1 LSU rDNA BASED RFLP ASSAYS FOR THE ROUTINE IDENTIFICATION OF

2 GAMBIERDISCUS SPECIES

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5 Abstract

6 Gambierdiscus is a genus of benthic dinoflagellates commonly associated with ciguatera 7 fish poisoning (CFP), which is generally found in tropical or sub-tropical regions around the world. Morphologically similar species within the genus can vary in toxicity; however, species 8 9 identifications are difficult or sometimes impossible using light microscopy. DNA sequencing of 10 ribosomal RNA genes (rDNA) is thus often used to identify and describe Gambierdiscus species 11 and ribotypes, but the expense and time can be prohibitive for routine culture screening and/or 12 large-scale monitoring programs. This study describes a restriction fragment length 13 polymorphism (RFLP) typing method based on analysis of the large subunit ribosomal RNA 14 gene (rDNA) that can successfully identify at least nine of the described Gambierdiscus species 15 and two Fukuyoa species. The software programs DNAMAN 6.0 and Restriction Enzyme Picker 16 were used to identify a set of restriction enzymes (SpeI, HpyCH4IV, and TaqaI) capable of distinguishing most of the known Gambierdiscus species for which DNA sequences were 17 available. This assay was tested using in silico analysis and cultured isolates, and species 18 identifications of isolates assigned by RFLP typing were confirmed by DNA sequencing. To 19 verify the assay and assess intra-specific heterogeneity in RFLP patterns, identifications of 63 20 Gambierdiscus isolates comprising ten Gambierdiscus species, one ribotype, and two Fukuyoa 21 22 species were confirmed using RFLP typing, and this method was subsequently employed in the routine identification of isolates collected from the Caribbean Sea. The RFLP assay presented 23

here reduces the time and cost associated with morphological identification via scanning electron
 microscopy and/or DNA sequencing, and provides a phylogenetically sensitive method for
 routine *Gambierdiscus* species assignment.

4

5 **1. Introduction**

6 Ciguatera fish poisoning (CFP) is a human poisoning syndrome caused by the consumption of 7 seafood contaminated with ciguatoxins. The genus Gambierdiscus represents a group of benthic 8 dinoflagellates known to produce ciguatoxins (CTX); however, toxin production is variable 9 among species (Holmes et al., 1991; Chinain et al., 2010). Incidences of CFP are more common 10 in tropical and subtropical latitudes, which correspond to the endemic range of Gambierdiscus spp., and the prevalence of poisonings and abundances of Gambierdiscus spp. are often site-11 12 specific (Dickey and Plakas, 2010). Gambierdiscus dinoflagellates have been reported in tropical or sub-tropical regions around the world, including Okinawa in Japan (Nishimura et al., 2013), 13 14 the South China Sea (Zhang et al., 2016), Hong Kong (Wong et al., 2005), Malaysia (Leaw et al., 15 2011), Thailand (Tawong et al., 2015), Texas, South Carolina, Hawaii, and Florida in U.S. (e.g., Babinchak et al., 1986; CDC, 2006; Villareal et al., 2007; Rains and Parsons, 2015), French 16 Polynesia (Chinain et al., 1991a, b), the Republic of Kiribati (Xu et al., 2014), Johnston Atoll 17 (Richlen and Lobel, 2011), and other island nations in the Pacific (Lewis et al., 1991; Smith et al., 18 19 2016), Australia (Gillespie et al., 1985; Kohli et al., 2014; Kretzschmar et al., 2016), and the Red 20 Sea (Saburova et al., 2013). More recently, *Gambierdiscus* was reported from temperate regions, 21 including the Kermadec Islands, New Zealand (Rhodes et al., 2017), Japan (Kuno et al., 2010; Nishimura et al., 2013, 2014, 2016), Korea (Jeong et al., 2012), Canary Islands, Northeast 22

Atlantic (Fraga et al., 2011; 2014), Pakistan (Munir et al., 2011), the Gulf of Aqaba, Jordan (Saburova et al., 2013), the Northern Gulf of Mexico (Tester et al., 2013), and the Mediterranean Sea (Aligizaki and Nikolaidis, 2008). The increased prevalence of CFP in recent years may be attributed to multiple factors including improved awareness and/or reporting, expanding international trade in tropical fish species, climate change, increased anthropogenic activities, and the continued absence of affordable and accurate methods for detecting ciguatoxins in fish (Lehane and Lewis, 2000; Poon-King et al., 2004; Lewis, 2006; Chan et al., 2011).

