SUPPLEMENT

Additional parameters of phylogenetic analysis. Homologous sequences were searched against NCBI GenBank (nucleotide collection nr/nt database) using BLAST (http://blast.ncbi.nlm.nih.gov/) [1]. Sixteen ITS1–5.8S rRNA–ITS2 sequences of microalgae from genus *Dunaliella*, and ITS1–5.8S rRNA–ITS2 fragment of *Spermatozopsis similis* (Dunaliellaceae) as outgroup were taken for analysis (table). Sequence data analysis was conducted in MEGA 6.06 [2]. Multiple alignment was performed using MUSCLE software [3] with default parameters. The analysis involved 19 (16 sequences from NCBI GenBank (table) and three sequences of interest) nucleotide sequences. All positions containing gaps and missing data were eliminated. Because the substitution rate of 5.8S rRNA gene is much slower than that of ITS1 and ITS2, this fragment was excluded as described in [4]. The final dataset contained 309 positions. The optimal model of DNA evolution for maximum likelihood (ML) analysis [5] was found in MEGA 6.06 under Bayesian Information Criterion (BIC) [6] with default parameters. The lowest BIC score corresponded to Tamura 3-parameter model (T92) [7]. A discrete Gamma distribution was used to simulate evolutionary rate differences among sites (five categories, +G parameter was 0.37). Nucleotide frequencies (f) and probabilities of the substitutions (r) as well as transition/transversion bias (R) were calculated: f(A) = 0.227; f(T) = 0.227; f(G) = 0.273; f(C) = 0.273; r(AT) = 0.035; r(AG) = 0.189; r(AC) = 0.042; r(CT) = 0.158; r(CG) = 0.042; r(GT) = 0.035; r(TA) = 0.035; r(TC) = 0.189; r(CA) = 0.035; r(GA) = 0.158; r(GC) = 0.042; R = 2.24.

A phylogenetic tree was constructed with the ML algorithm (using K2 + G; other parameters were default) as well as neighbor-joining (NJ) [8] and minimum evolution (ME) algorithm [9] under default parameters in MEGA 6.06. The accuracy of the tree topology was tested using bootstrap analysis [10] with 1000 replicates.

Sequences selected from the database NCBI GenBank for the phylogenetic analysis (see “Materials and Methods”)

Strain	Origin	GenBank ID	References
Dunaliella tertiolecta Dtsi	Italy: Venezia	EF473730.1	unpublished
Dunaliella tertiolecta SAG 13.86	Norway: Oslofjord, marine	EF473738.1	http://sagdb.uni-goettingen.de/
Dunaliella tertiolecta ATCC 30929	United Kingdom: Plymouth, marine	EF473742.1	http://www.lgcstandards-atcc.org/
Dunaliella salina CCAP 19/3	Soviet Union: dirty salt lake	KJ094609.1	http://www.ccap.ac.uk/
Dunaliella salina 9802	China	EF695405.1	unpublished
Dunaliella salina Ds18S3	unknown	FJ360758.1	unpublished
Dunaliella salina KMMCC 1064	hypersaline; hypersaline brines, Hutt Lagoon, Western Australia	JQ315780.1	[11]
Dunaliella parva CCAP 19/9	salt marsh, Northey Island, Essex, England	KJ094617.1	http://www.ccap.ac.uk/
Dunaliella salina CCAP 19/20	marine	KJ094624.1	http://www.ccap.ac.uk/
Dunaliella parva CCAP 19/26	unknown	KJ094630.1	http://www.ccap.ac.uk/
Dunaliella tertiolecta CCAP 19/27	Halifax, Canada	KJ094631.1	http://www.ccap.ac.uk/
Dunaliella salina CCAP 19/30	marine; salt pond, nr. Bardawil Lagoon, North Sinai, Israel	KJ094632.1	http://www.ccap.ac.uk/
Dunaliella salina CCAP 19/39	marine; sea salt sample from Arinaga Saltwork, Gran Canaria, Spain	KJ094637.1	http://www.ccap.ac.uk/
Dunaliella parva SAG 19-1	Romania, Lacul Sarat	DQ377091.1	http://sagdb.uni-goettingen.de/
Dunaliella tertiolecta CCMP 1302	Baja California, Mexico	DQ377096.1	https://ncma.bigelow.org/
Spermatozopsis similis SAG B1-85	United Kingdom, Cambridge, pond near Madingley	X69488.1	http://sagdb.uni-goettingen.de/

