

Supplementary Material

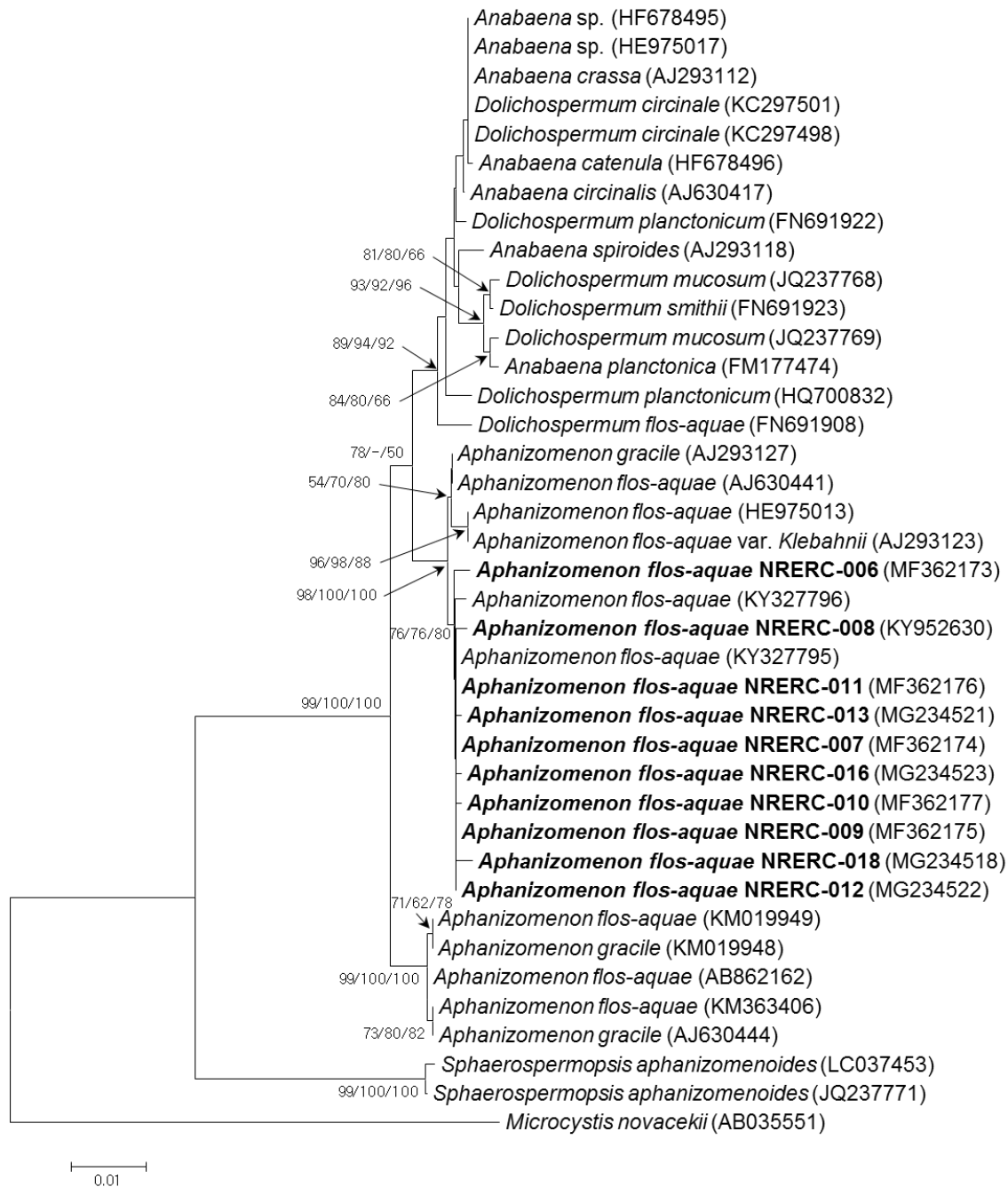


Figure S1. Neighbor-Joining (NJ) tree of 16S rRNA sequences from *Aphanizomenon flos-aquae* and Nostocales cyanobacterial strains. *Microcystis novacekii* (AB035551) was used as an outgroup. The numbers at the nodes indicated levels of bootstrap support (%) based on Neighbor-Joining (NJ), Maximum likelihood (ML), and Maximum parsimony (MP) analysis of 1,000 resampled datasets. Only bootstrap values (NJ/ML/MP) above 50% are shown at the nodes. Strains of the present study are marked in bold and the GenBank accession numbers for 16S rRNA gene sequences are shown in parentheses. The scale bar indicates substitutions per site.

Table S1. Nucleotide sequence of 16S-23S rRNA ITS of *Aphanizomenon flos-aquae* isolated from the Nakdong River. Sequence direction is 5' to 3'.

Type-1		
1	TAGGGAGACCTAATCCATTTAGAAATCGAAGGTGATGAAAATTGCCAATA	50
51	GAAACTAAATTGGTCTAACCTAGGTCGGTCGAGATTGGGAAAAATCTTTC	100
101	AAAGTATTATTTCCGGCTTAGTTAAATAGGAAAAAAGACAGCACCTAACTA	150
151	TAAAAGTTAGAATGCTGGATGAAATTCCAGTCAGAACCTTGAAAACCTGCA	200
201	TAAGAGAAAGAGAAAAAGCACCGCAGACACAGACATTTAGATGGATGTGG	250
251	AAGCAAAAGAAATTGT	266
Type-2		
1	TAGGGAGACCTAATCCATTTAGAAATCGAGGGTGTGAAAATTGCTAATA	50
51	GAAACTAAATCGGTCTAACCTAGGTCGGTCGCAGACTTGAAAGTAAAGCTT	100
101	TCAAACATGATTTGGTTCGATAAGGGCTATTAGCTCAGGTGGTTAGAGC	150
151	GCACCCCTGATAAGGGTGAGGTCCCTGGTTCGAGTCCAGGATGGCCACC	200
201	TGAAGGAAGTCAAAAATCAAAAAGTCAAAAAGTCAAAAAGTAAATATTTTGA	250
251	GCCGTGACTATAAATTTTGGATTCTTTTTGGGGTTTAGCTCAGTTGGTA	300
301	GAGCGCTGCTTTGCAAGCAGGATGTCAGCGGTTTCGAGTCCGCTAACCTC	350
351	CACATTGGAAAAAAGACAGCACCTAACTATAAAAAGTTAGAATGCTGGATG	400
401	AAATTCAGTCAGAACCTTGAAAACCTGCATAAGAGAAAAGAGAAAAAGCAC	450
451	CGCAGACACAGACATTTAGATGGATGTGGAAGCAAAAGAAATTGT	495