Assessing *Symbiodinium* diversity in scleractinian corals via next-generation sequencing-based genotyping of the ITS2 rDNA region

CHATCHANIT ARIF,* CAMILLE DANIELS,* TILL BAYER,† EULALIA BANGUERA-HINESTROZA,* ADRIAN BARBROOK,‡ CHRISTOPHER J. HOWE,‡ TODD C. LAJEUNESSE§ and CHRISTIAN R. VOOLSTRA*  

*Red Sea Research Center, King Abdullah University of Science and Technology (KAUST), 23955 Thuwal, Saudi Arabia, †GEOMAR Helmholtz Centre for Ocean Research Kiel, 24105 Kiel, Germany, ‡Department of Biochemistry, University of Cambridge, Building O, Downing Site, Tennis Court Road, Cambridge, CB2 1QW, UK, §Department of Biology, Penn State University, University Park, PA 16802, USA

Abstract

The persistence of coral reef ecosystems relies on the symbiotic relationship between scleractinian corals and intracellular, photosynthetic dinoflagellates in the genus *Symbiodinium*. Genetic evidence indicates that these symbionts are biologically diverse and exhibit discrete patterns of environmental and host distribution. This makes the assessment of *Symbiodinium* diversity critical to understanding the symbiosis ecology of corals. Here, we applied pyrosequencing to the elucidation of *Symbiodinium* diversity via analysis of the internal transcribed spacer 2 (ITS2) region, a multicopy genetic marker commonly used to analyse *Symbiodinium* diversity. Replicated data generated from isoclonal *Symbiodinium* cultures showed that all genomes contained numerous, yet mostly rare, ITS2 sequence variants. Pyrosequencing data were consistent with more traditional denaturing gradient gel electrophoresis (DGGE) approaches to the screening of ITS2 PCR amplifications, where the most common sequences appeared as the most intense bands. Further, we developed an operational taxonomic unit (OTU)-based pipeline for *Symbiodinium* ITS2 diversity typing to provisionally resolve ecologically discrete entities from intragenomic variation. A genetic distance cut-off of 0.03 collapsed intragenomic ITS2 variants of isoclonal cultures into single OTUs. When applied to the analysis of field-collected coral samples, our analyses confirm that much of the commonly observed *Symbiodinium* ITS2 diversity can be attributed to intragenomic variation. We conclude that by analysing *Symbiodinium* populations in an OTU-based framework, we can improve objectivity, comparability and simplicity when assessing ITS2 diversity in field-based studies.

Keywords: coral reefs, dinoflagellates, internal transcribed spacer 2, next-generation sequencing, operational taxonomic unit, *Symbiodinium*

Introduction

Coral reef communities depend critically on the relationship between scleractinian corals and photosynthetic endosymbionts in the genus *Symbiodinium*. While the coral host provides a light-rich, sheltered environment and inorganic nutrients, the dinoflagellate algae provide photosynthetically fixed carbon (Muscatine & Cernichiarri 1969). Some corals seem to rely strictly on a distinct symbiont type, whereas others harbour different types of *Symbiodinium* (Rowan & Knowlton 1995). Although host identity is the primary predictor of symbiont identity, coral-associated *Symbiodinium* diversity also covaries with geographical location, water depth and health state (Rodriguez-Lanetty et al. 2001; Toller et al.

Received 16 April 2014; revision received 17 July 2014; accepted 18 July 2014

© 2014 The Authors. *Molecular Ecology* Published by John Wiley & Sons Ltd.

This is an open access article under the terms of the Creative Commons Attribution License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited.
2001; LaJeunesse et al. 2004, 2010; Sampayo et al. 2007; Macdonald et al. 2008; Finney et al. 2010; Tonk et al. 2013b). The current decline in coral reef cover resulting from global (e.g. ocean warming) and local (e.g. pollution, overfishing) anthropogenic factors has intensified the need to examine the spatial, geographical and ecological distribution of Symbiodinium–coral associations and how these relate to environmental extremes.

Various DNA markers have been used to describe genetic diversity within Symbiodinium (Sampayo et al. 2009). Rowan & Powers (1991) were the first to examine Symbiodinium evolutionary relationships using restriction fragment length polymorphisms (RFLPs) of the small ribosomal subunit RNA (SSU) gene from dinoflagellates from various marine invertebrate hosts. Their phylogeny identified divergent lineages within this genus, which exhibited sequence differences comparable to those observed among dinoflagellates from different taxonomic families and orders (Rowan & Powers 1992). These lineages are commonly referred to as clades. So far, nine clades are identified (clades A–I), of which representatives in six clades (i.e. A, B, C, D, F and G) have been shown to persist in association with corals, other cnidarians, giant clams and sponges (Baker 2003; Pochon et al. 2006). It was soon recognized that the conserved SSU gene is not able to resolve species (Rowan & Powers 1991; McNally et al. 1994; LaJeunesse 2001). Researchers turned to more variable DNA regions, including the nuclear large subunit (LSU) (Wilson 1998; Loh et al. 2001), the internal transcribed spacer regions (Hunter et al. 1997; LaJeunesse 2001; van Oppen et al. 2001), the chloroplast large subunit (cp23S) (Santos et al. 2002; Pochon et al. 2006) and cytochrome oxidase b (Sampayo et al. 2009). A systematic survey by Sampayo et al. (2009) targeting ribosomal, mitochondrial and chloroplast genes employing 13 distinct genetic analyses found that different markers showed remarkable concordance, but differed in their relative ability to resolve ecologically distinct units. Other rapidly evolving markers, including the chloroplast psbA noncoding region (Moore et al. 2003; LaJeunesse & Thornhill 2011) and microsatellites, were recently employed, often in combination with each other, to improve genetic resolution further and delimit species boundaries (Thornhill et al. 2014). Only recently, Barbrook et al. (2014) sequenced the entire chloroplast genome of a Symbiodinium sp. type C3, where individual genes reside on minicircles that will provide additional genetic markers. Currently, however, the ITS2 region is still the most commonly employed DNA marker used to assess Symbiodinium diversity from a diverse array of hosts and over large geographical distances (LaJeunesse et al. 2010; Wicks et al. 2010; Silverstein et al. 2011; Putnam et al. 2012; Tonk et al. 2013a).

