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Draft genome sequences of green-pigmented Pseudoalteromonas luteoviolacea GB1 and Pseudoalteromonas rubra GB2 isolated from seawater of Chuuk lagoon

Jehyun Jeon
Korea Institute of Ocean Science and Technology
Tae-Yang Eom
Korea Institute of Ocean Science and Technology
Yoo Rim Roh
Korea Institute of Ocean Science and Technology
Youngdeuk Lee
Korea Institute of Ocean Science and Technology
Gun-Hoo Park
Korea Institute of Ocean Science and Technology
Chulhong Oh
och0101@kiost.ac.kr

Korea Institute of Ocean Science and Technology

Data Note

Keywords: Pseudoalteromonas luteoviolacea, Pseudoalteromonas rubra, Draft genome, Green pigmentation, Biosynthetic gene clusters, Antimicrobial activity, Marine bacteria

Posted Date: November 20th, 2026

DOI: https://doi.org/10.21203/rs.3.rs-10989452/v1

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Additional Declarations: No competing interests reported.

Abstract

Objectives

Pigmented *Pseudoalteromonas* strains are renowned for producing diverse bioactive secondary metabolites, yet genome-level characterization of green-pigmented strains—an unusual phenotype within species canonically exhibiting red or purple pigmentation—has not been reported. Here, we describe the draft genome sequences of two green-pigmented marine isolates, *Pseudoalteromonas luteoviolacea* GB1 and *Pseudoalteromonas rubra* GB2, both of which exhibited antimicrobial activity against bacteria and fungi, including *Candida* spp.

Data description

Both genomes were sequenced using the PacBio long-read platform. *P. luteoviolacea* GB1 was assembled into 37 contigs (6.06 Mb; N50 308,453 bp; 99.47% complete) and *P. rubra* GB2 into 4 contigs (5.84 Mb; N50 4,456,163 bp; 93.59% complete). Genome annotation, phylogenomic placement, and biosynthetic gene cluster (BGC) prediction were performed. Both strains were confirmed as members of their respective named species. BGC prediction identified clusters highly similar to the canonical violacein (GB1) and prodigiosin (GB2) biosynthetic pathways, despite the atypical green pigmentation in both strains. Multiple additional BGCs with predicted antimicrobial functions were identified. These datasets provide a resource for investigating the genomic basis of an unusual pigmentation phenotype and for mining novel bioactive compounds from marine *Pseudoalteromonas*.

Objective

The genus *Pseudoalteromonas* (order *Alteromonadales*, class *Gammaproteobacteria*) comprises strictly marine, Gram-negative bacteria distributed across diverse marine habitats [1]. Pigmented strains in particular harbor dense BGC repertoires, dedicating up to 15% of the genome to secondary metabolite production, and are a prolific source of antibacterial, antifungal, and antifouling compounds, including prodiginines, alterochromides, violacein, and pentabromopseudilin [2, 3].

Despite growing genomic resources for pigmented *Pseudoalteromonas*, published studies have focused almost exclusively on strains producing red (prodigiosin), purple (violacein), or yellow (alterochromide) pigments [2–5]. Green-pigmented isolates within species canonically associated with other pigment colors—*P. rubra* (normally red) and *P. luteoviolacea* (normally purple/violet)—have not been characterized at the genome level. Such phenotypic divergence raises questions about the integrity of canonical pigment biosynthetic pathways and the potential activation of alternative biosynthetic routes.

In this study, we report draft genome sequences of *P. luteoviolacea* GB1 and *P. rubra* GB2, two green-pigmented isolates recovered from seawater in Chuuk state in Micronesia. Both strains exhibited clear-zone inhibitory activity against bacterial and fungal indicator organisms, including *Candida* spp., in agar-based diffusion assays. These datasets are intended to support the investigation of the genetic basis of

an atypical pigmentation phenotype and to enable future mining of antimicrobial BGCs from these strains.

Data description

Pseudoalteromonas luteoviolacea GB1 and *Pseudoalteromonas rubra* GB2 were isolated from lagoon seawater of Chuuk, Micronesia, and cultured on Marine Agar 2216 (MA; Difco) at 30°C. Both strains produced a distinctly green pigment on MA, contrasting with the canonical purple/violet pigmentation of *P. luteoviolacea* and the red pigmentation of *P. rubra* type strains. Antimicrobial activity was assessed by agar-well diffusion using ethyl acetate culture extracts against *Staphylococcus aureus* ATCC 25923, *Bacillus subtilis* ATCC 6633, *Escherichia coli* ATCC 25922, and *Candida albicans* ATCC 10231; clear inhibition zones were recorded for both strains.

Genomic DNA was extracted using FastDNA Spin Kit for soil (MP Biomedicals, USA) and sequenced on the PacBio RSII platform at CJ Bioscience (Seoul, Korea) using PacBio DNA Template Prep Kit 1.0. Raw reads (CLR; continuous long reads) with an average coverage of 131.98x were assembled de novo using the HGAP2 protocol implemented in PacBio SMRT Analysis v2.3.0 (Pacific Biosciences, USA) [6]. Assembly quality was evaluated with CheckM v1.2.5 [7].

