

Supplementary Information

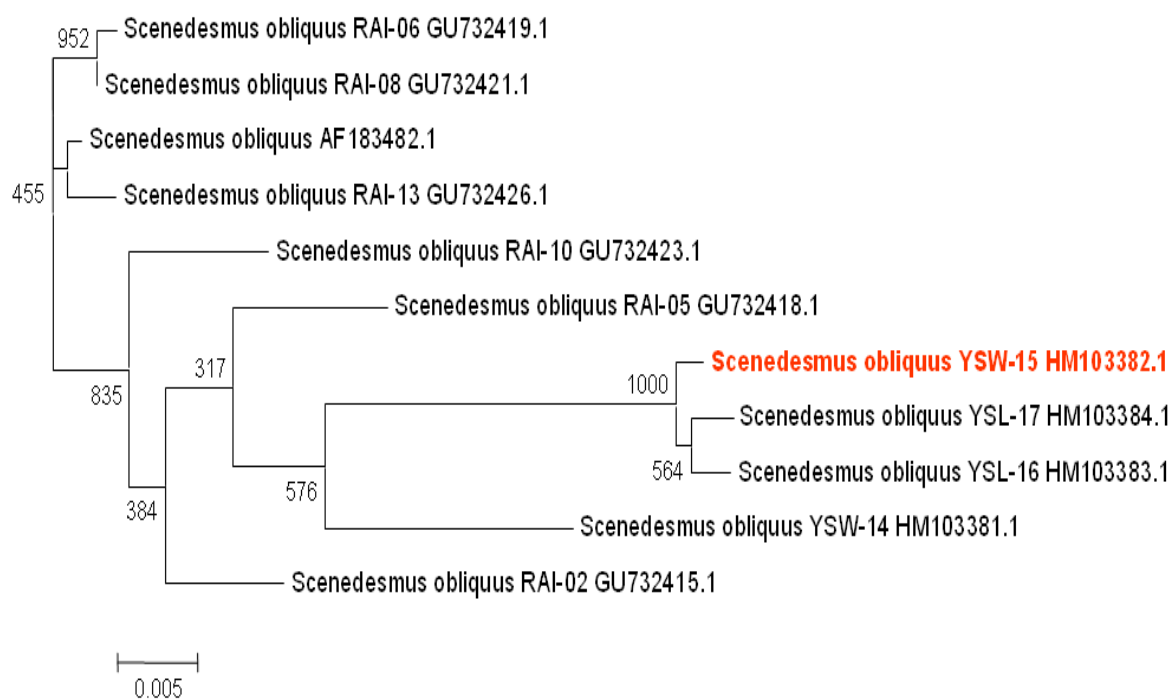
LSU-rRNA (D1-D2) coding region amplification and sequence

PCR amplification of the genomic DNA isolated from microalga with the universal forward and reverse primers was conducted. A single band of amplified LSU rDNA (D1-D2) product with a size of ~ 850-bp was recorded. The LSU-rRNA gene has a higher evolutionary rate compared with the SSU-rRNA gene¹ and should offer a better tool for the discrimination of closely related species using short diagnostic sequences. The DNA sequence was published in the NCBI databases under the specific accession number (HM103382). The phylogenetic tree constructed using MEGA 4.0 for the isolated strain (*S. obliquus* YSW15) was obtained from the LSU-rDNA D1-D2 sequence (SI Fig. 1). The LSU-rDNA sequence analysis showed that the isolated YSW15 can be ascribed to the *S. obliquus* AF183482 with a similarity of 97% (SI Table 1).

SI Table 1. The accession number, base pair length of the DNA fragment, and the similarity between amplified sequence and the closest relative sequence of the microalgae isolated from Wonju Wastewater Treatment Plant

Microalgae strain	Accession number	Length (nt ^a)	Closest relative and GenBank accession number	Similarity (%)
<i>Scenedesmus obliquus</i> YSW15	HM103382	864	<i>Scenedesmus obliquus</i> AF183482	97

^a nucleotide



SI Fig 1. Phylogenetic tree showing the relationship between the LSU rDNA D1-D2 sequence of *Scenedesmus obliquus* YSW15 and the most similar sequences retrieved from the GenBank database.

Reference

1. R. Sonnenberg, A. W. Nolte, D. Tautz, *Front Zool.*, **4**, 1-12.