LaJeunesse (2002) determined that ITS2, when analysed through targeting of numerically dominant intragenomic variants, provides sufficient resolution to resolve many ecologically distinct Symbiodinium spp. To achieve this, denaturing gradient gel electrophoresis (DGGE) was used to screen PCR amplifications for common ITS2 sequence variants diagnostic of a particular Symbiodinium ‘type’ (LaJeunesse 2002; Sampayo et al. 2007; LaJeunesse et al. 2010; Silverstein et al. 2011). More recently, researchers have also employed bacterial cloning and sequencing and found more sequence diversity within the populations of Symbiodinium residing in a host than identified with DGGE (Apprill & Gates 2007; Stat et al. 2009, 2011, 2013). Because rDNA represents an extreme example of a multicopy gene arrayed in tandem, intragenomic variation in the form of pseudogenes or numerous low-abundant functional variants affect how ITS2 data are interpreted (Thornhill et al. 2007; Sampayo et al. 2009; LaJeunesse & Thornhill 2011). For instance, it has been shown that cloning-and-sequencing-based approaches are potentially prone to inflated diversity estimates through the technique’s tendency to recover intragenomic variants that are of low abundance (i.e. limited diagnostic value), as well as by introducing additional sequence artefacts generated during the PCR and cloning steps (Thornhill et al. 2007). However, sequencing a substantial number of clones may resolve how rDNA data are best analysed and interpreted by allowing differentiation between intragenomic and interspecific ITS2 sequence variants, albeit at a high cost (Sampayo et al. 2009). Assessment has also shown that individuals from different species possess widely differing amounts of intragenomic variation (Thornhill et al. 2007), yet the full extent of this variation is at present unknown. In both regards, the application of pyrosequencing-based methods is projected to overcome the limited resolution and high cost associated with Sanger-based ITS2 diversity assessments, as a high number of sequences are produced at comparatively low cost per sequence.

While the study of prokaryotic diversity is now routinely conducted via pyrosequencing-based amplicon typing of the 16S ribosomal RNA gene (Sogin et al. 2006; Roesch et al. 2007), only a limited number of studies have utilized high-throughput sequencing to assess eukaryotic diversity. For instance, Stoeck et al. (2010, 2009) and Amaral-Zettler et al. (2009) sequenced the variable regions of the small subunit (SSU) and large subunit (LSU) of the 18S region to estimate eukaryotic diversity.

Pyrosequencing is now being applied to assess Symbiodinium diversity (Green et al. 2014; Quigley et al. 2014; Thomas et al. 2014), but there is a need to ground truth this new approach. In this study, we applied
pyrosequencing of ITS2 rDNA amplicons (320–360 bp) to genotype *Symbiodinium* diversity in several isoclonal and replicated cultures, two cultured isolates mixed at different ratios and field-collected coral specimens. The application of a high-throughput pyrosequencing approach holds the promise to improve assessment of the relative degree of sequence variation found in these eukaryotic genomes. Further, a pyrosequencing approach may provide a more accurate detection of low-abundance background *Symbiodinium*. Our aim was to understand diversity of the ITS2 gene at the genome level and to compare pyrosequencing results to data obtained from DGGE typing. Furthermore, we sought to analyse *Symbiodinium* diversity in an OTU-based framework in order to improve objectivity, comparability and simplicity when assessing ITS2 to study *Symbiodinium* composition in environmental samples of corals.

Materials and methods

**Sample collection and processing**

Isoclonal cultures of *Symbiodinium* sp. (CCMP2467: *Symbiodinium microadriaticum*, KB8: *S. microadriaticum*, rt-147: undescribed clade B type and rt-064: undescribed B1 type) were cultured at 23 °C in f/2 medium (Guillard & Ryther 1962) on a 12 h/12 h light–dark cycle (daytime: 6 am to 6 pm; nighttime: 6 pm to 6 am, light intensity 80 μmol/m²/s). The salt content in the medium was set to 40 g/L, matching the average salinity characteristic of the Red Sea. Coral samples were collected from various reefs in the Red Sea between 2011 and 2012 with SCUBA at depths between 4 and 12 m. More specifically, five specimens of *Pocillopora verrucosa* were collected from reefs at Maqna (*n* = 2), Al Wajh (*n* = 2) and Doga (*n* = 1) as well as one specimen of *Acropora hemprichii* from Al Fahal reef at Thuwal. Specimens of about 1–3 cm² tissue were collected with hammer and chisel and stored in Whirl-Paks during diving, subsequently washed with 0.22-μm-filtered sea water (FSW), preserved in DMSO/NaCl buffer (Gaither et al. 2010) and stored at 4 °C until further processing. For *Symbiodinium* culture DNA extraction, cells from each culture were counted using a haemocytometer (Hausser Symbiodinium culture DNA extraction, cells from each culture were used for DNA extraction. Mixed samples were generated by combining cells of two *Symbiodinium* species (a strain of *S. microadriaticum* CCMP2467 from clade A and strain rt-147 from clade B) in a ratio of 1:1 (4 × 10⁶ cells : 4 × 10⁶ cells) and in a ratio of 1:3 (2 × 10⁶ cells : 6 × 10⁶ cells), respectively. Cells were spun at 1934 g for 10 min and subsequently washed with DNase-free water. Five hundred microlitres of 0.5-mm sterile glass beads (BioSpec, Bartlesville, OK) was added to the pelleted cells together with 400 μL of buffer API and 4 μL RNase (Qiagen, Hilden, Germany). Samples were bead-beaten for 90 s with a Tissue Lyser II (Qiagen). DNA was isolated with the Qiagen DNeasy Plant Mini Kit (Qiagen) according to the manufacturer’s instructions. For the analysis of technical variation, DNA from isoclonal cultures of CCMP2467 and rt-147 was isolated once but amplified in distinct PCRs with a different barcoded primer. For DNA extraction of environmental samples, ~50 mg of coral tissue was transferred to 1.5-mL tubes (Eppendorf, Hamburg, Germany). Five hundred microlitres of 0.5-mm sterile glass beads (BioSpec) was added together with 400 μL of buffer API and 4 μL RNase (Qiagen). Samples were bead-beaten for 90 s with a Tissue Lyser II (Qiagen). DNA was isolated with the Qiagen DNeasy Plant Mini Kit (Qiagen) according to the manufacturer’s protocol.

**DGGE analysis of Symbiodinium ITS2 rDNA**

DGGE ITS2 diversity typing was performed following the protocol detailed in LaJeunesse (2002). Briefly, the *Symbiodinium* ITS2 region was amplified with the primer pair ITSinfor2 and ITS2CLAMP using PCR conditions described in LaJeunesse et al. (2003) with the following modifications: the annealing temperature was maintained at 52 °C for 27 cycles after 20 cycles of touchdown amplification. PCR products were mixed with 10 μL Ficoll-based loading buffer and concentrated by a speed vacuum before loading on an 8% polyacrylamide gel using a Cipher DGGE kit (CBS Scientific Company, Del Mar, CA). Gels were run at 150 V for 15 h, stained for 30 min with 1× SYBR Green (Invitrogen, Carlsbad, CA) and visualized on a Dark Reader Transilluminator (Clare Chemical Research, Dolores, CO). Prominent band(s) were excised from the DGGE gel with a sterile scalpel. Each band was transferred into an Eppendorf tube that contained 500 μL DNase-free water and incubated at 4 °C for 24 h. Two microlitres of this were used for reamplification as described in LaJeunesse (2002) and purified with Illustra ExoStar (SelectScience, Bath, UK) enzyme mix following the manufacturer’s instructions. Successful amplification was verified by running products on a 1% agarose gel stained with 1× SYBR Safe (Invitrogen). Samples were sent for bidirectional Sanger sequencing at the KAUST BioScience Core Laboratory (Thuwal, Saudi Arabia). Sequences were processed in CodonCode Aligner (CodonCode Corporation, Centerville, MA). After quality trimming, forward and reverse sequences were assembled into contigs. For phylogenetic assignment of ITS2 sequences, we built a custom BLAST database (File S1, Supporting information) of ITS2 types collected from 409 ITS2 sequences.
454 pyrosequencing of Symbiodinium ITS2 rDNA