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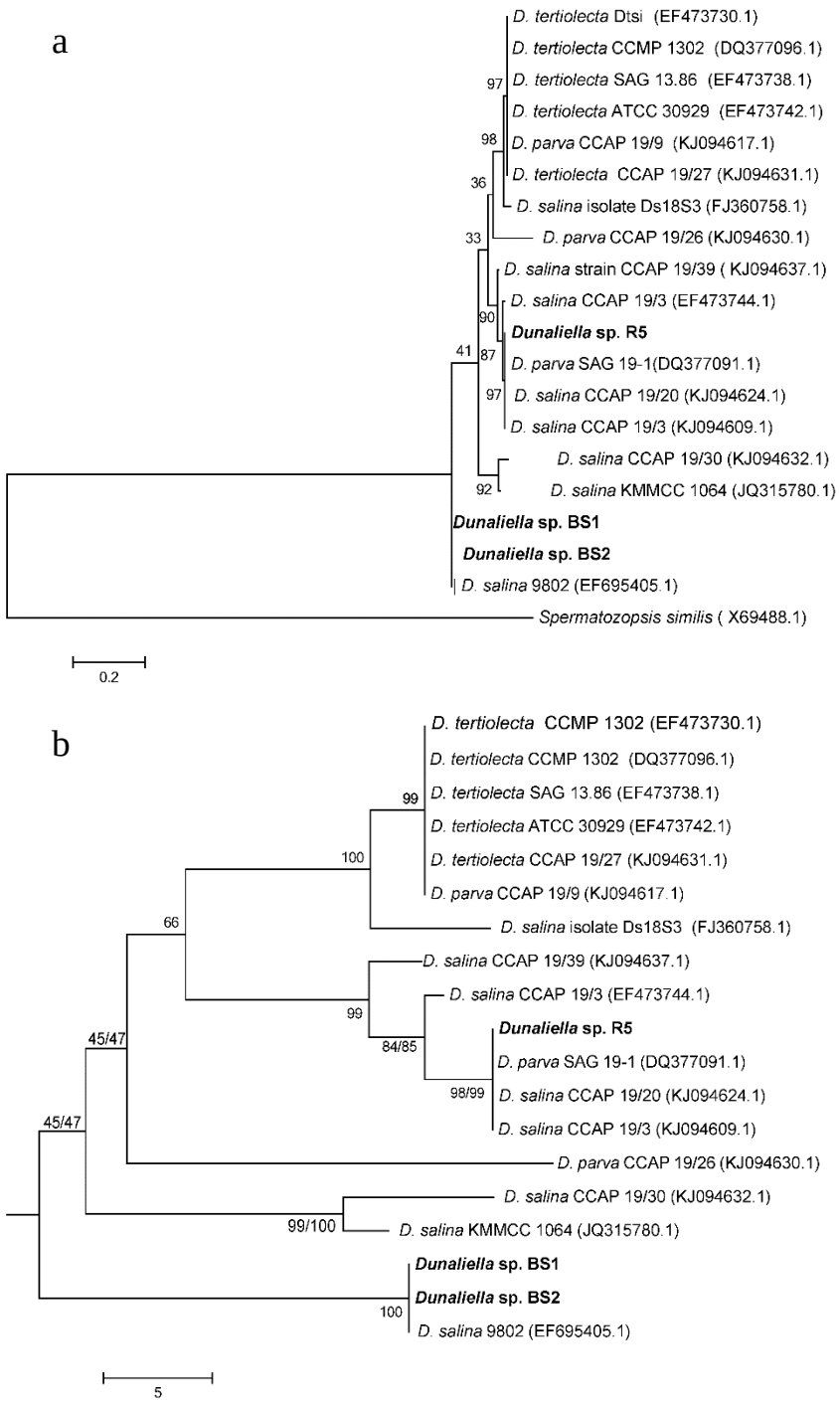

Fig. S1. Evolutionary relationships of strains *D. viridis* R5 and *D. salina* BS1 and BS2 based on the ITS1–5.8S rRNA–ITS2 sequences. The phylogenetic trees generated using (a) ML and (b) NJ/ME algorithms are shown, numbers are the results of the bootstrap test (see "Materials and Methods").

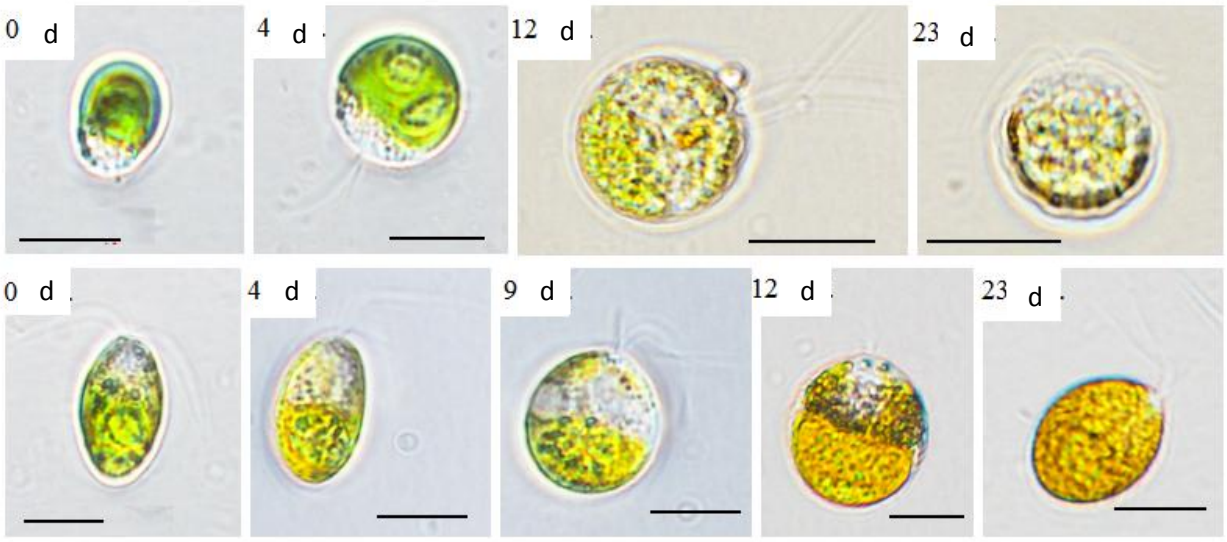

Fig. S2. Changes in the morphology of the *D. viridis* R5 (top) and *D. salina* BS1 (bottom) cells in the course of cultivation (cultivation time is specified on the figure) in medium containing 160 g/liter NaCl at 480 μmol quanta/(m^2·s). Scale bar: 10 μm.