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Rédou V, Kumar A, Matthieu Hainaut, Bernard Henrissat, Record E, et al.. Draft Genome Sequence of the Deep-Sea Ascomycetous Filamentous Fungus *Cadophora malorum* Mo12 from the Mid-Atlantic Ridge Reveals Its Biotechnological Potential: Draft Genome Sequence of the Deep-Sea Ascomycetous Filamentous Fungus *Cadophora malorum* Mo12. *Genome Announcements*, 2016, 4 (4), pp.e00467-16. 10.1128/genomeA.00467-16 . hal-01446811

HAL Id: hal-01446811

<https://amu.hal.science/hal-01446811>

Submitted on 4 May 2017

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Draft Genome Sequence of the Deep-Sea Ascomycetous Filamentous Fungus *Cadophora malorum* Mo12 from the Mid-Atlantic Ridge Reveals Its Biotechnological Potential

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***Cadophora malorum* Mo12 was isolated from the Rainbow hydrothermal site on the Mid-Atlantic Ridge. We present the draft genome sequence of this filamentous fungal strain, which has high biotechnological potentials as revealed by the presence of genes encoding biotechnologically important enzymes and genes involved in the synthesis of secondary metabolites.**

Received 14 April 2016 Accepted 23 May 2016 Published 7 July 2016

Citation Rédou V, Kumar A, Hainaut M, Henrissat B, Record E, Barbier G, Burgaud G. 2016. Draft genome sequence of the deep-sea ascomycetous filamentous fungus *Cadophora malorum* Mo12 from the Mid-Atlantic Ridge reveals its biotechnological potential. *Genome Announc* 4(4):e00467-16. doi:10.1128/genomeA.00467-16.

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Cadophora malorum is a filamentous fungus that has been largely reported in Antarctica in lakes (1) or on mosses (2) and even macroalgae (3). Ecophysiological analysis demonstrated that *Cadophora* spp. isolated from Antarctic environments were psychrotrophs (4), popularizing the idea that *Cadophora* sp. strains (including *C. malorum*) were strongly adapted to extreme environments. The strain *Cadophora malorum* Mo12 (UBOCC 108058) was isolated from the Mid-Atlantic Ridge endemic shrimp *Rimicaris exoculata* at the Rainbow hydrothermal site and characterized as a halophilic psychrotrophic fungus (5).

Here, we describe the draft genome sequence of *C. malorum* Mo12 (UBOCC 108058) as a putative producer of original bioactive compounds. High-quality genomic DNA was extracted using the hexadecyltrimethylammonium bromide (CTAB) and Genomic-tip (Qiagen) methods. Genomic DNA of *Cadophora malorum* Mo12 was used to generate shotgun and mate-pair libraries with insert sizes of approximately 350 bp and 8 kb, respectively. A shotgun library was made using the TruSeq DNA PCR-free sample preparation kit and a gel-plus mate-paired-end library was generated with the Nextera mate-pair sample preparation kit. Genome sequencing was performed using Illumina HiSeq 2500 sequencing technologies.

The shotgun library produced 39,507,284 reads. The mate-pair library produced 15,277,956 reads. After quality filtering, reads with more than 90% of bases with base quality greater than or equal to Q20, a total of 28,200,910 shotgun reads (2,848 Mb) and 8,857,004 mate-pair reads (815 Mb), were retained. The ALLPATHS-LG whole-genome shotgun assembler (6) was used for the creation of the *de novo* genome assembly from these short reads. The assembly contained a total of 164 scaffolds with an average read length of 299,210 bp. The N_{50} was 1,408 kb, and the maximum contig length was 1,707 kb. The total sequence length

of the resulting draft genome was 54,281,849 bp, with an overall GC content of 47.08%. A total of 374,040 bp were repeats, representing 0.76% of the assembled genome size as predicted by repeat masker tool (<http://www.repeatmasker.org/>). Gene prediction was performed using Augustus 3.0 (7), producing 17,781 protein-coding genes. Our Blast2GO-based annotation analyses (8) have revealed 79% of annotated genes while 21% remained unannotated. The genome analysis of secondary metabolite biosynthesis gene clusters using antiSMASH 3.0 software (9) highlighted the presence of 6 type I polyketide synthases, 5 nonribosomal peptide synthetases, 2 hybrid polyketide synthase/nonribosomal peptide synthesis (PKS/NRPS), and 2 terpene synthases genes. Analysis of the sequence with the CAZy database (10) identified 230 genes with activity involving carbohydrates, including 101 glycoside hydrolases, 74 glycosyltransferases, 1 polysaccharide lyase, 10 carbohydrate esterases, 29 carbohydrate-binding modules, and 15 auxiliary activities. As expected, the array of genes encoding enzymes for the deconstruction of terrestrial plant cell walls is very reduced and the genome does not encode any cellulase. Interestingly, the genome of *Cadophora malorum* Mo12 encodes a candidate alginate lyase, perhaps reflecting adaptation to marine carbohydrates. Due to the significant potential for synthesis of secondary metabolites and the presence of a particular portfolio of genes encoding carbohydrate-active enzymes, we believe that the genome sequence of *Cadophora malorum* Mo12 (UBOCC 108058) will result in the discovery of useful gene products that may be exploited for biotechnological application.

Nucleotide sequence accession numbers. The nucleotide sequence of the *Cadophora malorum* UBOCC 108058 (Mo12) genome is deposited in DDBJ/EMBL/GenBank under accession numbers [FKJQ01000001](https://www.ncbi.nlm.nih.gov/nuccore/FKJQ01000001) to [FKJQ01000591](https://www.ncbi.nlm.nih.gov/nuccore/FKJQ01000591). This paper describes the first version of the genome.

ACKNOWLEDGMENTS

We thank Macrogen Inc. (South Korea) for genome sequencing and assembly.

This study was granted by the UE project MaCuMBA (Marine Microorganisms: Cultivation the Methods section for Improving their Biotechnological Applications, FP7, grant agreement 311975, Brussels, Belgium).

FUNDING INFORMATION

This work, including the efforts of Vanessa Rédou, was funded by EC | Seventh Framework Programme (FP7) (311975).

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