PCR amplification of the ITS2 gene for pyrosequencing was performed using primers ITSinf1for2 and ITS2-reverse that generated an amplicon of around 320 bp. The primer sequences were 5'-CCATCTCATCCCTGCG-TGTCTCCGACTCAG(N)-GAATTGCAAGACTCCGTTG-3' (454-ITSinf1for2) and 5'-CTTATCCCCCTGTGTGCCCTTGG-CAGTCTCAGGGGATCCATATGCTTAAGTTCAGCGG-3' (454-ITS2-reverse). Primers included 454 Lib-L library adapters (underlined) and a barcode (shown as N) (Hamady et al. 2008). PCRs were run in triplicate per sample with 12.5 μL of Qiagen Multiplex PCR Kit (Qiagen), 0.1 μM primers, 20–50 ng DNA and DNase-free water to make a total volume of 25 μL. The following PCR conditions were used: initial denaturation for 15 min at 94 °C, followed by 35 cycles of 94 °C for 30 s, 51 °C for 30 s, 72 °C for 30 s and a final extension step of 10 min at 72 °C. PCR products were run on a 1% agarose gel stained with SYBR Safe (Invitrogen) to visualize successful amplification. For each sample, triplicate PCR products were pooled, and their DNA concentrations were measured using a Qubit 2.0 (Invitrogen). Twenty nanograms of the triplicated PCR samples from all specimens was combined and ran on a 1% agarose gel to remove excess primers. The gel band was excised, purified with the Qiagen MinElute Gel Extraction Kit (Qiagen) according to the manufacturer’s instructions, quantified with Qubit 2.0 and quality checked via Bioanalyzer (Agilent, Santa Clara, CA). Forty nanograms of this pooled library (i.e. pooled triplicated PCRs from all samples) was submitted to KAUST BioScience Core Laboratory for sequencing using Titanium FLX chemistry on a quarter of a picotiter plate. Raw sequencing data were retrieved with Roche 454 amplicon-processing pipeline.

454 pyrosequencing data analysis

A total of 218 475 reads with a median length of 314 bp were obtained from sequencing and processed using the software mothur version 1.31.2 (Schloss et al. 2009). Sequences were denoised using PyroNoise (Quince et al. 2011). Forward primer and barcode sequence were removed from reads by the trim.seqs function in mothur. All sequences that met the following criteria were discarded: barcodes (>0 mismatches), forward primer (>2 mismatches), ambiguities (>0 bp), homopolymers (>4 bp) and short sequence length (<250 bp). cutadapt version 1.1 (Martin 2011) was applied to remove the reverse primer (overall error rate set to 0.15). All identical sequences were subsequently collapsed, and representative sequences were retained via unique.seqs command in mothur. After chimera removal with UCHIME as implemented in mothur (Edgar et al. 2011), singletons (i.e. sequences detected only once across the entire data set) were also discarded. A total of 197 181 sequences were retained for the remainder of the analyses. From these data, frequency distributions of ITS2 variants for all samples were obtained via count.seqs command in mothur. Genetic distances for within-culture ITS2 diversity were calculated with the dist.seqs command in mothur based on MUSCLE-aligned ITS2 copies that were represented by at least 100 reads in any given isoclonal culture. For the OTU-based framework analysis, ITS2 sequences were assorted into their respective clades based on pairwise distances via pairwise.seqs command, and subsequent clustering with average neighbour algorithm using a cut-off value of 0.15 (empirically determined to effectively cluster sequences into clades). Sequences assigned to distinct clades were aligned using MUSCLE (Edgar 2004) and trimmed to equal length using the screen.seqs and filter.seqs commands in mothur. Sequences that were shorter than 90% of sequences in each clade were discarded, resulting in 197 128 sequences. A distance matrix was calculated using the aligned sequences within each clade. Sequences were clustered with the average neighbour algorithm (Schloss & Westcott 2011) at a 97% similarity cut-off, as this cut-off clustered ITS2 variants from isoclonal cultures into a single OTU (i.e. species). The most abundant sequence in each OTU was chosen as the representative ITS2 copy and was annotated via BLASTN against the custom ITS2 database to determine a specific Symbiodinium type. In addition, the most abundant ITS2 copy from each pyrosequenced sample was aligned to the sequence derived from the most prominent DGGE band of the same sample to verify whether they were identical. A list of succession of commands and an unattended script are available as supplementary information (Files S2 and S3).

Single-cell PCRs on Symbiodinium cells

To conduct single-cell PCRs on Symbiodinium, we developed an approach modified from Frommel & Iglesias-Rodríguez (2008). Cells from cultures CCMP2467, KB8,
rt-064 and rt-147 were harvested with the following changes: 1 mL of each culture was filtered through a 40-μm cell strainer (BD Biosciences, San Jose, CA), spun down at 1934 g for 10 min and washed 3 times with 1 mL of 1× TE buffer. Cell pellets were subsequently resuspended with 500 μL of 1× TE, counted using a haemocytometer (Haussner Scientific) and diluted to a concentration of 1 cell/μL. ‘(dilution-to-extinction’ approach). One microlitre was subsequently transferred into wells of 96-well plates, and the presence of single cells was confirmed using an inverted microscope (Leica DMI3000B). Cells were disrupted by triplicate freezing of cells for 2 min in liquid nitrogen and immediate thawing for 2 min at 95 °C. Next, a single 0.5-mm glass bead (BioSpec) was added to each well, and the cell was homogenized with a Tissue-Lyzer II (Qiagen) for 1 min. PCR master mix containing 12.5 μL Qiagen Multiplex PCR Kit, 0.1 μL of ITSinfor2 and ITS2-reverse (LaJeunesse 2002) and DNase-free water was added to make a total volume of 25 μL. PCR conditions were identical to the conditions used for 454 sequencing. Subsequently, 1 μL of the PCR product was used as template in a 25 μL clade-specific PCR containing 12.5 μL Qiagen Multiplex PCR Kit, DNase-free water, 0.1 μM of degenerated reverse primer (5’-TCWC YTGTCTGACTTCCATGC-3’) and 0.1 μM of clade A (5’-GGCAGTGGCATGC-3’), B (5’-ATTGGCTGTTGGCTTT CC-3’) or C (5’-TGCTTACTTGCCCCAAC-3’)–specific forward primers generating 100, 180 and 210 bp amplicons, respectively. PCR conditions were 94 °C for 15 min followed by 35 cycles of 30 s at 94 °C, 30 s at 53 °C and 30 s at 72 °C and a final step of 10 min at 72 °C. Amplicons were checked on a 1% agarose gel, cloned with Invitrogen TOPO-TA cloning kit and sent for Sanger sequencing to the KAUST BioScience Core Laboratory. Sequence variation among ITS2 copies in the genomes of Symbiodinium ITS2 database.

