



Figure S2. Maximum likelihood trees of *Tetradesmus* based on sequences of individual genes. Numbers associated with the nodes represent the bootstrap support values over 50% based on 1000 heuristic search replications. Aquatic strains are labeled in blue, strains isolated from desert soil crusts and other arid substrates are labeled in orange boldface font. (A) Best ML tree based on *tufA* gene (lnL = -2171.473). (B) Best ML tree based on the sequences of *rbcL* gene (lnL = -1645.418). (C) Best ML tree based on the sequences of ITS2 rDNA spacer (lnL = -987.906), and selected related genera, individual genes. Our ITS2 data set included a newly described species *T. arenicola* isolated from biological soil crusts on sand dunes along the Baltic Sea coast (Mikhailyuk et al. 2018). Sequences of *tufA* and *rbcL* were not generated in the other single gene analyses or the concatenated data set.