Data in brief

Draft genome sequence of the docosahexaenoic acid producing thraustochytrid Aurantiochytrium sp. T66

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Abstract

Thraustochytrids are unicellular, marine protists, and there is a growing industrial interest in these organisms, particularly because some species, including strains belonging to the genus Aurantiochytrium, accumulate high levels of docosahexaenoic acid (DHA). Here, we report the draft genome sequence of Aurantiochytrium sp. T66 (ATCC PRA-276), with a size of 43 Mbp, and 11,683 predicted protein-coding sequences. The data has been deposited at DDBJ/EMBL/Genbank under the accession LNGJ00000000. The genome sequence will contribute new insight into DHA biosynthesis and regulation, providing a basis for metabolic engineering of thraustochytrids.

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Keywords:
Thraustochytrid
Aurantiochytrium
Whole genome sequencing
Docosahexaenoic acid

Specifications

| Organism/cell line/tissue | Aurantiochytrium sp. T66 |
|---------------------------|--------------------------|
| Sex                       | N/A                      |
| Sequecer or array type    | Illumina HiSeq 2 × 100 bp paired-end and Roche 454 FLX ++ |
| Data format               | Analyzed                 |
| Experimental factors      | DNA extracted from a pure strain, no treatment |
| Experimental features     | Draft genome sequencing  |
| Consent                   | N/A                      |
| Sample source location    | The coast of Madeira, Portugal |

1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/bioproject/?term=LNGJ000000000

2. Introduction

Eicosapentaenoic acid (EPA; 20:5n−3), docosapentaenoic acid (DPA; 22:5n−3), and docosahexaenoic acid (DHA; 22:6n−3) are the main long chain polyunsaturated omega-3 fatty acids (ω-3 LC-PUFA). Over the past decades, the importance of ω-3 LC-PUFA in many aspects of human health, including brain and neural development, cardiovascular function and immune system regulation has been uncovered [1–4]. At present, marine fish and fish oils are the main sources of EPA and DHA. However, the need for new sustainable ω-3 LC-PUFA sources has attracted increasing attention in recent years [5,6].

Aurantiochytrium spp. belong to the thraustochytrids, which are unicellular, heterotrophic, marine protists, abundant in marine water, and able to grow on various carbon sources [7]. Recent studies have demonstrated that Aurantiochytrium spp. can be cultivated to high cell densities and produce biomass with up to 70% lipids of the dry cell weight, and up to 70% of the lipids may be DHA [8]. In a previous study of Aurantiochytrium sp. strain T66 (ATCC PRA-276), we demonstrated that its lipid content and fatty acid profile can be manipulated by changing the growth conditions [9]. The genetic, regulatory, and biochemical basis of DHA biosynthesis in thraustochytrids are largely unknown due to the scarcity of genome sequences. The genome sequences of the two thraustochytrids Schizochytrium sp. CCTCC M209059 [10] and Quahog Parasite Unknown (QPX) [11] as well as transcriptomes of QPX [12] and Aurantiochytrium sp. SD116 [13] were recently published. Here, we report the draft genome sequence of Aurantiochytrium sp. strain T66.

3. DNA extraction, library construction and sequencing

Aurantiochytrium sp. strain T66 was isolated from a mixture of marine sediment and seawater sampled from the coast of Madeira, Portugal [14]. Total genomic DNA was isolated with the Blood & Cell culture DNA kits (Qiagen, Hilden, Germany). DNA quality was assessed by gel electrophoresis, and the purity and quantity were determined by the
Nanodrop 1000 UV–Vis spectrophotometer (Thermo Scientific) and Qubit 2.0 fluorometer using the Qubit® dsDNA BR Assay Kit (ThermoFisher Scientific). The genome of Aurantiochytrium sp. T66 was sequenced using the Illumina HiSeq 2 × 100 bp paired-end and Roche 454 FLX + + platforms at Eurofins Genomics GmbH, Ebersberg, Germany. Three libraries of Illumina HiSeq were prepared (shotgun, 8 kbp and 20 kbp long jumping distance libraries). Following quality clipping and adapter trimming by Trimmomatic version 0.30 [15], genome sequence assembly was achieved by the combination of Velvet version 1.2.10 [16], Newbler v2.9 (454 Life Sciences), and Convey GraphConstructor (Cnykmer, Cnygc v2.2.5526, http://www.conveycomputer.com/). Gene prediction was done by a combination of homology-based approaches and de novo predictions [17–21].

4. Data analysis and results

The cleaned data output of Illumina HiSeq were 4.8 Gbp, 5.0 Gbp, and 3.6 Gbp, which represent estimated genome coverages of 102-fold, 115-fold and 82-fold, respectively. Roche 454 FLX + + sequencing resulted in 179 Mbp of cleaned data corresponding to an estimated genome coverage of 4.1-fold. The draft genome of Aurantiochytrium sp. T66 is 43 Mbp, with a G + C content of 62.8%, distributed on 495 large scaffolds (≥1000 bp) with an N50 length of 1,342,793 bp, L50 count of 3, N75 length of 594,063 bp, and a N50 length of 115,579 bp. A total of 11,683 putative protein-coding genes, 112 tRNA genes, 20 rRNA genes and 4 snRNA genes were predicted. Repetitive regions were estimated to comprise 7.1% of the genome. The Aurantiochytrium sp. T66 draft genome sequence generated in this study represents a new source of information that can be used as a reference to study thraustochytrids and it will help to further understand the genetic mechanisms of DHA biosynthesis and regulation. It will also be valuable in comparative genomic studies of other Aurantiochytrium sp. strains as well as for metabolic engineering of thraustochytrids.

5. Nucleotide accession number

This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession LNGJ00000000.

Conflict of interest

The authors declare that there is no conflict of interests on the work published in this paper.

Acknowledgments

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