**Results**

**Sequence variation among ITS2 copies in the genomes of Symbiodinium**

We applied 454-based amplicon sequencing of the ITS2 rDNA region from *Symbiodinium* to a collection of replicated isoclonal cultures (*n* = 7), pooled cultures (*n* = 2) and environmental samples (*n* = 6) (Table 1). A total of 218,475 reads were obtained from pyrosequencing with a median length of 314 bp (mean length = 323.11 ± 32.61 SD). After filtering of sequences, 197,181 reads were retained with an average of 13,145.40 sequences per sample, representing 1,487 unique ITS2 sequences (Table 1, File S4, Supporting information).

Depending on the taxon investigated, we identified between 102 and 331 distinct ITS2 sequence variants, including cultured strains and field-collected specimens (mean = 219.67). Taking only isoclonal culture samples into account, we identified on average 230.86 ITS2 sequence variants per culture, indicating that there is a substantial number of distinct ITS2 sequence variants found within *Symbiodinium* genomes (Table 1). Despite the high number of distinct ITS2 copies, read counts for the different ITS2 copies showed a highly uneven distribution (Fig. 1A). When sorting ITS2 variants of isoclonal cultures by sequence read abundance, the most abundant ITS2 copies were on average ~20 times more prevalent than the second most common ITS2 copy (all clades: 21.84-fold, clade A’s: 8.25-fold, clade B’s: 39.88-fold, clade C’s: 8.49-fold). Further, the five most abundant ITS2 copies from any culture made up >80% of associated reads, indicating that only few distinct ITS2 genes make up the majority of genomic gene copies. This was substantiated by a rarefaction analysis, which indicated that most of the numerous ITS2 copies were captured at very low abundance in each genome (Fig. 1B). For instance, subsampling of isoclonal cultures to 2000 reads yielded on average less than half of the distinct ITS2 copies we were able to recover taking all sequence reads into account. Additionally, the rarefaction curves at this sampling depth did not approach saturation. This effectively illustrates that intragenomic diversity lies in low-abundant genomic ITS2 copies, which also seems to far exceed what could be captured by ‘traditional’ sequencing methods. Comparison of pyrosequencing data of culture CCMP2467 (type A1) with 25 sequences generated by cloning and sequencing showed that both techniques identified the same most dominant sequence, but numerical ranking of the next most common sequences did not particularly match up well between cloning and 454 data (not shown). Comparing pyrosequencing data to DGGE fingerprinting of isoclonal *Symbiodinium* cultures, DGGE yielded a single dominant band accompanied by few, faint, background bands. The dominant ITS2 variants produced by 454 pyrosequencing (numerically abundant) and DGGE (brightest band) were identical in sequence and were representative sequences of the *Symbiodinium* type analysed (Table 1, Fig. 2). Accordingly, 454 pyrosequencing, cloning and sequencing and DGGE produced uniform results in regard to identifying the ITS2 variants most representative of the genome.

To further assess levels of intragenomic ITS2 diversity, we calculated uncorrected genetic distances between all ITS2 variants of a given isoclonal culture (Table 2). For each sample, we only considered ITS2 types represented by at least 100 reads. This was done to avoid diversity inflation by potential contamination,
Table 1  *Symbiodinium* ITS2 pyrosequencing overview. Depicted are clade types (when cultures were used), the respective animal host and collection site, and DGGE typing results (based on the brightest band). For ITS2 pyrosequencing data, the total number of sequence reads (after filtering) and the number of distinct ITS2 copies for each sample are provided. Sequence reads for each sample are further assigned to clade types detailing number of sequence reads, number of distinct ITS2 copies within clades and clade type of the most abundant ITS2 copy. In cases where the clade type of the most abundant ITS2 copy is different from the database sequence, the percentage identity is indicated. In cases where there are two or more equally abundant ITS2 copies, all clade types are indicated.

<table>
<thead>
<tr>
<th>Culture or Sample name</th>
<th>Clade type</th>
<th>Animal Host and Collection Site</th>
<th>DGGE typing</th>
<th>No. of sequences</th>
<th>No. of distinct ITS2 copies</th>
<th>No. of sequences</th>
<th>No. of distinct ITS2 copies</th>
<th>Clade type of most abundant ITS2 copy</th>
<th>No. of sequences</th>
<th>No. of distinct ITS2 copies</th>
<th>Clade type of most abundant ITS2 copy</th>
</tr>
</thead>
<tbody>
<tr>
<td>Isoclonal Cultures</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CCMP2467 (1) A1</td>
<td></td>
<td><em>Stylophora pistillata</em>, Gulf of Aqaba</td>
<td>A1</td>
<td>16 681</td>
<td>331</td>
<td>16 589</td>
<td>309</td>
<td>A1</td>
<td>26</td>
<td>5</td>
<td>B1</td>
</tr>
<tr>
<td>rt-147 (1) B1</td>
<td></td>
<td><em>Pseudoterogorgia bipinnata</em>, Jamaica</td>
<td>B1</td>
<td>16 843</td>
<td>225</td>
<td>6</td>
<td>3</td>
<td>A1</td>
<td>16 837</td>
<td>222</td>
<td>B1</td>
</tr>
<tr>
<td>rt-147 (2) B1</td>
<td></td>
<td><em>Pseudoterogorgia bipinnata</em>, Jamaica</td>
<td>B1</td>
<td>18 989</td>
<td>241</td>
<td>0</td>
<td>—</td>
<td>—</td>
<td>18 989</td>
<td>241</td>
<td>B1</td>
</tr>
<tr>
<td>rt-064 B1</td>
<td></td>
<td><em>Cassiopea xamachana</em>, Jamaica</td>
<td>B1</td>
<td>16 042</td>
<td>175</td>
<td>2</td>
<td>1</td>
<td>A1</td>
<td>16 040</td>
<td>174</td>
<td>B1</td>
</tr>
<tr>
<td>rt-152 C1</td>
<td></td>
<td><em>Discosoma sanctihomae</em>, Jamaica</td>
<td>C1</td>
<td>3116</td>
<td>111</td>
<td>1</td>
<td>1</td>
<td>A1 (99.61%)</td>
<td>11</td>
<td>4</td>
<td>B1</td>
</tr>
<tr>
<td>Pooled Cultures</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CCMP2467:rt-147 (1:3)</td>
<td>A1:B1</td>
<td>Pooled cultures</td>
<td>B1</td>
<td>14 915</td>
<td>223</td>
<td>18</td>
<td>7</td>
<td>A1</td>
<td>14 897</td>
<td>216</td>
<td>B1</td>
</tr>
<tr>
<td>Field-collected Coral specimens</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>P.Dog.R3.2</td>
<td></td>
<td><em>Pocillopora verrucosa</em>, Doga, Red Sea</td>
<td>A1</td>
<td>22 733</td>
<td>299</td>
<td>22 724</td>
<td>297</td>
<td>A1</td>
<td>7</td>
<td>1</td>
<td>B1</td>
</tr>
<tr>
<td>P.Maq.R2.19</td>
<td></td>
<td><em>P. verrucosa</em>, Maqna, Red Sea</td>
<td>C1h</td>
<td>3683</td>
<td>142</td>
<td>41</td>
<td>12</td>
<td>A1</td>
<td>30</td>
<td>3</td>
<td>B1</td>
</tr>
</tbody>
</table>