8 Until 1995, all Gambierdiscus cells were recorded as G. toxicus; however, taxonomic studies carried out over the past two decades have identified 13 additional genetically and 9 10 morphologically distinct species in the genus, including G. australes, G. balechii, G. belizeanus, G. caribaeus, G. carolinianus, G. carpenteri, G. cheloniae, G. excentricus, G. lapillus, G. 11 pacificus, G. polynesiensis, G. scabrosus, G. silvae, as well as several ribotypes (Chinain et al., 12 13 1999a; Litaker et al., 2009; Kuno et al., 2010; Litaker et al., 2010; Fraga et al., 2011, 2014, 2016; Nishimura et al., 2013, 2014; Xu et al., 2014; Kretzschmar et al., 2016; Smith et al., 2016), and 14 three closely related species recently reclassified as Fukuyoa paulensis, F. ruetzleri and F. 15 yasumotoi (Gómez et al., 2015). Gambierdiscus toxin production is thought to be genetically 16 17 determined, with significant variation in toxicity observed both within and among species (e.g., Bomber et al., 1989; Chinain et al., 2010; Holmes et al., 1991; Sperr and Doucette, 1996; 18 Pawlowiez et al., 2013). As Gambierdiscus populations found within a particular area can 19 20 comprise multiple species that vary with respect to their toxicity, the species composition of 21 blooms and particularly the presence of certain highly toxic species and/or strains have been 22 suggested as playing a prominent role in CFP events and the severity of outbreaks (Holmes and

Lewis, 1994; Chinain et al., 1999b; Chinain et al., 2010). Further investigation of *Gambierdiscus* species biogeography and toxicity is still needed to support this hypothesis.

Ribosomal RNA gene sequences have been used to document species and strain diversity of 3 Gambierdiscus populations globally and locally; however, DNA sequencing involves costly, 4 5 labor-intensive procedures, and is impractical to apply on a large scale. More recently, community diversity profiling methods using quantitative PCR (qPCR) were developed for 6 7 several Gambierdiscus species in field samples, including five Caribbean species (Vandersea et 8 al., 2012) and four Japanese Gambierdiscus species/phylotypes (Nishimura et al., 2016). To contribute to the molecular tools currently available for characterizing *Gambierdiscus* species 9 10 diversity, and specifically to aid in routine identification of cultures established from sampling sites in the Caribbean Sea, a restriction fragment length polymorphism (RFLP) assay based on 11 12 the hypervariable D1-D2 region of the large subunit ribosomal RNA gene (LSU rDNA) was 13 developed. To verify the assay and assess intra-specific heterogeneity in RFLP patterns, 63 Gambierdiscus isolates comprising ten Gambierdiscus species, one ribotype, and two Fukuyoa 14 species were identified using RFLP typing. The assay was subsequently and successfully 15 employed in the routine identification of cultures established from samples collected from the 16 17 Bahamas, St. Thomas, USVI, and the Florida Keys, FL, USA over the period of approximately 18 two years. The assay presented here provides a rapid, phylogenetically sensitive, and inexpensive alternative to morphological identification via scanning electron microscopy (SEM) and/or DNA 19 20 sequencing, and provides an alternative method for routine Gambierdiscus species assignment. 21 The approach is also operationally simple, requiring basic molecular laboratory capabilities 22 (PCR amplification and gel electrophoresis), and thus it could be useful in countries where DNA 23 sequencing and/or SEM facilities are costly and/or unavailable.

2 2. Materials and Methods

3 2.1 RFLP assay design and in silico testing

4 For the assay design and *in silico* testing, sequences of the D1-D3 hypervariable region of the 5 LSU rDNA from 12 Gambierdiscus species, one ribotype, and three Fukuyoa species were 6 downloaded from the NCBI GenBank database, and the D1-D2 region was selected and used in 7 subsequent analyses. Sequence data from this region was not available for G. lapillus and G. 8 balechii, so these species were excluded from this analysis. The software programs DNAMAN 9 6.0 (Lynnon Biosoft, Quebec, Canada) and Restriction Enzyme Picker (Collin and Rocap, 2007) were used to identify restriction enzymes that could distinguish these species. DNAMAN ENZ 10 (Enzyme file), which contains 2523 enzymes, was used in the *in silico* analysis. The fragments 11 12 with all cutters and ends were considered. Restriction Enzyme Picker was then used to optimize the enzyme combination, according to the principle of minimum fragments and enzyme number. 13 14 SpeI was selected to distinguish G. australes from G. carolinianus, TaqoI for F. ruetzleri and F. *yasumotoi*, and *Hpy*CH4IV for the remaining *Gambierdiscus* species. 15

16 2.2 Strain isolation and culture maintenance

Live cultures established for the assay testing were isolated from St. Thomas, USVI, the Florida Keys, USA, and San Salvador, Bahamas (Parsons and Richlen, 2016). Additionally, cell pellets or DNA extracts were provided for several *Gambierdiscus* species from French Polynesia and Japan (*G. australes* and *G. scabrosus*). For culture establishment, individual *Gambierdiscus* or *Fukuyoa* spp. cells were isolated by micropipetting at 100× magnification, rinsed in sterile seawater, and established in 25% modified K medium (Morton and Norris, 1990). Clonal isolates were subsequently transferred into tissue culture flasks and maintained in 100% modified K
medium at 23°C, 32 psu, ~100 µmol photons m⁻² s⁻¹ of light, and 12h:12h light:dark photoperiod.
A complete list of the isolates used in this study is provided in Table 1.

