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Draft Genome Sequences of Three *Janthinobacterium lividum* Strains Producing Violacein

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Purple pigment producing bacterium strains AMJK, AMJM, and AMRM were isolated from sediment in sinan-gun, Korea and their draft genomes were sequenced using Illumina Hiseq 4000 platform. The lengths of AMJK, AMJM, and AMRM genomes were 6,380,747 bp, 6,381,259 bp, and 6,380,870 bp, respectively and G+C contents were 62.82%, 64.15%, and 62.82%, respectively. Comparative analysis of genomic identity showed that three strains were closely related to the group of *Janthinobacterium lividum*. Functional analysis of AMJK, AMJM, and AMRM genomes showed that all strains harbor genes related to producing violacein (VioABCDE).

Keywords: *Janthinobacterium lividum*, draft genome, violacein producing bacteria

The genus *Janthinobacterium lividum* is a Gram-staining negative, psychrotolerant, rod shape with flagella, and aerobic bacterium [1]. The bacterium is reported for producing violacein, a purple pigment of the bis-indol family, which has been known as its functionality for antioxidant-, anti-virus- and anti-fungal-activities [2]. Although the violacein produced by *Janthinobacterium lividum* is of great industrial value, research based on the optimization for production of violacein from microbes has not been conducted. Strains AMJK, AMJM, and AMRM, which exhibit purple-colored colonies, were isolated from tidal flat in Sinan-gun, Korea (34.8605 N 126.0252 E). To isolate the genomic DNAs from strains AMJK, AMJM, and AMRM, colonies of three strains were cultured on R2A broth at 30°C for 3 days. The genomic DNAs from cultured cells were extracted using FastDNA™ SPIN Kit for Soil (MP Bio-medicals), following the manufacturer's instructions. The libraries from extracted genomic DNAs were constructed using the Illumina NGS library prep kit and sequenced by Illumina HiSeq 4000 platform at Macrogen (Republic of Korea). A total of 55,545,794 (N50, 809,585 bp), 63,501,590, (N50, 809,585 bp) and 50,518,042 bp (N50, 809,585 bp) was generated after quality control of sequencing results for strains AMJK, AMJM, and AMRM, respectively, using FastQC version 0.11.5 (http://www.bioinformatics.babraham.ac.uk/projects/fastqc). Through de novo assembly using SPAdes version 3.15.0 [3] and quality analysis using CheckM v1.2.2 [4] and BUSCO v.5.7.0 [5], draft contigs with high quality for strains AMJK, AMJM, and AMRM were produced (Table 1). The genome annotation was conducted using NCBI Prokaryotic Genome Annotation Pipeline v6.6 [6] (Table 1). The genomic identities of strains AMJK, AMJM, and AMRM with their phylogenetically closely related type strains were compared using POCP (https://github.com/hoelzer/pocp) [7], ANI (OrthoANIu, EzBioCloud) [8], and AAI (EzAAI, EzBioCloud) [9]

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Table 1. Genomic features of draft genomes in the strains AMJK, AMJM, and AMRM.

Genome feature	AMJK	AMJM	AMRM
Genome length (bp)	6,380,747	6,381,259	6,380,870
G + C content (%)	62.82	64.15	62.82
Total number of genes	5,745	5,746	5,747
Number of protein-coding genes	5,630	5,631	5,632
Total number of RNA genes	90	90	90
rRNA genes (5S, 16S, 23S)	5, 4, 1	5, 4, 1	5, 4, 1
tRNA genes	76	76	76
ncRNA genes	4	4	4
Pseudo genes	25	25	25
Coverage (×)	150	147	150
GenBank accession NO.	JAVFKP000000000	JAVFKR000000000	JAVFKQ000000000
Completeness (%)*	99.3	99.2	99.3
Contamination rate (%)*	7.2	7.2	7.2
Complete BUSCOs (%)	98.8	99.0	99.0

* These analyses were conducted using CheckM [4].

Table 2. Comparison of genomic identities of strains AMJK, AMJM, and AMRM with their phylogenetically closely related type strains using POCP, ANI, and AAI. Strains: 1, *Janthinobacterium lividum* NCTC9796[T]; 2, *Janthinobacterium rivuli* FT68W[T]; 3, *Janthinobacterium violaceinigrum* FT13W[T]; 4, *Janthinobacterium agaricidamnosum* NBRC 102515[T]

Program	Strains	1	2	3	4
POCP (%)	AMJK	92.96	88.44	89.84	68.96
	AMJM	92.96	88.45	89.85	68.97
	AMRM	92.98	88.42	89.85	68.93
ANI (%)	AMJK	97.76	92.59	91.65	79.68
	AMJM	97.83	92.64	91.68	79.68
	AMRM	97.79	92.65	91.60	79.78
AAI (%)	AMJK	98.46	94.67	93.88	79.27
	AMJM	98.46	94.68	93.89	79.28
	AMRM	98.46	94.67	93.89	79.27
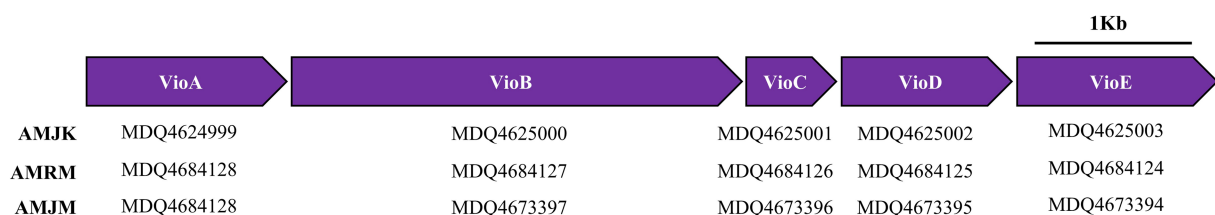
Fig. 1. A physical map of genes and their corresponding accession numbers responsible for producing violacein in the draft genomes of AMJK, AMJM, and AMRM.

(Table 2). The proposed POCP cut-off value for delineating genus are ≥ 50%, indicating that the strains of AMJK, AMJM, and AMRM belong to the genus of *Janthinobacterium*. ANI and AAI cut-off value for delineating species are both ≥ 95%. The ANI and AAI results for strains of AMJK, AMJM, and AMRM showed that these three strains belong to the *Janthinobacterium lividum* group. Through KEGG database [10] and

BLASTP searches, genes (VioABCDE) related to producing violacein [11] were identified in the genomes of strains AMJK, AMJM, and AMRM (Fig. 1).

Nucleotide Sequence Accession Number

The draft genome sequencing data of strains AMJK, AMJM, and AMRM derived in this study are publicly available in the GenBank database under accession numbers JAVFKP000000000, JAVFKR000000000, and JAVFKQ000000000, respectively (NCBI Bioproject number: PRJNA1007897, PRJNA1007939, and PRJNA1007934, respectively).

Acknowledgments

Conflicts of Interest

The authors have no financial conflicts of interest to declare.

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