

Draft Genome Sequence of *Cladonia macilenta* KoLRI003786, a Lichen-Forming Fungus Producing Biruloquinone

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The lichen-forming fungus *Cladonia macilenta* strain KoLRI003786 is capable of producing an acetylcholinesterase inhibitor, biruloquinone, which effectively prevents neurodegeneration in Alzheimer's disease. Laying the foundation to unravel the biruloquinone biosynthetic pathway, we present the 37.11-Mb draft genome sequence of strain KoLRI003786.

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Lichens are remarkable symbionts with a vault of potentially valuable chemical compounds as secondary metabolites. Biruloquinone is one such high-value metabolite produced by lichen-forming fungi and belongs to the *ortho*-phenanthraquinone group. It has been shown to be a potent antioxidant and an effective preventative agent against neurodegeneration in Alzheimer's disease (AD) (1). Two lichen-forming fungi, *Parmelia birulae* (2) and *Cladonia macilenta* (1), are currently known to produce this chemical. In particular, a mass liquid culture system for the production of biruloquinone by *C. macilenta* has been established (1). However, no information is available on the genes that are responsible for the biosynthesis of biruloquinone in these fungi.

C. macilenta strain KoLRI003786 was isolated from rotten bark at Mt. Cangshan (26°31'52.7"N, 100°02'14.0"E), Yunnan Province, China, in 2005. DNA from an axenic culture of the fungus was extracted using the DNeasy mini kit (Qiagen, Valencia, CA). Sequencing was performed using a whole-genome shotgun strategy with Illumina HiSeq 2000 (Macrogen, Inc., Seoul, Korea). The total size of the assembled genome of *C. macilenta* KoLRI003786 is 37,117,081 bp, with a G+C content of 44.68%, representing 540-fold coverage. The short reads were assembled by using Allpaths-LG (3), yielding 240 scaffolds ($\geq 1,000$ bp) generated from 1,310 contigs. Gene prediction was performed by using MAKER (4), producing 7,322 protein-coding sequences. According to three gene family pipelines (5–7), 141 transcription factor (TF) genes, 58 cytochrome P450 genes, and 1,362 genes encoding secretory proteins were predicted. In addition, 8 putative polyketide synthase genes, containing ketoacyl synthase, acyl-transferase, and acyl carrier domains, were predicted by a domain search (8).

The genome sequence of *C. macilenta* KoLRI003786 is a valuable resource to identify the genes for the biosynthesis of biruloquinone and many other chemicals, and it also serves as a platform to facilitate comparative genomics with other lichen-forming fungi, as well as species in the phylum *Ascomycota*.

Nucleotide sequence accession numbers. The draft genome sequence of *C. macilenta* KoLRI003786 has been deposited in DDBJ/EMBL/GenBank under the accession no. [AUPP000000000](https://www.ncbi.nlm.nih.gov/nuccore/AUPP000000000). The version described in this article is the first version, accession no. AUPP01000000.

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