Curr Genet (1992) 22:173

Current Genetics

© Springer-Verlag 1992

Erratum

On page 396 of the paper starting on page 395 of volume 19 there were unfortunately several errors. The paragraph concerned is now printed correctly below.

Curr Genet (1991) 19:395–398

Rubisco spacer sequence divergence in the rhodophyte alga *Gracilaria verrucosa* and closely related species

Christophe Destombe [1] **and Susan E. Douglas** [2]

[1] Institut Maurice Lamontagne, C. P. 1000, Mont Joli, Quebec G5H 3Z4, Canada
[2] Institute of Marine Biosciences, National Research Council, 1411 Oxford Street, Halifax, Nova Scotia B3H 3Z1, Canada

Received December 27, 1990

Materials and methods

Total DNA isolation and sequencing. Total DNA from the isolates used in the interpopulation study was donated by C. Bird and E. Rice. DNA from the five isolates used in the intrapopulation study was purified using the CTAB method of Doyle and Doyle (1990). Double-stranded DNA of the spacer region was amplified by the polymerase chain reaction (PCR) (Saiki et al. 1988). Primers were chosen from conservative regions of the small and large subunit genes by comparing the sequences of *Cryptomonas Φ* (Douglas et al. 1990), *O. luteus* (Boczar et al. 1989), *Porphyra linearis* (Douglas, unpublished) and *Gymnogongrus* sp. (Douglas et al., in preparation). Amplification primers (5′-TGTGGACCTCTACAAACAGC-3′ and 5′-CCCCATAGTTCCCAAT-3′) and internal sequencing primers (5′-GTGAGATTAACACAAGGAA-3′ and 5′-TTCCTT-GTGTTAATCTCAC-3′) were synthesized on a Milligen Biosearch Oligonucleotide synthesizer. Both strands of the amplified DNA were directly sequenced using a modification (Bachman et al. 1990) of the dideoxy chain termination procedure developed by Sanger et al. (1977) and the DNA sequencing kit "Sequenase 2.0" (US Biochemicals, Cleveland, Ohio).