this pathogen, which will aid in analyzing possible virulence genes and contribute to the development of control strategies.

Keywords Genome, Plant-associated bacteria, Phaseolus vulgaris, Sequence

Objective

The genus *Microbacterium* belongs to the family *Microbacteriaceae* with the phylum *Actinobacteria* [1]. Members of the genus are widely distributed in diverse environments such as soil, sediment, or activated sludge, clinical specimens, plants, freshwater, and seawater [2]. Some species have been isolated from animal feces [3, 4], insects [5, 6], and plants [7–9]. GM-13 was isolated from the leaf surface of bean with symptoms associated with bacterial wilt disease in Culiacán, Sinaloa, México (25.544444 N, 108.376389 W) in 2022. Bacteria isolate GM-13 is described as a Gram-positive bacterium with yellow-pigmented colonies on peptone yeast glycerol agar (NYGA) medium. A DNA genomic library was prepared with the MiSeq Reagent Nano Kit v2 (MS-103–1001, Illumina). High-throughput sequencing was performed with a Miseq instrument (SY-410-1003, MiSeq; Illumina) with a 2 × 150 bp maximum read length. Then, sequence reads were trimmed with trimmomatic, assembled, and analyzed in the BV-BRV server and the complete genome was deposited in NCBI under accession number JBHZTD000000000, Biosample SAMN44027483

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(BioProject accession number PRJNA1168145). FastANI and phylogenetic analysis suggests that GM-13 is a strain of *Microbacterium enclense*.

Data description

Bean leaf samples with symptoms associated with bacterial wilt were collected from Sinaloa agronomic fields. A yellow-pigmented bacterial strain was grown on peptone yeast glycerol agar, and an individual colony was placed in 5 ml of peptone yeast glycerol medium and cultivated overnight at 28 °C with 150 rpm shaking. Next, 1.5 ml was centrifuged at 13,000 rpm for 4 min. DNA was isolated from the bacterial cells [10]. 16 S RNA was amplified using primers fD1/rD1 [11] and SANGER senquenced. 16 S sequence (data file 1) [12] was analyzed using BLASTn [13]. The complete genome was sequenced using the illumina MiSeq platform, generating 2 × 150 bp paired-end reads. Illumina reads were trimmed with Trimmomatic (v = 0.39) parameters (threads 10, phred 33, illuminaclip, leading 3, trailing 3, slidingwindows 4:15, minlen 36) [14], then the files were submitted to the server of the Bacterial and Viral Bioinformatics Research Center "BV-BRC", version = 3.39.10 [15]. For assembly and analysis, we utilized the PATRIC service´s Compressive genome analysis strategy [16], with parameters set to auto-assembly for *Microbacterium enclense*, and default settings for genome annotation, and phylogenetic analysis [16–18]. Average nucleotide identity (ANI) was analyzed using FastANI (V = 1.3.3) [19] included in the Proksee server [20]. Phylogenetic tree information obtained from BV-BRC server was drawn using MEGA v = 10.2.6 [21]. The complete genome was deposited in NCBI and annotated with PGAP v = 6.8 for genome release [22]. Bacteria with a yellow-pigmented shape were isolated named "GM-13". 16 S analysis shows (Data file 1) [12] 99% and 98% nucleotide identity to *Microbacterium testaceum* and *Microbacterium enclense* respectively. Then Bacterial DNA was summited to the sequence service. The complete genome sequence resulted in 3,489,266 raw reads (Data set 01) [23]. Whole genome conformed of 35 contigs, genome length of 3,172,320 pb, 98.7% of completeness (Data file 2) [24] and QUAST analysis shows GC content of 71.74% (Data file 3) [25, 26]. PATRIC annotation shows, GM-13 genome has 3,076 protein coding sequences (CDS), 47 transfer RNA (tRNA) genes, and 3 ribosomal RNA (rRNA) genes (Data file 4) [27]. The annotation included 1,033 hypothetical proteins and 2,043 proteins with functional assignments. The proteins with functional assignments included 740 proteins with Enzyme Commission (EC) numbers [28], 632 with Gene Ontology (GO) assignments [29], and 554 proteins that were mapped to KEGG pathways [30]. Also, PATRIC annotation includes two types of protein families [31], and this genome has 2,505 proteins that belong to the genus-specific protein families (PLFams), and 2,545 proteins that belong to the cross-genus protein families (PGFams). According to NCBI PGAP annotation shows 3,018 genes, with 2,966 CDSs, 46 tRNAs, 3 ncRNAs, 2,954 coding genes with protein associated. A circular graphical representation of the genome from PATRIC annotation distribution (Data file 5) [32]. Annotation by PATRIC includes an analysis of the subsystems unique to each genome. A subsystem is a set of proteins that together implement a specific biological process or structural complex [33]. An overview of the number of subsystems for this genome (Data file 6) [34]. Specialty genes were annotated including one and twenty-nine genes for drug resistance according to CARD and PATRIC respectively [35, 36] and two genes using DrugBank databases [37]. The Genome Annotation Service in PATRIC uses a k-mer-based AMR genes detection method, which utilizes PATRIC's curated collection of representative AMR gene sequence variants [16] and assigns to each AMR gene functional annotation, broad mechanism of antibiotic resistance, drug class, and, in some cases, specific antibiotic it confers resistance. Within the CDS of *M. enclense* GM-13, three M23 peptidase-related CDS were found. Protein domains M23 are related to cell restructuration in growth and division [38], as well as weapons against other bacteria in the same niche [39] and as bacteria virulence factor [40]. Peptidase M23B in GM-13 corresponds to a Metallopeptidase. BLAST protein analysis using the non-redundant protein sequences database [41] shows that M23B metallopeptidase protein shares 100% amino acid identity with M23 metallopeptidase of *Microbacterium sp* strain LMI1 [42]. Average nucleotide identity (ANI) analysis shows GM-13 has 84.06% and 83.67% nucleotide identity to *Microbacterium enclense* and *Microbacterium testaceum*, respectivelly (Data file 7) [43]. Phylogenetic analysis shows GM-13 is related to *Microbacterium enclense* and *Microbacterium testaceum* (Data file 8) [44], suggesting a closer relationship with *Microbacterum enclense*. The complete genome was deposited under Sequence Read Archive (SRA) [23], the assembly (Data set 02) [45] and nucleotide report (Data set 03) [46] (Table 1).

