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GENOME SEQUENCES

Draft Genome Sequence of *Sinomicrobium* sp. Strain PAP.21, Isolated from a Coast Sample of Papua, Indonesia

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ABSTRACT *Sinomicrobium* sp. strain PAP.21 (EXT111902) was isolated from the coast of Cenderawasih Bay National Park in West Papua, Indonesia. Its genome was assembled into 151 contigs with a total size of 5.439 Mbp, enabling the prediction of its specialized metabolite production capacity.

The phylum *Bacteroidetes* is a promising, although underexplored, bioresource for natural product discovery (1, 2). *Bacteroidetes* are among the most abundant bacteria within marine ecosystems (3), and their known bioactive natural products represent a remarkable diversity. This diversity is, e.g., exemplified by the lanthipeptide pinensin from *Chitinophaga pinensis* exhibiting antifungal activity (4). Expecting a positive correlation between the *Bacteroidetes* diversity and their produced chemical diversity, we aimed at accessing new strains.

In this study, *Sinomicrobium* sp. PAP.21 was isolated from marine sediment of the upper layer (5 to 10 cm) collected at a coast area of Cenderawasih Bay National Park, Papua, Indonesia (2°23′06.8″S 134°57′53.5″E). The strain was deposited in the Fraunhofer strain collection (5) under its identifier EXT111902.

The marine sediment sample was stored in a sterile plastic bag before being plated onto artificial seawater (1.5% agar, 0.01% KBr, 2.3% NaCl, 1.1% $MgCl_2 \cdot 6\,H_2O$, 0.1% $CaCl_2 \cdot 2H_2O$, 0.1% KCl, 0.004% $SrCl_2 \cdot 6\,H_2O$, 0.4% Na_2SO_4, 0.02% $NaHCO_3$, and 0.003% H_3BO_3 in H_2O), including *Escherichia coli* prey, and incubated at 30°C. Grown colonies were purified on marine agar (Carl Roth GmbH; product no. CP73.1 + 1.5% agar), and a sequencing sample was prepared by growing EXT111902 aerobically in marine broth (30°C for 24 h; Carl Roth GmbH; product no. CP73.1). The cell pellet was resuspended in ATL buffer (Qiagen) containing RNase A. BashingBead lysis tubes (Zymo Research) were used for cell disruptions. DNA was isolated using QIAmp 96 DNA QIAcube high-throughput (HT) kits with the addition of proteinase K (Qiagen). Libraries for short-read sequencing were prepared using the Illumina DNA prep tagmentation kit with 500 ng DNA input and 5 cycles of indexing PCR. Library quality was evaluated (Agilent 2100 bioanalyzer) and sequenced on an Illumina NovaSeq instrument using a NovaSeq 6000 SP v1 sequencing kit with a 2 × 150 bp read length and a depth of 4.0 to 5.0 Mio reads. For sequence processing and analysis, software tools were run with default settings unless otherwise stated. The sequencing was demultiplexed (Illumina bcl2fastq, v2.19.0.316), quality checked (Fastp [6] v0.20.1), and visualized (MultiQC [7] v1.7). A total of 11.98 million paired-end reads were quality filtered (Fastp [6] v0.20.1; additional parameter "–detect_adapter_for_pe –cut_by_quality5 –cut_by_quality3

