

Molecular Characterization of Twenty-Five Marine Cyanobacteria Isolated from Coastal Regions of Ireland

Supplementary Material

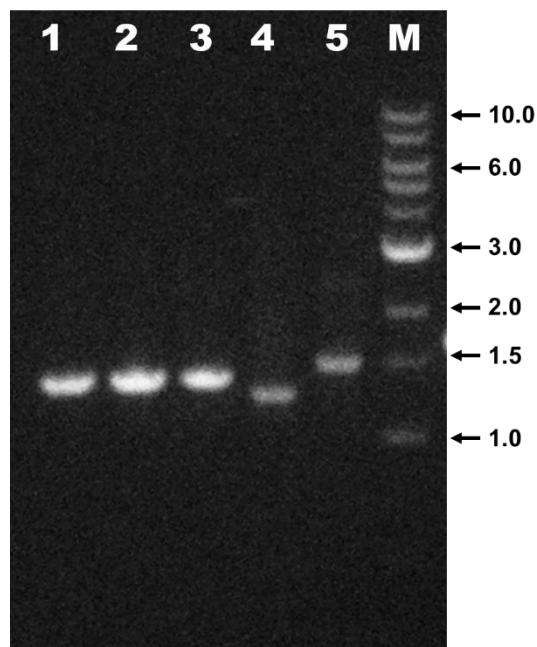


Figure S1. Representative 1% agarose gel showing PCR amplified products of 16S rRNA gene of selected cyanobacteria. Lane 1, *Chlorogloea microcystoides* SABC011701; Lane 2, *Chlorogloea microcystoides* SABC022904; Lane 3, *Kamptонема оkenii* SABC011902; Lane 4, *Tychonema decoloratum* SABC011901; Lane 5, *Leptolyngbya valderiana* SABC022801; M, 1 kb DNA ladder (New England Biolabs).

CLUSTAL O(1.2.4) multiple sequence alignment

Figure S2. Alignment of 16S rRNA gene sequences of *Hyella patelloides* LEGE 07179 (*Hyella patelloides*) and *Hyella gigas* SABC011201 (*Hyella gigas*).

Figure S3. Alignment of 16S rRNA gene sequences of *Typhonema decoloratum* SABC011901 (TycDec) and *Kamptonema okenii* SABC011902 (KamOke).

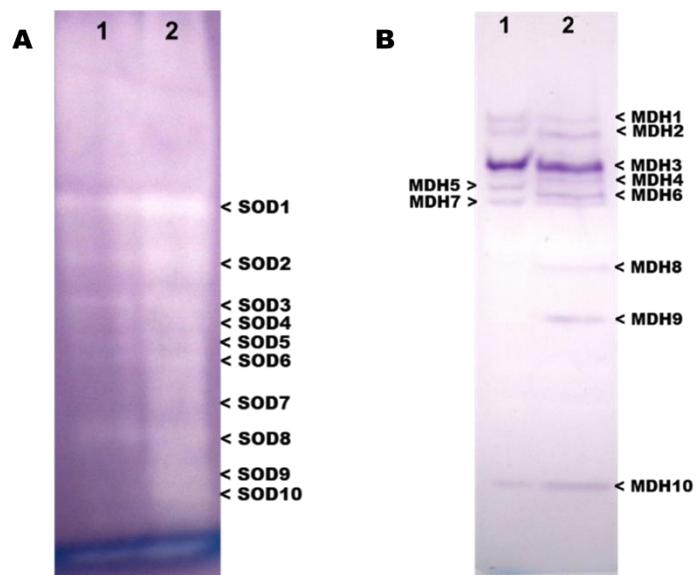


Figure S4. Native-PAGE gels showing superoxide dismutase (SOD) (A) and malate dehydrogenase (MDH) (B) isoenzymes profile of *Tychonema decoloratum* SABC011901 (lane 1) and *Kamptonema okenii* SABC011902 (lane 2).