4 2.3. *RFLP analysis and sequencing*

5 To verify the RFLP method, forty Gambierdiscus isolates, primarily from the Caribbean Sea, 6 were identified using RFLP typing, and the species identity was confirmed using DNA sequencing. For these analyses, DNA was extracted from 1 ml of dense culture using the MoBIO 7 PowerSoil DNA Isolation Kit (MoBio Laboratories, Inc., Carlsbad, CA, USA) following the 8 9 manufacturer's instructions and eluted in a final volume of 100 µl. Partial fragments of the LSU rRNA gene were amplified from isolates using either the primers D1R and D2C (Scholin et al., 10 1994) or FD8 and RB (Chinain et al., 1999a). Each PCR reaction (25 µl) contained ~5 ng 11 template DNA, 1 x PCR Buffer (500 mM KCl and 100 mM Tris-HCl, pH 8.3), 2 mM MgCl₂, 0.8 12 mM dNTPs, 0.5 µM of each primer, and 0.5 U of AmpliTaq DNA Polymerase (Applied 13 14 Biosystems Inc., Foster City, CA, USA). Hot start PCR amplifications were performed in an Eppendorf Mastercycler Nexus thermal cycler (Eppendorf, Hamburg, Germany) with the 15 following cycling conditions: 94 °C for 4 min; then 35 cycles of 94 °C for 30 s, 57 °C for 1 min, 16 17 72 °C for 2 min, and a final extension of 72 °C for 10 min. PCR products were visualized by electrophoresis on 2% TAE agarose gel to verify that the PCR reaction was successful, and to 18 assess the uncut PCR product size. PCR products used in the RFLP assay were then purified 19 using the Qiaquick PCR purification kit (Qiagen, Hilden, Germany). 20

21 RFLP reactions (25 μl) contained 4 μl of purified D1-D2 PCR product (variable, but
22 generally ranging from ~100-200 ng), 18 μl water, 2.5 μl 1× CutSmart® Buffer, and 0.5 μl (5 U)

of *Spe*I and *Hpy*CH4IV (New England Biolabs, Inc., Ipswich, MA, USA). Samples were covered
with plastic wrap to prevent evaporation and incubated at 37 °C for 15 min in the Eppendorf
thermal cycler. The temperature was reduced to 4 °C and 0.5 µl (50 U) *Taq*αI (New England
Biolabs, Inc.) was added to each reaction, then samples were incubated at 65 °C for 15 min
followed by 80 °C for 20 min to deactivate the enzymes. RFLP digestion products, along with a
100 bp DNA ladder, were separated by electrophoresis on 2% TAE agarose gel at 75V for 1.5
hours.

For DNA sequencing, unpurified PCR products were cloned into the pGEM T Easy Vector
(Promega, Madison, WI, USA). Clones were screened with plasmid primers M13F and M13R,
and sequenced in both the forward and reverse direction (Eurofins MWG Operon, Ebersberg,
Germany). DNA sequences were aligned in Geneious Pro 8.1 (Biomatters, Auckland, NZ), and
the consensus sequences were compared with those in GenBank using BLAST sequence
similarity searches (NCBI). Restriction maps used to analyze DNA sequences from isolates
exhibiting aberrant RFLP patterns were created with Geneious Pro 8.1.

15 3. **Results**

In silico analyses identified a combination of three enzymes (SpeI, HpyCH4IV, and TaqαI) that
produced fragments unique to the Gambierdiscus species examined, as well as two
morphologically similar Fukuyoa species. SpeI distinguished G. australes and G. carolinianus,
TaqαI distinguished F. ruetzleri and F. yasumotoi, and HpyPYCH4IV differentiated among the
remaining Gambierdiscus species. Gambierdiscus toxicus did not contain any restriction
recognition sites, and generated a PCR product of ca. 726 bp. Enzyme recognition sites are listed
in Table 2, and expected fragment sizes from the *in silico* analysis are provided in Table 3.

1 Ten Gambierdiscus species, one ribotype (Gambierdiscus ribotype 2), and two Fukuyoa species were analyzed using this assay to verify the fragment sizes generated by the in silico 2 analysis (Fig. 1). These analyses showed that the fragment bands produced by the RFLP 3 4 digestion were comparable to those predicted by *in silico* analysis. All fragments greater than 100 base pairs were clearly visible in the agarose gel; however, fragment bands smaller than 100 5 base pairs were sometimes faint or difficult to visualize (Fig. 1). Efforts to improve the 6 visualization of these smaller bands by increasing the amount of digested product used in gel 7 electrophoresis (up to 12 µl) were unsuccessful, as the smaller fragments still appeared faint 8 9 regardless of the amount analyzed (data not shown).

10 The RFLP assay was then tested with multiple *Gambierdiscus* isolates from the Caribbean 11 Sea and the Pacific to further assess the assay's consistency and accuracy, including potential intra-specific variability. DNA sequence data were also collected from these isolates to verify 12 13 species identifications assigned by RFLP typing. Consensus sequences were compared with those deposited in GenBank using BLAST sequence similarity searches (National Centre for 14 Biotechnology Information, NCBI) to confirm the species identification. Results from both the 15 RFLP digestion and DNA sequencing are listed in Table 1, and a subset shown in Fig. 2. 16 Fragment sizes were generally uniform within species (exceptions described below), and the 17 species identifications from the RFLP assay correctly corresponded to previously assigned 18 species identifications. Undigested PCR product was occasionally observed in digest patterns of 19 G. carpenteri (Fig. 1 and Fig. 2G, H) and G. australes (Fig. 1 and Fig. 2I), but this did not 20 21 interfere with species identification.