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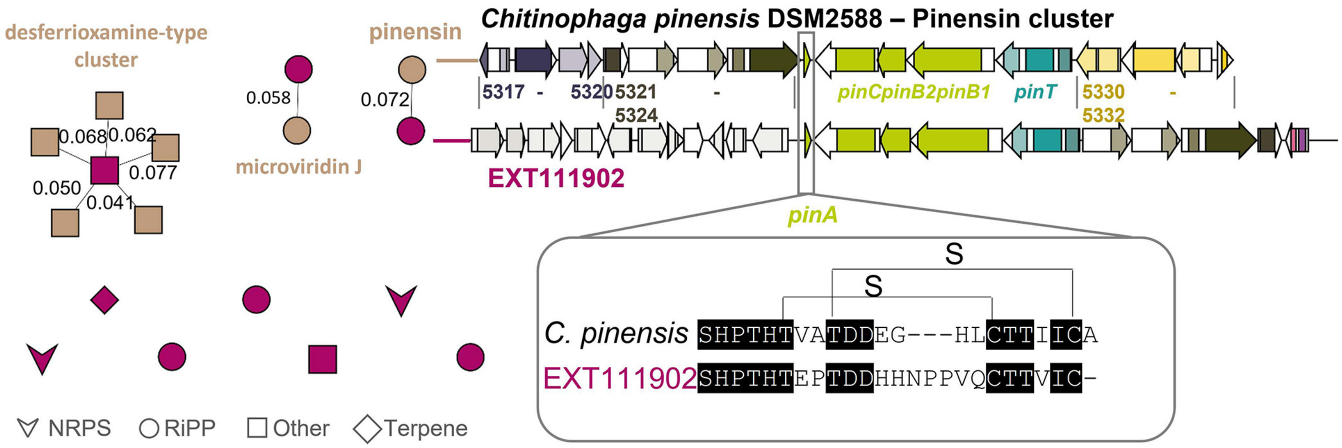

FIG 1 BiG-SCAPE network (16) (left) of strain EXT111902 (magenta) (manually curated). EXT111902 carries five ribosomally synthesized and posttranslationally modified peptides (RiPPs; circle), two nonribosomal peptides (NRPSs; arrow), one terpene (diamond), and two other BGCs (rectangle). By networking with the MIBiG reference clusters (brown), a desferrioxamine-like NRPS-independent siderophore BGC (similarity index up to 0.077, BGC0001478), a microviridin-like BGC (similarity index of 0.058, BGC0000593), and a pinensin-like BGC (similarity index of 0.072) were annotated. Alignment of the pinensin-like cluster of EXT11902 to the pinensin BGC0001392 of *C. pinensis* DSM2588 (right) shows the presence of homologous genes to the biosynthetic core genes *pinA* to *C* (light green) and *pinT* (turquoise), including the split dehydratase genes *pinB1* and *pinB2*. Homologous genes to Cpin5321 to 5324 (dark green) of BGC0001392, suggested to be involved in the perception and import of pinensin, are present. Homologs to Cpin5330 to 5332 (yellow), proposed to be responsible for pinensin export, instead are not detected in the EXT111902 BGC. Alignment of the pinensin core peptide (bottom right) suggests a sequence of 24 amino acids for EXT111902, while the pinensin A peptide contains 22 amino acids.

–low_complexity_filter –length_required 21 –correction”), assembled (Unicycler [8] v0.4.8), and annotated (Bakta [9] v1.5.1). The genome consists of 5,438,544 bp (coverage, 320×; N_{50}, 141,686 bp; L_{50}, 13) in 151 contigs and has a GC content of 44.4%. Using CheckM (v1.0.18) (10), the degree of genome completeness was determined at 99.34% with 3.9% contamination. The genome encodes 4,679 protein-coding genes, 47 tRNAs, 1 transfer-messenger RNA (tmRNA), 3 rRNAs and 6 noncoding RNAs (ncRNAs). The taxonomical rank was established using the Type Strain Genome Server (11). This process revealed *Sinomicrobium oceani* CGMCC 1.12145 (12) as the closest related type strain. Digital DNA-DNA hybridization (dDDH) values exceed the species delineation threshold of 70% (76.9% [d0], 92.1% [d4], and 82.3% [d6]). An average nucleotide identity (ANI) (13) value of 98.89% supports the affiliation of EXT111902 to the species *S. oceani*.

antiSMASH v6.0 (14) was employed to predict the biosynthetic gene clusters (BGCs). BGC annotation was achieved by their clustering with MIBiG (15) reference clusters into gene cluster families (GCFs) using BiG-SCAPE (16) and setting a cutoff value of 0.6. EXT111902 carries one BGC clustering with BGC0001478, encoding the synthesis of the siderophore desferrioxamine E (17) and another BGC was annotated to BGC0000593, encoding microviridin J (18). The third database annotation refers to pinensin (BGC0001392) (4). Pinensin-like BGCs were detected previously in the genomes of certain *Chitinophaga*, *Chryseobacterium*, *Elizabethkingia*, *Pedobacter*, and *Sinomicrobium* strains (19). Variations in the amino acid sequence of the core peptides indicate a yet undiscovered structural diversity within this lantipeptide type. Such alterations toward the known pinensins are also predicted for EXT111902 (Fig. 1).