© 2014 The Authors. Molecular Ecology Published by John Wiley & Sons Ltd.
methodological artefacts or ultralow-abundant ITS2 copies. The resulting median genetic distance between ITS2 copies from isoclonal cultures was in all cases below 0.02, and median intragenomic variation ranged from 0.003 to 0.017 (Table 2). Therefore, most sequence variants within any culture differed by only one or two nucleotide substitutions from each other.

The reproducibility of pyrosequencing rDNA varied depending on the scale of comparison. In some cases, different tallies of distinct ITS2 copies were calculated between the sequencing of different PCR amplifications conducted from the same DNA extract. Our replicated analysis of culture CCMP2467 recovered 331 and 241 distinct ITS2 sequences from 16 681 and 8565 sequence reads, respectively. Of these ITS2 sequences, 184 were identical (55.59 and 76.35%, respectively). Repeated sequencing of the culture rt-147 was less variable and retrieved 225 and 241 distinct ITS2 variants at a comparable sequencing depth, of which 168 were identical (74.67 and 69.71%, respectively). The comparison between the top 10 most abundant sequence variants showed consistency, but there were some discrepancies between replicated samples (Fig. 3). Sequence variants that represented 2–3% of the total variation were typically recovered between replicates, but not always in the same relative abundance. The top three most common sequences, however, were always recovered, and in the same order of abundance between replicates (Fig. 3). To further elucidate this pattern, the top 10 most common variants from pyrosequencing ITS2 of culture rt-152 (*Symbiodinium goreaui* or type C1) were compared to the composition of top 10 variants identified from several field-collected samples representing clade C *Symbiodinium*, including types C1c, C1h and C41 (Fig. 4). For each of these samples, there were one to five common sequence variants representing >5% of sequence reads for the respective specimen. Each sequence set contained the C1 sequence, *sensu* LaJeunesse (2001), but in very different proportions. The C1 sequence comprised 68.36% of the genome of *S. goreaui* (rt-152 or type C1), 34.00% for type C1c (P.Waj.D7), 34.08% for type C1h (P.Maq.R2.19) and 11.82% in type C41 (A.Af.B6). These proportions were similar to the relative band intensities observed from their respective DGGE fingerprint profile (Fig. 2). The ‘c’ sequence found in codominance with C1 (19.95% vs. 34.00%) in the ribosomal array of *Symbiodinium* type C1c also was detected in two other types (C1h and C1) at significantly lower concentrations and explains why this sequence variant was not resolved by DGGE fingerprinting (Fig. 2).

Among sequences recovered from PCRs of DNA extracted from the artificially mixed cultures, CCMP2467 (*S. microadriaticum* or type A1) and rt-147

<table>
<thead>
<tr>
<th>Culture or Sample name</th>
<th>Animal Host and Collection Site</th>
<th>Clade type</th>
<th>DGGE typing</th>
<th>ITS2 pyrosequencing</th>
<th>Sequences assigned to clade A</th>
<th>Sequences assigned to clade B</th>
<th>Sequences assigned to clade C</th>
</tr>
</thead>
<tbody>
<tr>
<td>P.Waj.R1.5</td>
<td>P. verrucosa, A l Wajh, Red Sea</td>
<td>A1</td>
<td>20 284</td>
<td>20 080 297</td>
<td>20 284 297</td>
<td>20 284 297</td>
<td>20 284 297</td>
</tr>
<tr>
<td>PWaj.R1.5</td>
<td>P. verrucosa, A l Wajh, Red Sea</td>
<td>A1</td>
<td>20 284</td>
<td>20 080 297</td>
<td>20 284 297</td>
<td>20 284 297</td>
<td>20 284 297</td>
</tr>
<tr>
<td>P.Waj.D7</td>
<td>P. verrucosa, A l Wajh, Red Sea</td>
<td>C1c</td>
<td>3279 102</td>
<td>3279 102</td>
<td>3279 102</td>
<td>3279 102</td>
<td>3279 102</td>
</tr>
<tr>
<td>P.Maq.R2.7</td>
<td>P. verrucosa, A l Maqna, Red Sea</td>
<td>B1</td>
<td>33 5</td>
<td>33 5</td>
<td>33 5</td>
<td>33 5</td>
<td>33 5</td>
</tr>
<tr>
<td>P.Maq.R2.7</td>
<td>P. verrucosa, A l Maqna, Red Sea</td>
<td>B1</td>
<td>33 5</td>
<td>33 5</td>
<td>33 5</td>
<td>33 5</td>
<td>33 5</td>
</tr>
<tr>
<td>PWaj.D7</td>
<td>P. verrucosa, A l Wajh, Red Sea</td>
<td>B1</td>
<td>33 5</td>
<td>33 5</td>
<td>33 5</td>
<td>33 5</td>
<td>33 5</td>
</tr>
<tr>
<td>PWaj.D7</td>
<td>P. verrucosa, A l Wajh, Red Sea</td>
<td>B1</td>
<td>33 5</td>
<td>33 5</td>
<td>33 5</td>
<td>33 5</td>
<td>33 5</td>
</tr>
<tr>
<td>PWaj.D7</td>
<td>P. verrucosa, A l Wajh, Red Sea</td>
<td>B1</td>
<td>33 5</td>
<td>33 5</td>
<td>33 5</td>
<td>33 5</td>
<td>33 5</td>
</tr>
<tr>
<td>A.Af.B6</td>
<td>Acropora hemprichii, A l Fahal Reef, Red Sea</td>
<td>C41</td>
<td>102 4</td>
<td>102 4</td>
<td>102 4</td>
<td>102 4</td>
<td>102 4</td>
</tr>
<tr>
<td>A.Af.B6</td>
<td>Acropora hemprichii, A l Fahal Reef, Red Sea</td>
<td>C41</td>
<td>102 4</td>
<td>102 4</td>
<td>102 4</td>
<td>102 4</td>
<td>102 4</td>
</tr>
<tr>
<td>A.Af.B6</td>
<td>Acropora hemprichii, A l Fahal Reef, Red Sea</td>
<td>C41</td>
<td>102 4</td>
<td>102 4</td>
<td>102 4</td>
<td>102 4</td>
<td>102 4</td>
</tr>
</tbody>
</table>

© 2014 The Authors. *Molecular Ecology* Published by John Wiley & Sons Ltd.
In a 1:1 or 1:3 cell ratio, more than 99% of ITS2 reads were identified only as clade B. This result was consistent with DGGE profiling conducted on the same samples, which showed only a single prominent band matching that of the fingerprint for culture rt-147.