Gambierdiscus belizeanus, G. silvae, and *Gambierdiscus* ribotype 2 exhibited consistent, but
 similar, fragment sizes that required further evaluation (Fig. 3A). Analyzing the band size of the

uncut D1-D2 PCR product enabled identification of *G. belizeanus*, as this species consistently
produced two bands that were easily distinguished using gel electrophoresis (Fig. 3B).
Distinguishing between *G. silvae* and *Gambierdiscus* ribotype 2, however, was more difficult. *Gambierdiscus silvae* has a shorter D1-D2 sequence length (ca. 688 bp) compared to that of *Gambierdiscus* ribotype 2 (ca. 744 bp), but this size difference was not readily apparent on an
agarose gel unless these taxa were analyzed side by side (Fig. 3B).

7 In order to investigate the intra-specific uniformity in RFLP patterns for species distributed in both the Pacific Ocean and Caribbean Sea, isolates of G. caribaeus and G. carpenteri from 8 9 French Polynesia were analyzed and their RFLP profiles compared with conspecific isolates 10 from St. Thomas, USVI. Restriction site analysis of LSU rDNA sequences (D1-D2 region) 11 collected from these isolates was also carried out to determine if differences in RFLP profiles could be attributed to sequence heterogeneity. Pacific isolates of both species exhibited variation 12 13 in RFLP patterns, which was consistently observed in multiple digests of these particular strains. For example, the ~ 278 bp digestion fragment that was clearly visible in restriction profiles of G. 14 *caribaeus* isolates from the Caribbean (Fig. 2A) appeared to be absent from RFLP profiles of the 15 Pacific G. caribaeus isolates from French Polynesia (Fig. 2B). Restriction site analysis of D1-D2 16 sequences of the G. caribaeus isolate NH-1 from French Polynesia showed that certain clones 17 exhibited a single base change directly adjacent to the HpyCH4IV recognition site, which may 18 19 have resulted in the loss of this restriction site in these strains (Supplementary Fig. S1). Information about this phenomenon is scarce, but the loss of recognition sites due to point 20 21 mutations in flanking bases has been reported previously (Klein et al., 1991). Despite this 22 difference, the Pacific isolates were readily identified as G. caribaeus based on the other observed fragments. Additionally, RFLP analysis of the two Pacific isolates of G. carpenteri 23

1 generated banding patterns that differed from conspecific isolates from the Caribbean (Fig. 2G), 2 and also from each other (Fig. 2H). Both isolates produced the expected ca. 233 bp fragment; however, additional bands observed did not match the species-specific RFLP pattern (Fig. 2G, 3 4 H). Sequence analysis confirmed that both isolates are indeed G. carpenteri (Supplementary Fig. 5 S2), but species identification could not be assigned with the RFLP assay due to these unique banding patterns. Restriction site analysis of the D1-D2 sequences of these isolates showed that 6 isolate NH-2 contained internal deletions (Supplementary Fig. S2). These particular sequences 7 were ~60 bp shorter than the full-length sequences. Additionally, some of the sequences 8 9 obtained from these isolates included base changes that produced additional recognition sites for the enzymes used in this assay. 10

11 Discussion

12 Over the past two decades, significant progress has been made in identifying and describing the considerable species and strain diversity within the Gambierdiscus genus, thus advancing our 13 14 knowledge of the biogeography and community composition of *Gambierdiscus* populations. The toxin producing capabilities of these newly described species and ribotypes are not fully known, 15 although prior laboratory studies have shown that toxin production is highly variable among 16 species (e.g., Chinain et al., 1999a) and strains (e.g., Holmes et al., 1994). As multiple 17 Gambierdiscus species can co-exist within a particular reef ecosystem, information on the 18 community diversity and the prevalence of toxin-producing species and strains is an important 19 part of assessing and understanding spatial and temporal trends in the prevalence of toxic fish 20 21 and cases of ciguatera. The goal of this study was to develop a rapid and low-cost method for 22 routine species identification that can be used in conjunction with monitoring programs, either as a screening method prior to the selection of species and strains for further study, or in 23

combination with other methods of community diversity profiling (e.g., qPCR; Vandersea et al.,
 2012; Nishimura et al., 2016). This assay was employed in the routine identification of isolates
 from the Caribbean Sea, but is also capable of distinguishing several *Gambierdiscus* species
 commonly observed in the Pacific.