Data availability. The whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under BioProject PRJNA904543 with accession number SAMN31846359. Raw data can be obtained from the Sequence Read Archive (SRP421602). The draft genome sequence has been deposited in GenBank under the accession number JAPPSR000000000.

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Complete Genome Sequence of the Carboxydotrophic Knallgas Bacterium *Pseudomonas carboxydohydrogena* Strain DSM 1083

- Daniel Siebert,
- Tobias Busche,
- Ezgi Saydam,
- Jörn Kalinowski,
- Christian Rückert-Reed,
- Bastian Blombach

https://doi.org/10.1128/mra.01277-22

Draft Genome Sequence of *Granulicatella* sp. Strain S8, Isolated from a Marine Fish, *Seriola quinqueradiata*

- Myunglip Lee,
- Adeel Farooq,
- Joon Bum Jeong,
- Man-Young Jung

https://doi.org/10.1128/mra.01352-22

Genome Resources for the *Colletotrichum gloeosporioides* Species Complex: 13 Tree Endophytes from the Neotropics and Paleotropics

- Stephen A. Rehner,
- Romina Gazis,
- Vinson P. Doyle,
- Willie A. S. Vieira,
- Philip M. Campos,
- Jonathan Shao

https://doi.org/10.1128/mra.01040-22

Complete Genome Sequences of Monkeypox Virus from a French Clinical Sample and the Corresponding Isolated Strain, Obtained Using Nanopore Sequencing

- Charlotte Balière,
- Véronique Hourdel,
- Aurelia Kwasiborski,
- Quentin Grassin,
- Maxence Feher,
- Damien Hoinard,
- Jessica Vanhomwegen,
- Fabien Taieb,
- Paul-Henri Consigny,
- Jean-Claude Manuguerra,
- India Leclercq,
- Christophe Batéjat,
- Valérie Caro

https://doi.org/10.1128/mra.00009-23

Complete Genome Sequences of 11 *Staphylococcus pseudintermedius* Isolates from Dogs in the United States

- Ashkan Roozitalab,
- Ola Elsakhawy,
- Lufuno Phophi,
- Stephen A. Kania,
- Mohamed A. Abouelkhair

https://doi.org/10.1128/mra.00002-23

Complete Genomic Analysis of the Novel Phage BUCT-3589, Infecting *Klebsiella pneumoniae*

- Xiaoxuan Zhang,
- Yanze Mi,
- Shan Xu,
- Lihua Song,
- Huahao Fan,
- Mengzhe Li,
- Yigang Tong

https://doi.org/10.1128/mra.01223-22

Whole-Genome Sequence of Endophytic Bacteria Associated with Poison Ivy Vine (*Toxicodendron radicans*)

- Han Ming Gan,
- Trevor S. Penix,

- Peter C. Wengert,
- Narayan H. Wong,
- André O. Hudson,
- Girish Kumar,
- Michael A. Savka

https://doi.org/10.1128/mra.01232-22

Complete Genome Sequence of *Nitrospina watsonii* 347, Isolated from the Black Sea

- Linnea F. M. Kop,
- Hanna Koch,
- Eva Spieck,
- Theo van Alen,
- Geert Cremers,
- Holger Daims,
- Sebastian Lücker

https://doi.org/10.1128/mra.00078-23

Complete Sequence of the Closed Circular Extrachromosomal Element of *Naegleria jadini* Willaert and Ray (Strain ITMAP400)