The band diagnostic of type A1, S. microadriaticum, was absent in both mixed samples (Fig. 2). Sequences derived from 454 (most abundant) and DGGE (brightest band) of both pooled samples were identical and identified as type B1 via BLASTN. These results suggest that clade B has either a far greater copy number of rDNA than clade A, or PCR bias of rt-147 over CCMP2467. This bias might arise from differences in DNA isolation efficiency or preferential primer amplification as discussed in Thornhill et al. (2013). In conclusion, we could not detect both entities in their initially mixed proportions.

Looking further at ITS2 type composition from pyrosequencing reads of isoclonal cultures, we found that besides the majority of sequences being representatives of the underlying ITS2 type, very low-abundant ITS2 types were present that were representatives of other clades (Table 1). These variants matched with the dominant sequence variants (or nearly so) of isolates representing other Symbiodinium clades also under analysis and occurred between 0.01 and 0.40% of all reads (Table 1). To understand the cause of this observation further, we conducted a series of single-cell PCRs on cultures CCMP2467, KB8, rt-064 and rt-147 with primers specific to clades A, B and C. Clade-specific PCRs performed on single Symbiodinium cells from these cultures yielded PCR products with the corresponding clade-specific primers and failed to yield amplicons using primers specific to a clade other than the template, with the exception of culture rt-064 (type B1). For this culture, we retrieved PCR products in two of seven cases upon amplification with clade A-specific primers. From both PCR products, a total of eight clones were sent for sequencing, of which five were

Fig. 1 (A) Frequency distribution of sequence reads for the 10 most common ITS2 copies from isoclonal culture samples. (B) Rarefaction curve illustrating ITS2 sequence diversity distribution in isoclonal cultures.

Fig. 2 Denaturing gradient gel electrophoresis (DGGE) fingerprint of samples used in this study with clades/subclades indicated.
identical to the identified clade B1 in 454 sequences and three were discarded due to reduced quality.

**Taxon-based analysis of Symbiodinium ITS2 diversity in isoclonal cultures**

Studies of microbial diversity in an OTU framework based on pyrosequencing of the 16S rRNA gene have revolutionized our understanding of bacterial diversity and distribution (Sogin et al. 2006). Similarly, the ITS2 gene is amenable to analysis in a taxon-based framework under the premise of derivation of appropriate cut-offs to denoting clades and species/types. Given the deep divergence between Symbiodinium species from different clades (comparable to differences between orders in other dinoflagellates), we had to devise a strategy where taxonomic delineation was conducted on the clade level first and subsequently at the type level.

Clade separation was empirically determined by pairwise similarity calculation of all sequences and subsequent clustering using a similarity cut-off of >0.10. This approach consistently clustered reads into different clades, which was confirmed by BLASTing representatives of each cluster against our custom ITS2 database. As mothur calculates exact distance cut-offs, the next higher distant cut-off from 0.10 was chosen for data analysis (here: 0.15). After aligning, trimming and discarding sequences that were shorter than 90% of the reads in each clade, 197 128 sequences remained, of which 101 239 sequences belonged to clade A, 82 273 belonged to clade B, and 13 616 sequences belonged to clade C (Table 3).

For the determination of species- or type-level cut-offs, we used data from isoclonal cultures. Our aim was to determine a cut-off that effectively clustered all reads from culture samples assorted to a clade (step above) into one corresponding OTU at the ‘species’ level. Average neighbour clustering of reads based on uncorrected pairwise distances at 0.03 provided the cut-off where all cultures collapsed into one OTU for a given clade (Table 3). Therefore, 97% sequence similarity was implemented as a cut-off value for species/type-level OTU-based analyses within clades. Comparing results from sequence- (Table 1) and OTU-based (Table 3) analyses effectively illustrates that the high number of distinct ITS2 copies that we identified in isoclonal culture samples could be collapsed to within-species (i.e. within OTU<sub>0.03</sub>) ITS2 variation in a taxon-based analysis. Three distinct OTU<sub>0.03</sub> (1 of each clade A, B and C) represented data from all cultures. For the pooled culture samples, two OTU<sub>0.03</sub> were
correctly identified, but the relative abundances of reads did not reflect the initial ratio of cells used. Accordingly, while diversity was correctly recovered for cells from pooled isoclonal cultures, the relative abundances were not.

Taxon-based analysis of ITS2 diversity in environmental samples

We applied our OTU-based framework to analyse ITS2 diversity in environmental samples based on the
Discussion

Sequence variation among ITS2 copies in the genomes of Symbiodinium

We applied 454 pyrosequencing to analyse intra- and intergenomic Symbiodinium rDNA diversity in order to gain an in-depth perspective on the relative homogeneity of this high multicopy gene (Thornhill et al. 2007). By utilizing isoclonal cultures, we further resolved the degree of genomic homogeneity relative to abundance of ITS2 sequence variants across the ribosomal array. In addition, we extended sequencing resolution in comparison with classical cloning-and-sequencing-based approaches, and we were able to empirically derive cut-offs for application of these types of data in a taxon-based framework. Our analysis protocol was then applied to environmental samples to assess overall feasibility of the approach.