5 Because RFLP analysis is operationally straightforward, comparatively inexpensive, and 6 does not require specialized equipment, it has obvious advantages compared to other methods 7 such as DNA sequencing, which for *Gambierdiscus* requires bacterial cloning of PCR products to distinguish pseudogenes (Richlen and Barber, 2005), and may not be practical for the 8 9 identification of large numbers of cultured strains. RFLP assays provide a rapid and reliable means for screening large numbers of cultures, and have been widely used for species 10 11 identifications and in the study of the community structure of many different groups of microorganisms such as fungi and algae, including taxa responsible for HABs (Scholin et al., 12 13 1994; Chang et al., 2006; Dickie and FitzJohn, 2007). For example, RFLP assays for Alexandrium spp. were described by Scholin and Anderson (1994), Scholin et al. (1996), and 14 Adachi et al. (1994), based on multiple restriction enzyme cleavage of small subunit (SSU) 15 rRNA gene, LSU rRNA gene, and 5.8S rDNA-ITS regions, respectively. RFLP profiling has also 16 been used to distinguish Alexandrium affine and A. margalefii from Bahía Concepción, Mexico 17 (Band-Schmidt et al., 2003). These methods have been used with great success to identify 18 19 several toxin-producing species responsible for paralytic shellfish poisoning (PSP), which prompted the approach outlined here. 20

In this study, the restriction enzymes *Spe*I, *Hpy*CH4IV, and *Taq*αI were selected for the assay based on successful *in silico* analysis, and this combination was tested using DNA extracts of ten *Gambierdiscus* species, one ribotype, and two morphologically similar *Fukuyoa* species.

1 Subsequent to these analyses, we used RFLP profiling to analyze a culture collection comprising 2 63 isolates to assess intra-specific length heterogeneity and RFLP pattern uniformity. In these in silico and laboratory analyses, the selected enzyme combination generated apparent and unique 3 4 DNA fragment patterns for all species tested, with the exception of G. silvae and Gambierdiscus ribotype 2, which exhibited similar RFLP patterns (Fig. 3A), and required longer electrophoresis 5 6 duration (>1.5 h) to separate them (Fig. 3B). Examination of the uncut PCR product aided in 7 distinguishing these groups, as the D1-D2 region exhibits length heterogeneity that can be visualized on an agarose gel (ca. 688 bp and 744 bp for G. silvae and Gambierdiscus ribotype 2, 8 9 respectively; see Fig. 3B). However, this size difference was not readily apparent on an agarose 10 gel unless these taxa were analyzed side by side. Increasing the duration of gel electrophoresis or separation on an acrylamide gel may aid in resolving these species, or an alternative means of 11 identification may occasionally be required. Several quality control (QC) procedures to ensure 12 that the assay is functioning properly can also be employed, and include: (1) analyzing uncut 13 PCR product using gel electrophoresis to ensure that PCR amplification was successful, and to 14 assess uncut PCR product length; (2) analyzing both uncut and digested DNA on the same gel to 15 better distinguish length heterogeneity of the uncut DNA and identify undigested PCR product; 16 17 (3) measure and standardize the PCR product concentration used in each digestion reaction (for labs with access to a nanodrop or some other means of analyzing DNA concentration); (4) 18 including one or more positive controls (i.e., DNA extraction from an identified culture) in PCR 19 20 amplifications and RFLP digestions; and (5) including one or more positive controls (digested PCR product) along with unknowns in the gel electrophoresis analysis. To the extent feasible, 21 22 multiple isolates of each species were tested, but for some species only one DNA extract was

analyzed due to the limited availability of these isolates, and recently described species were not
 tested due to the unavailability of cultures.

During these analyses, the smaller fragments (<100 bp) used to help distinguish *G*. *carolinianus*, *G. polynesiensis*, and *G. toxicus* were often faint (Fig. 1), possibly due to the low
resolution of agarose electrophoresis, differences in DNA concentrations, and limitation of visual
observation. Increasing the digestion volume (up to 12 μl) did not improve the appearance of
these fragments; however, using polyacrylamide rather than agarose gels would likely improve
the resolution. Fortunately, differences in banding patterns were such that this limitation did not
affect the assay's ability to effectively discriminate among these species.

Additionally, RFLP digests of G. carpenteri and G caribaeus strains from the Pacific 10 11 (French Polynesia) produced fragment patterns that differed from the Caribbean isolates (Figs. 2A-B, 2G-H), despite multiple repeats of the digest. One of the fragments present in restriction 12 13 profiles of G. caribaeus isolates from the Caribbean appeared to be absent from profiles of the 14 Pacific isolates (Figs. 2A-B). Gambierdiscus carpenteri from the Pacific also exhibited banding patterns that were different from the Caribbean isolates, and also from each other. Three bands 15 (ca. 443, 320, and 233 bp) were observed in digests of isolate Rik-5 and three distinct bands (ca. 16 385, 233, and 115 or 118 bp) were observed in digests of NH-2 (Fig. 2H). Based on restriction 17 18 site analysis of the D1-D2 sequences of these isolates, these RFLP patterns are likely due to the presence of nucleotide substitutions that either eliminated restriction sites (G. caribaeus, 19 Supplementary Fig. S1), or produced additional recognition sites for the enzymes used in this 20 assay (G. carpenteri, Supplementary Fig. S2). Pseudogenes containing internal deletions are 21 22 well-documented in Gambierdiscus spp. (Richlen and Barber, 2005) and may have also contributed to these aberrant RFLP patterns. With the exception of these isolates, aberrant 23

patterns were infrequently observed; however, the variation we observed in these globally
 distributed and closely related species illustrates that an alternative confirmation method may
 occasionally be needed to confirm an isolate's identity.