- Brian T. Nguyen,
- Nora M. Chapman,
- Holly A. F. Stessman,
- Steven Tracy,
- Kristen M. Drescher

https://doi.org/10.1128/mra.00061-23

Complete Genome Sequence of *Streptococcus gallolyticus* Strain XH2168

- Siyuan Yang,
- Yue Yao,
- Feng Zhao,
- Yunsong Yu,
- Xiaoting Hua

https://doi.org/10.1128/mra.00105-23

Complete Genome Sequence of New *Cronobacter*-Specific Bacteriophage Dev_CS701

- Michal Kajsik,
- Peter Durovka,
- Maria Kajsikova,
- Diana Rusnakova,
- Tomas Szemes,
- Hana Drahovska

https://doi.org/10.1128/mra.00034-23

Draft Genome Sequence of *Bacillus anthracis* N1, Isolated from a Recreational Freshwater Kettle Lake in Ontario, Canada

- Noah Bryan,
- Rebecca Anderson,
- Opeyemi U. Lawal,

- Valeria R. Parreira,
- Lawrence Goodridge

https://doi.org/10.1128/mra.01262-22

Draft Genome Sequences of Endophytic *Pseudomonas* Strains, Isolated from the Interior of *Brassicaceae* Plants

- Hiroki Kaneko,
- Toshiki Furuya

https://doi.org/10.1128/mra.01337-22

Draft Genome Sequence of the Fluconazole-Resistant *Yarrowia lipolytica* Clinical Isolate CBS 18115

- Rose-Anne Lavergne,
- Paul Barbier,
- Lenha Mobuchon,
- Atanu Banerjee,
- Rajendra Prasad,
- Florent Morio

https://doi.org/10.1128/mra.01260-22

Complete Genome Sequence of *Staphylococcus capitis* CCSM0123, Isolated from Healthy Facial Skin

- Laiji Ma,
- Hong Jiang,
- Suzhen Yang,
- Yan Li,
- Li Shao

https://doi.org/10.1128/mra.00132-23

Genome Sequences of Two Grapevine Rupestris Stem Pitting-Associated Virus Variants from *Vitis vinifera* cv. Riesling in Idaho, USA

- Jennifer Dahan,
- Gardenia E. Orellana,
- Jungmin Lee,
- Alexander V. Karasev

https://doi.org/10.1128/mra.01366-22

Complete Genome Sequence of Bacteriophage vB_Hercules_Set, Which Infects Enteric Pathogen *Salmonella enterica* Serovar Typhimurium

- Evan N. Bennett,
- Ibrahim Ayyash,
- Joshua Hughes,
- Teagen Comeau,
- Shallee T. Page

https://doi.org/10.1128/mra.01282-22

Draft Genome Sequences of 14 Fluoroquinolone-Resistant *Escherichia coli* Isolates from Imported Shrimp

- Khulud Alotaibi,
- Javier Revollo,

- Kidon Sung,
- Jaime A. Miranda,
- Saeed A. Khan,
- Ashraf A. Khan,
- Mohamed Nawaz

https://doi.org/10.1128/mra.01116-22

Whole Genome Sequencing of *Brucella melitensis* Isolated from Patients in Hohhot, China

- Shana Chen,
- Quan Fu,
- Mandlaa Mandlaa,
- Qingchun Wang,
- De Sheng,
- Saijilahu Saijilahu,
- Tana Tana,
- Dezhi Yang

https://doi.org/10.1128/mra.00032-23

Draft Genome Sequence of *Aspergillus ochraceus* Strain DY1, a Lignin-Degrading Fungus Isolated from Wood Rot

- Menaka Devi Salam,
- Namdol Nilza,
- Ajit Varma

https://doi.org/10.1128/mra.01278-22

Draft Genome Sequences of Marine Bacteria, Degraders of the Sulfated Polysaccharide Ulvan, Extracted from a Green Alga, *Ulva meridionalis*

- Bubai Bhakta,
- Miho Satoh,
- Kouhei Ohnishi

https://doi.org/10.1128/mra.01288-22

Genome Sequence Analysis of a *Wohlfahrtiimonas chitiniclastica* Strain Isolated from a Septic Wound of a Hospitalized Patient in Uganda

