

1 Details of molecular strain characterisation. Characterisation of the strains started with the
2 determination of their ITS1 lengths by PCR and agarose gel electrophoresis. For this PCR, a
3 new *Ectocarpus*-specific forward primer which annealed in the last variable loop near the 3'-
4 end of the SSU gene was used in combination with a more general reverse primer which
5 annealed to the 5.8S gene (Supplementary Table 1). The PCR product contained the entire
6 ITS1 with 224bp of flanking sequences (129bp from SSU, 95bp from 5.8S). The same primer
7 pair was used for subsequent sequencing of ITS1 in at least one member of each ITS1 length
8 type per locality, thereby obtaining the ITS1 genotypes (GT). Because three ITS1 genotypes
9 (incl. that of the genome strain; GT4) had an ITS1 length of ca. 350 bp but nevertheless
10 exhibited significant sequence differences (see Results), a genotype-specific reverse primer
11 was designed based on a motif in the highly variable first part of the ITS1 of the genome
12 strain to test all strains with this particular ITS1 length of ca. 350 bp. In combination with the
13 *Ectocarpus*-specific forward primer it amplified a fragment of 169bp. ITS1 was sequenced in
14 strains for which this primer pair did not amplify a fragment; this led to the discovery of GT2.

15 Details of PCR and sequencing. PCR reactions were run in 12.5 or 18 µl volumes on a
16 Corbett Research (Mortlake, Australia) CGI-96 cyclor using Taq polymerase from MBI
17 Fermentas (Lithuania). The PCR protocols usually included 35 cycles, annealing at the
18 temperature corresponding to the primers (Supporting Table S1) and extension at 72°C for
19 90s except for the PCR with GT4-specific primer in which extension time at 72°C was 15s.
20 Direct cycle sequencing of PCR products was undertaken using the same primers and
21 annealing temperatures as for the PCR and the Applied Biosystems BigDye® Terminator
22 v3.1 Cycle Sequencing Kit according to the manufacturer's instructions. The products from
23 cycle sequencing were sent to a commercial sequencing facility (Source Bioscience plc,
24 Cambridge, United Kingdom) for processing.

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1 **Supporting Table S1.** Primers used for polymerase chain reaction (PCR) and sequencing. F and R in the end of
 2 primer names designate forward and reverse directions.

Organelle	Marker amplified	Primer Name	Sequence 5'-3'	Annealing	Reference
				T of PCR (°C)	
Nucleus	ITS1	EcSSU1695F†	GAGGATCTCGGATTTTGTG	53 and 60	New primer
		5.8S1R	TGATGATTCACTGGATTCTG	53	Peters <i>et al.</i> , 2004b
	begin of				
	ITS1	EcPeITS1R‡	AAGTTGCCCGCAGCATACA	60	New primer
	ITS2	5.8S3F	CGACGGATGTCTTGGCTC	50	Peters <i>et al.</i> , 2010
LSU410R		TCCTTCGCTTCCCTTTCAG	50	Peters <i>et al.</i> , 2010	
Mitochondrion	cox3	cox3F23	AGCTAAAATCRTTCAACGRCATC	48	Cho, unpublished
		cox3R20	AACAAARTGCCAATACCA	48	Cho, unpublished
Rubisco					
Plastid	spacer	rbcL1273F	GTGCGACAGCTAACCGTG	50	Peters <i>et al.</i> , 2004b
		rbcS139R	AGACCCCATTAATCCCAATA	50	Peters <i>et al.</i> , 2004b

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4 †Primer specific for *Ectocarpus* and *Kuckuckia*

5 ‡Primer specific for ITS1 of genome-sequenced strain; working with EcSSU1695F