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Journal Article**Author(s):**

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Publication date:

2020

Permanent link:

<https://doi.org/10.3929/ethz-b-000403798>

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Originally published in:

Microbiology Resource Announcements 9(8), <https://doi.org/10.1128/MRA.01305-19>

Funding acknowledgement:

184666 - Towards building microbial consortia for pest control: exploring adaptation to insect hosts and intraspecific diversity of pathogenicity and competition traits in insecticidal pseudomonads (SNF)



Draft Genome Sequence of *Pseudomonas* sp. Strain LD120, Isolated from the Marine Alga *Saccharina latissima*

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ABSTRACT We report the draft genome sequence of *Pseudomonas* sp. strain LD120, which was isolated from a brown macroalga in the Baltic Sea. The genome of this marine *Pseudomonas protegens* subgroup bacterium harbors biosynthetic gene clusters for toxic metabolites typically produced by members of this *Pseudomonas* subgroup, including 2,4-diacetylphloroglucinol, pyoluteorin, and rhizoxin analogs.

Pseudomonas bacteria occur in many terrestrial and aquatic ecosystems, where they interact with various hosts, including plants, invertebrates, and humans (1–3). Pseudomonads can serve as a source for novel secondary metabolites, and some are used as bioremediation and biological control agents (4–6). The genus *Pseudomonas* is composed of different lineages, divided into groups and subgroups (7–9). The *Pseudomonas protegens* subgroup harbors mainly isolates from soil or roots that are active against plant pathogens and pest insects (5, 10, 11).

Here, we sequenced the genome of *Pseudomonas* sp. strain LD120 using PacBio technology. Strain LD120 was isolated from a blade of the brown macroalga *Saccharina latissima*, from the Baltic Sea (12). A 16S rRNA gene-based analysis placed LD120 in a close phylogenetic relationship with the *P. protegens* type strain CHA0 (13, 14). LD120 exhibits broad-spectrum antimicrobial activity, including activity against algal pathogens (12), which involves the toxic metabolites 2,4-diacetylphloroglucinol (DAPG) and pyoluteorin (14).

The MagAttract high-molecular-weight (HMW) DNA kit (Qiagen) was used to extract LD120 genomic DNA from 400 μ l of an overnight nutrient yeast broth culture prepared from an individual colony derived from the original stock of the strain. Sequencing was performed by the Lausanne Genomic Technologies Facility. DNA samples were sheared in Covaris g-TUBEs to obtain fragments with a mean length of 10 kb. The sheared DNA was used to prepare a library with the PacBio SMRTbell template preparation kit v1.0. The resulting library underwent size selection on a BluePippin system (Sage Science, Inc.) for molecules larger than 7 kb, which excluded smaller plasmids. The library was multiplexed and sequenced using one single-molecule real-time (SMRT) cell and a Sequel system (movie length, 600 min). Genome assembly was performed using the RS_HGAP_Assembly.4 protocol in SMRT Link v6.0.

The resulting assembly generated six contigs with a maximum length and N_{50} value of 3,219,715 bp and 1,709,349 bp, respectively, providing a total genome length of 6,672,566 bp (G+C content, 61.61%; coverage, 136 \times). Annotation of the LD120 genome with the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) identified 5,987 coding sequences. In addition, 68 tRNAs and 16 rRNAs were detected.

The average nucleotide identity (calculated based on BLAST+ results [15]) between the genomes of strain LD120 and the type strain CHA0 (16) was 87.32%, which identified LD120 as a member of the *P. protegens* subgroup. The LD120 genome

Citation Heiman CM, Wiese J, Kupferschmied P, Maurhofer M, Keel C, Vacheron J. 2020. Draft genome sequence of *Pseudomonas* sp. strain LD120, isolated from the marine alga *Saccharina latissima*. Microbiol Resour Announc 9:e01305-19. <https://doi.org/10.1128/MRA.01305-19>.

Editor Julie C. Dunning Hotopp, University of Maryland School of Medicine

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Received 24 October 2019

Accepted 28 January 2020

Published 20 February 2020

harbors biosynthetic gene clusters for DAPG and pyoluteorin and also for rhizoxin analogs, which are produced by a subset of *P. protegens* strains (17–19). Unlike other *P. protegens* subgroup strains, LD120 does not harbor gene clusters for production of the antimicrobial pyrrolnitrin and the entomotoxin FitD (11, 20). This difference could be a result of coevolution with the algal host and points to genomic diversity within the *P. protegens* subgroup.

Data availability. This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under accession number [WVHL00000000](https://doi.org/10.1128/aem.66.12.5448-5456.2000). The version described in this paper is the first version, WVHL01000000. The sequences for the *de novo* assembly have been deposited in EMBL/GenBank under accession number [ERR3588830](https://doi.org/10.1128/aem.66.12.5448-5456.2000).

ACKNOWLEDGMENTS

This study was supported by grant 310030-184666 from the Swiss National Science Foundation.

We thank the staff of the Genomic Technologies Facility of the University of Lausanne for sample processing and bioinformatic analysis.

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