P. luteoviolacea GB1 assembled into 37 contigs totaling 6,064,542 bp (GC content: 42.0%; N50: 308,453 bp; L50: 7; completeness: 99.47%; contamination: 0.59%) (Table 1, data file 1). *P. rubra* GB2 assembled into 4 contigs totaling 5,836,493 bp (GC content: 49.3%; N50: 4,456,163 bp; L50: 1; completeness: 93.59%; contamination: 0.97%) (Table 1, data file 1). Genome annotation was performed with Prodigal v2.62 [8], identifying 5,354 and 6,816 CDS, 37 and 31 rRNA genes, and 127 and 114 tRNA genes for GB1 and GB2, respectively. Phylogenomic placement (GTDB-Tk v2.4.0 [9]; MEGA v12 [10]) confirmed that GB1 and GB2 belong to *P. luteoviolacea* and *P. rubra*, respectively (Table 1, data file 2), with pairwise ANI values of 71.7% and 71.2% relative to their respective type strains (Table 1, data file 3). BGC prediction with antiSMASH v8.0 [11] identified a total of 16 BGCs in each of GB1 and GB2 (Table 1, data file 4). In GB1, a BGC with high similarity to the violacein biosynthetic pathway (indole/T3PKS type) was identified. In GB2, a BGC highly similar to the prodigiosin BGC (PKS type) was predicted. The presence of violacein- and prodigiosin-related BGCs in strains exhibiting green pigmentation warrants further chemical and transcriptomic investigation to elucidate the biosynthetic basis of the atypical phenotype.

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	Genome assembly and annotation summary of *P. luteoviolacea* GB1 and *P. rubra* GB2	MS Excel file (.xlsx)	Figshare (https://doi.org/10.6084/m9.figshare.33457459) [12]
Data file 2	Phylogenomic tree of *Pseudoalteromonas* genomes	PDF file (.pdf)	Figshare (https://doi.org/10.6084/m9.figshare.33457924) [13]
Data file 3	Average nucleotide identities of *Pseudoalteromonas* genomes	MS Excel file (.xlsx)	Figshare (https://doi.org/10.6084/m9.figshare.33457519) [14]
Data file 4	Biosynthetic gene cluster (BGC) prediction summary of *P. luteoviolacea* GB1 and *P. rubra* GB2	MS Excel file (.xlsx)	Figshare (https://doi.org/10.6084/m9.figshare.33457924) [15]
Data set 1	PacBio raw sequencing reads of *P. luteoviolacea* GB1	Sequence file (.fastq)	Sequence Read Archive (https://identifiers.org/ncbi/insdc.sra:SRR40497444) [16]
Data set 2	PacBio raw sequencing reads of *P. rubra* GB2	Sequence file (.fastq)	Sequence Read Archive (https://identifiers.org/ncbi/insdc.sra:SRR40497445) [17]
Data set 3	Genome assembly of *P. luteoviolacea* GB1	Sequence file (.fasta)	Nucleotide Sequence Database (https://identifiers.org/ncbi/insdc:JCDGSG000000000) [18]
Data set 4	Genome assembly of *P. rubra* GB2	Sequence file (.fasta)	Nucleotide Sequence Database (https://identifiers.org/ncbi/insdc:JCDGSH000000000) [19]

Limitations

Several limitations should be noted. First, neither genome is complete: *P. luteoviolacea* GB1 comprises 37 contigs (N50 308 kb) and *P. rubra* GB2 comprises 4 contigs (N50 4.46 Mb); additional sequencing or chromosomal conformation methods would be required to fully close the assemblies. Second, functional characterization of individual BGCs—including compound isolation and direct linkage to observed antimicrobial activity—was not performed. Third, the chemical identity of the green pigments

has not been determined; genomic evidence of the absence or disruption of the canonical pigment pathway is presented, but chemical characterization is needed to confirm this. Fourth, analyses are based on single isolates of each species, precluding assessment of intraspecies genomic diversity. Fifth, antimicrobial assays used crude ethyl acetate extracts; minimum inhibitory concentration (MIC) values and identification of active compounds were not determined.

Abbreviations

BGC
Biosynthetic gene cluster
CLR
Continuous long read
HGAP
Hierarchical Genome Assembly Process
SMRT
Single-molecule real-time
GC
Guanine and cytosine
CDS
Coding sequence
GTDB-Tk
Genome Taxonomy Database Toolkit
MEGA
Molecular Evolutionary Genetics Analysis
ANI
Average nucleotide identity
PKS
Polyketide synthase
SRA
Sequence Read Archive
MIC
Minimum inhibitory concentration
NCBI
National Center for Biotechnology Information.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Availability of data and materials

The raw sequencing reads and draft genome assemblies are publicly available at the National Center for Biotechnology Information (NCBI) under BioProject PRJNA1521116 (data files 1–4, data sets 1–4). Accession numbers and persistent identifiers are provided in Table 1 and references [16-19].

Competing interests

The authors declare that they have no competing interests.

Acknowledgments

This research was supported by the development of an advanced platform for recombinant drug production based on marine-derived nanomachines of the Korea Institute of Marine Science & Technology Promotion (KIMST), funded by the Ministry of Oceans and Fisheries (RS-2026-25541458).

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Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

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- Datafile3.xlsx
- Datafile2.pdf