A concern regarding utilization of ITS2 genes for estimating Symbiodinium diversity is the multicopy nature of ribosomal DNA (LaJeunesse 2002). The genomes of eukaryotes contain one to several numerically dominant sequence variants (Dover 1986; Hillis & Dixon 1991; LaJeunesse & Pinzon 2007). Species lineages of Symbiodinium exist that have two or more codominant ITS2 copies that together are diagnostic of the species (Sampayo et al. 2009). The rank abundance plot of ITS2 variants from isoclonal samples (Fig. 1A) revealed that while there seems to be extensive intragenomic variation in ITS2 sequences, each genome was characterized (in these particular examples) by the presence of one numerically dominant ITS2 sequence. Provided that the process of concerted evolution is correctly understood (Dover 1986), common intragenomic variants persist in the genomes among the individuals of a genetically recombining population over long evolutionary timescales (Sampayo et al. 2009; Thornhill et al. 2014). The number of ITS2 sequence variants follows a long-tail abundance distribution with dominant variants (often one or two) being present at high frequency and a high number of rare variants at much lower frequencies (Fig. 1). This disparity among intragenomic variants
indicates that gene conversion drives the relative homogenization of this gene array, but is not rapid enough to dampen out the appearance and partial spread of new mutations. As rare variants are removed or replaced through concerted evolution, variants derived from the dominant sequence are continually being generated. This process, however, leads to evolutionary stability of the dominant sequence variant(s). For this reason, the numerically dominant intragenomic variant is used to conservatively characterize Symbiodinium (LaJeunesse 2002; Thornhill et al. 2007). Accordingly, DGGE-based analyses focus only on the dominant Symbiodinium ITS2 sequence variants in a sample to resolve the most abundant Symbiodinium species present in the host. However, DGGE-based analyses are relatively labour- and time intensive, which might prohibit studying a large number of samples. In comparison, pyrosequencing requires little hands-on time and has become comparatively cheap. In addition, the resolution of additional Symbiodinium that might occur at low abundances (<5%) may be detected. DGGE can usually detect the coexistence of a second or third Symbiodinium if present at >5–10% of the sample (Thornhill et al. 2006), with some species (e.g. type D1 in Porites) requiring 10–30% abundance to be detected (LaJeunesse et al. 2008). In contrast, pyrosequencing detected sequences below 1% in our data. Accordingly, DGGE-based ITS2 typing can miss the presence of background species that may be ecologically important (LaJeunesse et al. 2009).

The application of deep sequencing can be used to better understand intragenomic rDNA diversity and its evolution within a genome. Pyrosequencing repeatedly identified a large number of ITS2 sequence variants diagnostic of a particular genome (Fig. 3) beyond the resolution of DGGE- or cloning-based approaches. Still, the median intragenomic sequence divergence was <0.02 (Table 2) similar to the values calculated when only the most abundant sequence variants were considered (Sampayo et al. 2009; Stat et al. 2013), and this value was subsequently used to inform cut-off estimates for the resolution of separate taxa.

The analysis of mixed cultured isolates at different ratios showed that one must be conservative when interpreting abundance in samples with two or more Symbiodinium species. This is mainly due to the differences in rDNA copy number between Symbiodinium species (Rowan & Knowlton 1995; Rowan et al. 1997; Mieog et al. 2007; LaJeunesse et al. 2008), or differences in DNA extraction efficiency among different Symbiodinium spp. Pooled cultures of Symbiodinium A1 (CCMP2467) and B1 (rt-147) in a 1:1 ratio generated far more sequence reads for Symbiodinium B1, despite pooling the same number of Symbiodinium cells from both cultures (Table 1). While genomic complexity in terms of distinct copies was similar for both cultures, clade B has several times more ITS copies than clade A, explaining the unequal read distribution we recovered (T. C. LaJeunesse, unpublished data). Accordingly, this has to be taken into account when using rDNA in estimating the relative abundances of samples containing members of two or more clades.

Our discovery of ITS2 sequence variants diagnostic of a different clade in pyrosequencing data from isoclonal cultures prompted further investigations via single-cell PCRs. Given the absence of consistent foreign clade amplification in single-cell PCRs as well as the vast evolutionary timescales between Symbiodinium clades (estimated at tens of millions of years), the most parsimonious explanation is DNA contamination (e.g. in the form of aerosols). In a recent review, van Oppen & Gates (2006) report on the retrieval of highly divergent sequences (diagnostic of other clade entities) at ultralow abundance, indicating that contamination is potentially a significant issue in laboratories that extensively employ PCRs of the ITS2 marker. The finding of unexpected ‘background’ sequences would need to be confirmed by next-generation sequencing these samples in laboratories that have not previously worked on Symbiodinium ITS2.

**Taxon-based analysis of ITS2 diversity**

While many studies have applied cluster-based approaches to analyse Symbiodinium ITS2 diversity within environmental samples (Correa & Baker 2009; Stat et al. 2013), few studies yet have targeted analysing Symbiodinium diversity with high-throughput sequencing data in an OTU-based framework (Green et al. 2014; Thomas et al. 2014). We think that this is the most suitable approach in dealing with data produced from next-generation sequencing of rDNA. It should be noted that the application of high-throughput sequencing of the ITS2 region is not limited to the Roche 454 platform. Given current read-length improvements of the Illumina MiSeq platform (2*300 bp Paired-End libraries) in addition to its higher throughput, data from this platform can readily be applied to the analysis of ITS2 in a taxon-based framework. In particular, our OTU-based pipeline developed here for mothur is compatible and portable to data generated on the Illumina MiSeq platform with minor changes to the quality trimming steps (Phase I, File 2, Supporting information) based on differences in the sff (Roche 454) and fastq (Illumina MiSeq) file format. The challenge lies in the derivation of appropriate cut-offs for the separation of sequences into clades and species or types. Even for a well-studied marker such as 16S, taxonomic cut-offs are not necessarily accurate (Ghyselinck et al. 2013; Preheim et al. 2013). Here, we used (replicated) sequencing of
isoclonal cultures representing clades A, B and C to better understand inter- and intragenomic diversity and empirically derive taxonomic cut-offs. Future studies should sequence rDNA from additional cultures representing a diverse set of Symbiodinium species.

On the clade level, due to the large evolutionary distance in the genus Symbiodinium, ITS2 sequences from different clades are difficult if not impossible to align correctly. Accordingly, taxon-based framework analyses will fail to separate ITS2 sequences into ecological and evolutionarily discrete entities when sequences from all clades are considered at the same time. Rather, it will lead to exaggerated genetic distance estimates retrieved from the alignment of nonhomologous DNA characters. To resolve ITS2 types more accurately, we found that sequences need to be separated into distinct clades first, and a subsequent OTU-based analysis has to be carried out for each clade separately. For our data, ITS2 sequences separated into clades upon applying a cut-off value of 0.15. However, application of this cut-off to ITS2 sequences from our database considering all clades (i.e. A–I) did not correctly cluster ITS2 sequences into all distinct clades (data not shown). This might be due to difficulties in calculating pairwise similarities between sequences when all subtypes of Symbiodinium, for example A1, A2, A3 or B1, B2, B3 are present in one data set. To separate ITS2 sequences into Symbiodinium clade levels, we suggest manual binning upon determination of an appropriate similarity cut-off before conducting OTU-based ITS2 type analyses (File S5, Supporting information).

Similarly as for the separation of ITS2 reads into clades, there is no a priori cut-off value that consistently sorts ITS2 sequences into distinct species (Thornhill et al. 2014). In fact, Symbiodinium species classification should not be conducted using ITS2 sequence divergence alone, as ITS2 may not consistently resolve species. For instance, two distinct Symbiodinium lineages that are not undergoing genetic exchange can have the same ITS2 sequence (Thornhill et al. 2014). Accordingly, a taxonomic cut-off value that clusters existent ITS2 variants into OTUs should be regarded as provisional, pending subsequent analysis with independent and more rapidly evolving markers. For this reason, grouping of ITS2 variants into provisional OTUs for the (initial) characterization and comparison of Symbiodinium diversity seems a more feasible approach than trying to definitely resolve ITS2 sequence differences into species.