Limitations

Analysis of the *Microbacterium enclense* GM-13 assembly was performed with Illumina 2 × 150 sequences and the lack of a third-generation sequencing system like PacBio could have improved our genome assembly.

Table 1 Overview of data files/data sets

Label	Name of data file/data set	File types (file extension)	Data repository and identifier (DOI or accession number)
Data file 1	GM-13 16 S Amplification	Portable Document Format file (.pdf)	Figshare (https://doi.org/10.6084/m9.figshare.27253032) [12]
Data file 2	Sequencing and assembly metrics	Portable Document Format file (.pdf)	Figshare (https://doi.org/10.6084/m9.figshare.27131967) [24]
Data file 3	QUAST report	Portable Document Format file (.pdf)	Figshare (https://doi.org/10.6084/m9.figshare.27131970) [25]
Data file 4	Annotation report	Portable Document Format file (.pdf)	Figshare (https://doi.org/10.6084/m9.figshare.27131853) [27]
Data file 5	Circular genome illustration	Portable Document Format file (.pdf)	Figshare (https://doi.org/10.6084/m9.figshare.27131940) [32]
Data file 6	Genome Subsystem identified	Portable Document Format file (.pdf)	Figshare (https://doi.org/10.6084/m9.figshare.27131934) [34]
Data file 7	FastANI analysis	Portable Document Format file (.pdf)	Figshare (https://doi.org/10.6084/m9.figshare.27131937) [43]
Data file 8	Phylogenetic tree	Portable Document Format file (.pdf)	Figshare (https://doi.org/10.6084/m9.figshare.27131931) [44]
Data set 01	*Microbacterium enclense* strain: GM-13 Genome sequencing Sequence Read Archive (SRA)	SRA file (.fastq)	NCBI, *Sequence Read Archive*, (https://identifiers.org/insdc.sra:SRP536676) [23]
Data set 02	Genome assembly of *Microbacterium enclense* strain GM-13	Fasta file (.fasta)	NCBI, Genome Assembly, (https://identifiers.org/assembly:GCA_042879275.1) [45]
Data set 03	Nucleotide report of *Microbacterium enclense* strain GM-13	Fasta file (.fasta)	NCBI, Nucleotide, (https://www.ebi.ac.uk/ena/browser/view/JBHZTD000000000.1) [46]

Abbreviations

GC	Guanine-Cytosine
CDSs	Coding sequences
rRNA	Ribosomal ribonucleic acid
tRNA	Transfer ribonucleic acid
ncRNAs	Non-coding ribonucleic acids
ANI	Average nucleotide identity
KEGG pathways	Kyoto Encyclopedia of Genes and Genomes

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12863-025-01376-5.

Supplementary Material 1

Supplementary Material 2

Supplementary Material 3

Supplementary Material 4

Supplementary Material 5

Supplementary Material 6

Supplementary Material 7

Supplementary Material 8

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Author contributions

The project was conceived and designed by ECB and GRE. Data acquisition was performed by ECB. Data analysis and interpretation was performed by ECB, JJMA, MLM, EEQA and GRE. The project was jointly supervised by JJMA, MLM, EEQA and GRE. GRE was the principal investigator. The manuscript was written by ECB and revised by JJMA, MLM, EEQA and GRE. All authors read and approved the final manuscript.

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Data availability

The data described in this note can be freely and openly accessed on NCBI Bioproject PRJNA1168145, Biosample SAMN44027483 and Accession number JBHZTD000000000 (Data set 03). Please see Table 1 and references [12, 23–25, 27, 32, 34, 43–46] for details and links to the data.

Declarations

Ethics approval and consent to participate

Tissue sampling was undertaken on private land in Culiacán, Sinaloa with full landowner permission.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

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