4 The RFLP approach offers several advantages over other approaches to species identification (DNA sequencing, SEM) and the analysis of community diversity, although the 5 6 method does require some laboratory skill and resources, and there are biases inherent in using 7 this approach to assess community diversity. As cells must be isolated from field samples and established in culture, the survival of particular strains over others may skew the perception of 8 9 species composition. The RFLP also requires both a PCR and digestion step, but the cost to 10 perform these reactions is far lower than both qPCR and DNA sequencing costs. Another 11 advantage of this method is its sensitivity. For example, this method readily discriminates groups separated by very low phylogenetic distance (e.g., G. toxicus and G. pacificus; G. 12 13 caribaeus and G. carpenteri). Overall, the RFLP method greatly benefits labs with culturing facilities that are interested in a low cost, phylogenetically sensitive, and rapid screening 14 approach to identify *Gambierdiscus* isolates. The approach is also operationally simple, requiring 15 basic molecular laboratory capabilities (PCR amplification and gel electrophoresis), making the 16 method useful in countries where DNA sequencing facilities and/or SEM are costly and/or 17 unavailable. 18

Following its development, this method was successfully used in conjunction with DNA sequencing for the identification of cultures established during monthly sampling in St. Thomas, USVI, and the Florida Keys, USA, as well as isolates established from San Salvador, Bahamas. These cell isolation and culture establishment activities were carried out routinely as part of a broader program to assess the *Gambierdiscus* population dynamics, community composition, and

1 growth physiologies of *Gambierdiscus* species/ribotypes at these study locations. The 2 development of this assay was motivated by the labor and expense associated with traditional 3 methods of species identification of the large numbers of cultures established during this 4 research (e.g., DNA sequencing and morphological analysis). The enzyme combination used in 5 this assay proved to be a sensitive and effective method for distinguishing most of the described 6 *Gambierdiscus* species, and complements other existing, validated methods for species 7 identification and the analysis of community diversity.

8 Conclusions

Here the development of a RFLP assay that effectively distinguishes at least nine Gambierdiscus 9 10 species, and two morphologically similar *Fukuyoa* species is described. This method was tested 11 using cultures established during monthly monitoring to assess *Gambierdiscus* abundance and toxicity in St. Thomas, USVI, the Bahamas, and the Florida Keys, USA, and with isolates from 12 13 French Polynesia and Japan. This LSU rDNA-based RFLP assay readily distinguished most of 14 the known Gambierdiscus species, and was successfully used over a period of two years to identify isolates established from field sampling in the Caribbean. Where possible, multiple 15 isolates of each species were examined, many of which exhibited intra-specific uniformity in 16 their electrophoretic patterns; however, additional work is still needed to investigate the 17 18 interference of pseudogenes, and to better document intra-specific sequence heterogeneity observed in Pacific versus Caribbean strains of G. caribaeus and G. carpenteri. Nonetheless, this 19 assay proved to be an effective method for routine identification of Gambierdiscus species, and 20 21 could supplement or in some instances replace current methods for the analysis of laboratory 22 cultured isolates.

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1 Tables

Table 1. Isolate name and geographic origin of *Gambierdiscus* and *Fukuyoa* spp. used for RFLP assay testing, and comparison between RFLP typing results and identification based on DNA sequencing or alternative method. Percent identity levels based on BLAST sequence similarity searches in GenBank are shown in parentheses. In the interest of simplifying the assay description and results, the first four letters of each species name (shown in alphabetical order) is used to represent each *Gambierdiscus* and *Fukuyoa* species, except for *Gambierdiscus* ribotype 2 (Ribo2).

Isolates	Geographic Origin	Abbreviation	Species identification based on DNA sequencing or alternative method	RFLP Recognition
BB Apr 11-11	St. Thomas, USVI	Cari1	G. caribaeus (100%)	G. caribaeus
BB May 10-12	St. Thomas, USVI	Cari2	G. caribaeus (99%)	G. caribaeus
BP Aug 08	St. Thomas, USVI	Cari3	G. caribaeus (99%)	G. caribaeus
HGB7	Florida Keys, FL, USA	Cari4	G. caribaeus (100%)	G. caribaeus
LKH4	Florida Keys, FL, USA	Cari5	G. caribaeus (99%)	G. caribaeus
Tenn10	Florida Keys, FL, USA	Cari6	G. caribaeus (100%)	G. caribaeus
STT_Cari6	St. Thomas, USVI	Cari7	G. caribaeus (99%)	G. caribaeus
STT_Cari19	St. Thomas, USVI	Cari8	G. caribaeus (100%)	G. caribaeus
NH-1	Nuku-Hiva, Marquesas, French Polynesia	Cari9	G. caribaeus (100%)	G. caribaeus
Rik-1	Mangareva, Gambier, French Polynesia	Cari10	G. caribaeus ^a	G. caribaeus