- Denis K. Byarugaba,
- Bernard Erima,
- Godfrey Wokorach,
- Florence Najjuka,
- James Kiyengo,
- Yoon I. Kwak,
- Ana Ong,
- Rosslyn Maybank,
- Lan Preston,
- Emma Mills,
- Patrick McGann,
- Hannah Kibuuka,
- Ambrose K. Musinguzi,
- Fred Wabwire-Mangen

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Whole-Genome Sequencing of Pig Gut *Lactobacillus amylovorus* CICC 6090

- Yeshi Yin,
- Zongyan Li,
- Huahai Chen

https://doi.org/10.1128/mra.01197-22

Complete Genome Sequence of *Enterobacter roggenkampii* RX.G5M56, a C1-Metabolizing Strain from a Freshwater Stream in Hong Kong

- D. Y. Xu,
- K. M. Leung,
- G. K. K. Lai,
- F. C. C. Leung,
- S. D. J. Griffin

https://doi.org/10.1128/mra.00015-23

Complete Genome Sequence of *Gordonia polyisoprenivorans* 135, a Promising Degrader of Aromatic Compounds

- Ekaterina Frantsuzova,
- Viktor Solomentsev,
- Anna Vetrova,
- Vasili Travkin,
- Inna Solyanikova,
- Yanina Delegan

https://doi.org/10.1128/mra.00058-23

Complete Genome Sequence of the Thermophilic *Enterococcus faecalis* Strain K-4, Isolated from a Grass Silage in Thailand

- Meimi Kuwabara,
- Rei Irimajiri,
- Shun Togo,
- Yasuhiro Fujino,
- Masanori Honsho,
- Shiro Mawatari,
- Takehiko Fujino,
- Katsumi Doi

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Draft Genome Sequence of *Sinomicrobium* sp. Strain PAP.21, Isolated from a Coast Sample of Papua, Indonesia

- Riyanti,
- Celine M. Zumkeller,
- Marius Spohn,
- Sanja Mihajlovic,
- Oliver Schwengers,
- Alexander Goesmann,
- Riviani Riviani,

- Maria D. N. Meinita,
- Till F. Schäberle,
- **Harwoko Harwoko**

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Omics Data Sets

Seasonal and Spatially Distributed Viral Metagenomes from Comau Fjord (42°S), Patagonia

- Eduardo Castro-Nallar,
- Valentín Berríos-Farías,
- Beatriz Díez,
- Sergio Guajardo-Leiva

https://doi.org/10.1128/mra.00082-23

Amplicons, Metagenomes, and Metatranscriptomes from Sediment and Water

- Madison R. Newman,
- Darlenys Sanchez,
- Anna M. Acosta,
- Bernadette J. Connors

https://doi.org/10.1128/mra.01230-22

Amplicon Sequence Collections

16S Amplicon Metabarcoding of the Nest Materials of Native Australian Stingless Bees

- Boyd Tarlinton,
- Flavia Carmelina Massaro,
- Caroline Hauxwell

https://doi.org/10.1128/mra.01181-22

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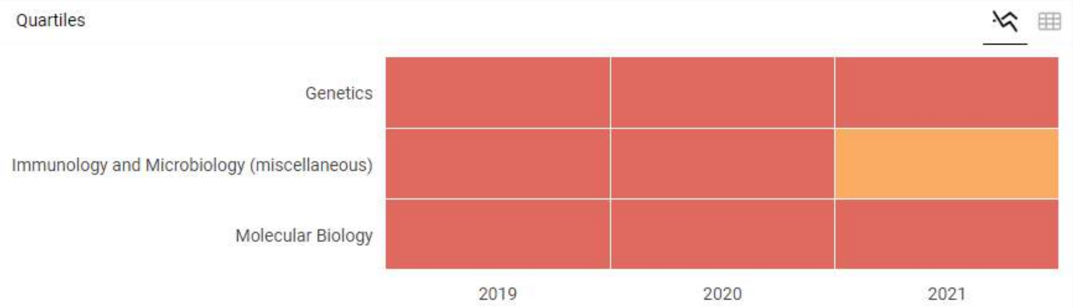


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