

1 **The Complete Chloroplast Genome of *Tetraselmis desikacharyi*** 2 **(Chlorodendrophyceae) and Phylogenetic Analysis**

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14 *Tetraselmis desikacharyi* is a marine alga, known as an important plankton for
15 aquaculture as a feed organism. However, the genomic study on this class is rare.
16 Here, we present a complete Chlorodendrophyceae chloroplast genome of *T.*
17 *desikacharyi*, belonging to Chlorodendrophyceae with a full length of 149,934bp,
18 characterized by a very small single-copy (SSC) region without any genes and a large
19 inverted repeat (IR) region. A maximum-likelihood (ML) phylogenetic analysis was
20 performed using three kinds of data comprising 50 protein-coding genes, which
21 placed the Chlorodendrophyceae as a deep-diverging lineage of the core Chlorophyta.

22 *T. desikacharyi*, characterized by their intense green colored chloroplast, is
23 important for aquaculture as a feed organism, and for studying plankton growth cycles
24 due to their fast growth rate (Arora et al., 2013; Norris et al., 1980). However, only

two chloroplast genomes have been published in the past years for Chlorodendrophyceae (Turmel et al., 2016), which makes the phylogenetic relationship between Chlorodendrophyceae and UTC clade (Ulvophyceae, Trebouxiophyceae, Chlorophyceae) a mystery.

Here, we reported a complete chloroplast genome of *T. desikacharyi*. The samples were collected from marine environment at Rochigou, Ile de Batz, Bretagne, France (48°44'43"N, 4°00'35"W). The voucher specimen has been deposited in the Culture Collection of Algae at the University of Cologne (Strain number: CCAC 0023) and were grown in Waris-H culture medium (<http://www.ccac.uni-koeln.de/>) (McFadden and Melkonian, 1986). Total DNA was extracted using a modified CTAB protocol (Sahu et al., 2012). BGISEQ-500 platform was used to generate approximately 50Gb high quality, paired-end (100bp) reads. CLC-Assembly-Cell-5.1.1 (<http://www.clcbio.com/>) was used to remove the adapter and unpaired reads. The complete chloroplast genome was assembled by the seed-extension-based *de novo* assembler NOVOPlasty2.5.9 (Dierckxsens et al., 2017), based on an *rbcL* seed gene sequence of *Chlamydomonas reinhardtii*. The assembled chloroplast genome was annotated using a web-based program GeSeq (Tillich et al., 2017), and the protein-coding genes were further annotated by GeneWise v2.4.1 (Birney and Durbin, 2000). The plastid genome has been submitted to the CNGB Nucleotide Sequence Archive (CNSA: <https://db.cngb.org/cnsa>; accession number: CNP0000390).

The complete plastid genome of *T. desikacharyi* has a total length of 149,934 bp, with a typical quadripartite structure composed of a large single-copy (LSC) region (71,639bp) and an SSC region (1,611bp) interspersed between the IRa/b region (38,343bp). It encodes a total of 81 protein-coding genes, 6 ribosomal RNAs, and 37

49 transfer RNAs.

50 To further investigate its phylogenetic position, a maximum likelihood
51 phylogenetic tree was generated using RAxML based on complete chloroplast
52 genome sequences along with 20 other Chlorophyta species. Three different data sets
53 were used for the phylogenetic tree construction: (1) all nucleotide positions; (2) the
54 first and second codon nucleotide positions; (3) the amino acid of 50 protein-coding
55 genes. GTRCAT (PROTGAMMAWAG for AA) model was used with 500 bootstraps.
56 The results revealed that the phylogenetic relationship using the three different data
57 sets were highly consistent at the family level, which places the Chlorodendrophyceae
58 as a deep-diverging lineage of the core Chlorophyta (Figure 1).

59 **Disclosure statement**

60 No potential conflict of interest was reported by the authors

61 **Funding**

62 Financial support was provided by the Shenzhen Municipal Government of China
63 (grant numbers No. JCYJ20151015162041454). This work is part of the 10KP project
64 led by BGI-Shenzhen and China National GeneBank.

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