BB May 10-11	St. Thomas, USVI	Carol	G. carolinianus (99%)	G. carolinianus
-				
FC Apr 11-2	St. Thomas, USVI	Caro2	G. carolinianus (99%)	G. carolinianus
BP May 10-5	St. Thomas, USVI	Caro3	G. carolinianus (99%)	G. carolinianus
LKH10	Florida Keys, FL, USA	Caro4	G. carolinianus (99%)	G. carolinianus
GHCG2-C6	San Salvador, Bahamas	Caro5	G. carolinianus (99%)	G. carolinianus
TRL26	Florida Keys, FL, USA	Caro6	G. carolinianus (99%)	G. carolinianus
GHCG2-A6	San Salvador, Bahamas	Caro7	G. carolinianus (99%)	G. carolinianus
GHCG2-B8	San Salvador, Bahamas	Caro8	G. carolinianus (99%)	G. carolinianus
CCMP399	St. Barthelemy Island	Beli1	G. belizeanus ^b	G. belizeanus
FC Dec 10-13	St. Thomas, USVI	Beli2	G. belizeanus (99%)	G. belizeanus
BP Apr 11-7	St. Thomas, USVI	Beli3	G. belizeanus (99%)	G. belizeanus
BP Mar 10-18	St. Thomas, USVI	Beli4	G. belizeanus (99%)	G. belizeanus
BP Mar 10-22	St. Thomas, USVI	Beli5	G. belizeanus (99%)	G. belizeanus
BP Mar 10-25	St. Thomas, USVI	Beli6	G. belizeanus (99%)	G. belizeanus
BP Mar 10-31	St. Thomas, USVI	Beli7	G. belizeanus (99%)	G. belizeanus
BP Mar 10-7	St. Thomas, USVI	Beli8	G. belizeanus (99%)	G. belizeanus
MUR-4	Moruroa, Gambier, French Polynesia	Paci1	G. pacificus °	G. pacificus
Hao1 (or HO-91)	Hao, Tuamotu, French Polynesia	Paci2	G. pacificus °	G. pacificus
Tub ET1	Tubuai, Australes, French Polynesia	Paci3	G. pacificus ^a	G. pacificus
BP Apr 11-6	St. Thomas, USVI	Ribo21	G. ribotype 2 (99%)	G. ribotype 2
BP Apr 11-6	St. Thomas, USVI	Ribo21	G. ribotype 2 (99%)	G. ribotype 2

SH Dec 10-10	St. Thomas, USVI	Ribo22	<i>G</i> . ribotype 2 (99%)	G. ribotype 2
SH Dec 10-12	St. Thomas, USVI	Ribo23	<i>G</i> . ribotype 2 (99%)	G. ribotype 2
TRL29	Florida Keys, FL, USA	Ribo24	<i>G</i> . ribotype 2 (100%)	G. ribotype 2
HGB	Florida Keys, FL, USA	Yasu	F. yasumotoi (94%)	F. yasumotoi
HGB6	Florida Keys, FL, USA	Carp1	G. carpenteri (99%)	G. carpenteri
KML1	Florida Keys, FL, USA	Carp2	G. carpenteri (99%)	G. carpenteri
TPH12	Florida Keys, FL, USA	Carp3	G. carpenteri (99%)	G. carpenteri
STT_Carp5	St. Thomas, USVI	Carp4	G. carpenteri (99%)	G. carpenteri
STT_Carp8	St. Thomas, USVI	Carp5	G. carpenteri (99%)	G. carpenteri
STT_Carp9	St. Thomas, USVI	Carp6	G. carpenteri (99%)	G. carpenteri
STT_Carp11	St. Thomas, USVI	Carp7	G. carpenteri (99%)	G. carpenteri
STT_Carp24	St. Thomas, USVI	Carp8	G. carpenteri (99%)	G. carpenteri
Rik-5	Mangareva, Gambier, French Polynesia	Carp9	G. carpenteri (98%)	Inconclusive
NH-2	Nuku-Hiva, Marquesas, French Polynesia	Carp10	G. carpenteri (99%)	Inconclusive
РО	Tahiti, Society, French Polynesia	Aust1	G. australes ^a	G. australes
RAV-1	Raivavae, Australes, French Polynesia	Aust2	G. australes ^a	G. australes
G3-93	Mangareva, Gambier, French Polynesia	Aust3	G. australes ^a	G. australes
S080911_1	Kutsu, Kochi, Japan	Aust4	G. australes ^e	G. australes
ISC5G	Touzato, Ishigaki Island, Okinawa, Japan	Aust5	G. australes ^e	G. australes
I080606_1	Sawada Beach, Irabu Island, Okinawa, Japan	Aust6	G. australes ^e	G. australes

Rai1	Raivavae, Australes, French Polynesia	Poly1	G. polynesiensis ^c	G. polynesiensis
Rik-8	Mangareva, Gambier, French Polynesia	Poly2	G. polynesiensis ^a	G. polynesiensis
RG-92	Rangiroa, Tuamotu, French Polynesia	Poly3	G. polynesiensis ^c	G. polynesiensis
TB-92	Tubuai, French Polynesia	Poly4	G. polynesiensis ^e	G. polynesiensis
GTT-1	Tahiti, Society, French Polynesia	Toxi1	G. toxicus ^a	G. toxicus
Rik-13	Mangareva, Gambier, French Polynesia	Toxi2	G. toxicus ^a	G. toxicus
HIT-0	Tahiti, French Polynesia	Toxi3	G. toxicus ^c	G. toxicus
CCMP 3143	Carrie Bow Cay, Belize	Ruez	F. ruetzleri ^b	F. ruetzleri
BP Mar 10-23	St. Thomas, USVI	Silv1	G. silvae (100%)	G. silvae
FC May 10-9	St. Thomas, USVI	Silv2	G. silvae (99%)	G. silvae
SH Apr 11-1	St. Thomas, USVI	Silv3	G. silvae (99%)	G. silvae
TRL23	Florida Keys, FL, USA	Silv4	G. silvae (99%)	G. silvae
M080828_3	Muroto Promontory, Kochi, Japan	Scab	G. scabrosus ^d	G. scabrosus