As ITS2 rDNA is not a single-copy gene, a cut-off value that clusters intragenomic ITS2 variants into a single OTU might be indicated as a valid cut-off value. In our data, clustering sequences from isoclonal cultures assorted to clades with the average neighbour algorithm (Schloss & Westcott 2011) at a pairwise genetic distance cut-off of 0.03 collapsed intragenomic ITS2 variation into a single OTU. For this reason, we adopted 0.03 as a cut-off to determine Symbiodinium community composition from pyrosequencing data retrieved from field-collected coral specimens. The application of this cut-off to samples from coral host tissues resulted in only six distinct OTUs describing Symbiodinium diversity, despite numerous sequenced ITS2 variants. This provides an indication of how much of the variation we sequenced might be attributable to actual intra- rather than intergenomic diversity. Applying an OTU-based approach to the analysis of coral symbiont diversity suggests that most coral colonies appear to be dominated by a single genetic entity (Sampayo et al. 2009; Pettay et al. 2011; Baums et al. 2014; Thornhill et al. 2014). However, ITS2 sequences of types C1, C1h, C1c and C41 were represented by the same OTU at a 0.03 cut-off underscoring the difficulties that are associated with matching ITS2 sequence variants to closely related Symbiodinium with separate ecological distributions. Because these entities share a recent common ancestor as members of the CI radiation (sensu Thornhill et al. 2014), the genomes of these Symbiodinium shared the ancestral sequence, CI, at different relative abundances (Fig. 4). An exception was a Pocillopora verrucosa specimen (P.Maq.R2.7, Table 3): in this sample, we detected all six OTUs representing the entire OTU diversity from our data. The significance of colonies possibly harbouring highly mixed Symbiodinium assemblages is not fully understood and should be the effort of future studies.

Considerations for the application of an OTU-based pipeline to the analysis of Symbiodinium ITS2 diversity

There is probably no single genetic marker that can correctly classify all Symbiodinium diversity into distinct species (LaJeunesse et al. 2012; Pochon et al. 2012). Typically, a distinct ITS2 variant that is numerically dominant in the genome is tentatively regarded as a new type, or ‘species’, of Symbiodinium (LaJeunesse 2002; LaJeunesse et al. 2010), and only when diagnostic of an ecologically distinct population. However, for (initial) characterization of Symbiodinium diversity in a large number of samples, elucidation of Symbiodinium species using multimarker molecular evidence in combination with morphological, ecological and physiological data (as detailed in, e.g., LaJeunesse et al. 2012) is not (yet) feasible. Here, we suggest adoption of an OTU-based framework to analyse high-throughput Symbiodinium ITS2 sequence data to provisionally assess species diversity (similar to the use of DGGE fingerprinting of ITS2 rDNA) until ‘true’ species are formally described using the convergence of independent lines of genetic, ecological and in some cases morphological evidence.

© 2014 The Authors. Molecular Ecology Published by John Wiley & Sons Ltd.
(LaJeunesse et al. 2014). Although the application of a taxon-based framework will miss some ecologically and evolutionarily distinct entities, most importantly, it provides a conservative and comparable estimate of Symbiodinium diversity based on rDNA. The development of sensible cut-offs to delineate Symbiodinium diversity in an OTU-based framework allows harmonization and reanalysis of existing and new data under a common set of rules. We specifically acknowledge that some Symbiodinium species will be contained in a single OTU and not resolve at a cut-off of >97% similarity. For instance, clade C, which is by far the most diverse clade with a broad radiation, would require higher cut-off values to resolve species. But as ITS2 data alone are unable to unequivocally diagnose species, our intentions were to provide a reasonable cut-off that investigators can apply to compare diversity within and between their samples and that deflates rather than inflates Symbiodinium species diversity estimates. Further, continuing efforts in the (genetic) description of Symbiodinium species (LaJeunesse et al. 2012, 2014; Jeong et al. 2014) and the ease of typing a large number of samples might encourage the use of multiple markers in the analysis of Symbiodinium diversity, which will facilitate analysis of high-throughput sequencing data in a phylogeny-based context. This perspective stimulates further comparative analyses of ocean basins and species in a standardized framework that might provide greater insight into symbiont diversity of marine invertebrates and the acclimation of corals to environmental change.

Acknowledgements

We would like to thank the KAUST BioScience Core Lab and S. Neelamegam for 454 library generation and sequencing. We would also like to thank Y. Sawall and A. Al-Sofyani for provision and collection of coral samples, and three anonymous reviewers for helpful comments. This project was funded by a KAUST Academic Excellence Alliance (AEA) Award to CRV and CJH, baseline research funds to CRV and a National Science Foundation grant to TCL (OCE-0928766).

References


Jeong HJ, Lee SY, Kang NS et al. (2014) Genetics and morphology characterize the dinoflagellate Symbiodinium voratum, n. sp., (Dinophyceae) as the sole representative of Symbiodinium Clade E. Journal of Eukaryotic Microbiology, 61, 75–94.

LaJeunesse TC (2001) Investigating the biodiversity, ecology, and phylogeny of endosymbiotic dinoflagellates in the genus...


LaJeunesse TC, Petay DT, Sampaio EM et al. (2010) Long-standing environmental conditions, geographic isolation and host-symbiont specificity influence the relative ecological dominance and genetic diversification of coral endosymbionts in the genus *Symbiodinium*. *Journal of Biogeography*, 37, 785–800.

LaJeunesse TC, Parkinson JE, Reimer JD (2012) A genetics-based description of *Symbiodinium minutum* sp. nov. and *S. psamnophilum* sp. nov. (Dinophyceae), two dinoflagellates symbiotic with cnidaria. *Journal of Phycology*, 48, 1380–1391.


Silverstein RN, Correa AMS, Lajeunesse TC, Baker AC (2011) Novel algal symbiont (Symbiodinium spp.) diversity in reef corals of Western Australia. Marine Ecology Progress Series, 422, 63–75.


Data accessibility

ITS2 DNA variants were uploaded as online supplemental material. Pyrosequencing analysis pipeline overview and motuor script were uploaded as online supplemental material. The sequences determined in this study have been deposited in the NCBI Sequence Read Archive under accession no. PRJNA244965.

Supporting information

Additional supporting information may be found in the online version of this article.

File S1 ITS2 BLAST database.

File S2 Symbiodinium ITS2 analysis pipeline with motuor (version 1.31.2).

File S3 Script file for unattended motuor ITS2 analysis.

File S4 Overview over ITS2 classification, read counts, and reference sequence for all ITS2 variants identified.

File S5 Overview over ITS2 Symbiodinium 454 Data Analysis Pipeline.