2 ^a Isolate from culture collection maintained by the Institut Louis Malardé, Tahiti, French Polynesia

3 ^b Isolate from culture collection maintained by the National Center for Marine Algae and Microbiota at Bigelow Laboratory, East Boothbay, ME,

4 USA

^c see Chinain et al. (2010)

6 ^d see Nishimura et al. (2013)

^e see Chinain et al. (1999a)

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Table 2. Recognition sites of the restriction enzymes *Spe*I, *Hpy*CH4IV, and *Taq*αI.

	Enzyme	SpeI	HpyCH4IV	TaqaI
	Recognition site	A/CTAGT	A/CGT	T/CGA
8				
9				
10				
11				
12				
13				
14				
15				
16				

Table 3. Fragment sizes for 12 *Gambierdiscus* species, one ribotype, and three *Fukuyoa* species.
 Abbreviated species names are represented by the first four letters of each species name except
 for *Gambierdiscus* ribotype 2 (Ribo2). Fragments are listed from 5^{-/} to 3^{-/} end of each D1-D2
 LSU rDNA sequence.

Gambierdiscus spp.	Abbreviation	Uncut PCR product size	Restriction fragment sizes (bp)
G. australes	Aust	687	493, 194
G. belizeanus	Beli	770, ~640*	617, 153
G. caribaeus	Cari	676	389, 278, 184, 98
G. carolinianus	Caro	691	635, 56
G. carpenteri	Carp	676	443, 233
G. cheloniae	Chel	712	659, 53
G. excentricus	Exce	741	500, 262, 49
G. pacificus	Paci	763	487, 153, 123
G. polynesiensis	Poly	706	626, 80
G. scabrosus	Scab	778	512, 276
G. silvae	Silv	688	573, 115
G. toxicus	Toxi	726	726
Gambierdiscus ribotype 2	Ribo2	744	609, 135
F. ruetzleri	Ruet	747	530, 142, 75
F. paulensis	Paul	708	432, 103, 98, 40, 35
F. yasumotoi	Yasu	697	434, 188, 75

^{*} Smaller fragment size estimated from agarose gel.

1 Figures

Figure 1. RFLP profiles of LSU rDNA (D1-D2 hypervariable regions) from ten *Gambierdiscus*species, one ribotype, and two *Fukuyoa* species. Cari: *G. caribaeus* (BP Aug 08), Caro: *G. carolinianus* (GHCG2-C6), Beli: *G. belizeanus* (CCMP399), Paci: *G. pacificus* (Tub ET1),
Ribo2: *Gambierdiscus* ribotype 2 (SH Dec 10-10), Yasu: *F. yasumotoi* (HGB), Carp: *G. carpenteri* (HGB6), Aust: *G. australes* (RAV-1), Poly: *G. polynesiensis* (Rai1), Toxi: *G. toxicus*(GTT-1), Ruez: *F. ruetzleri* (CCMP 3143), Silv: *G. silvae* (SH Apr 11-1), Scab: *G. scabrosus*

8 (M080828_3), Mk: DNA marker.

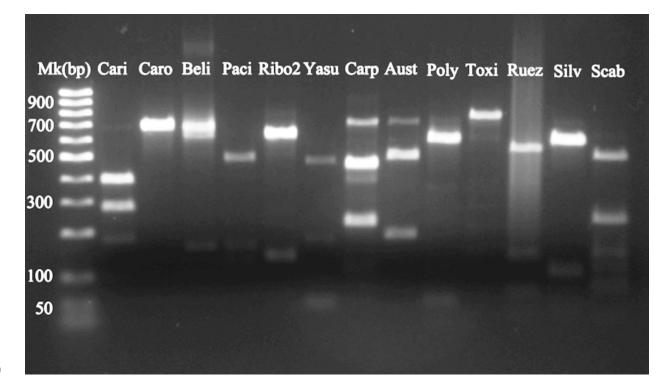
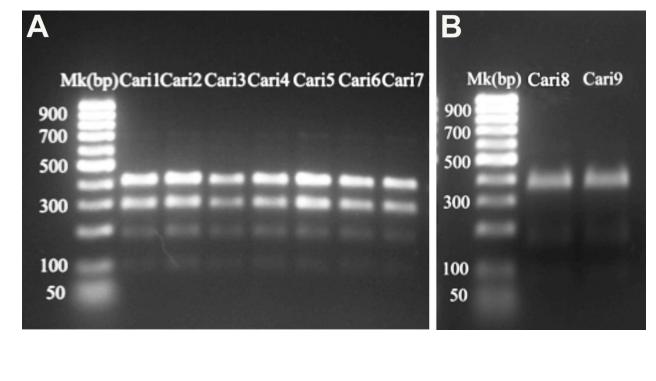
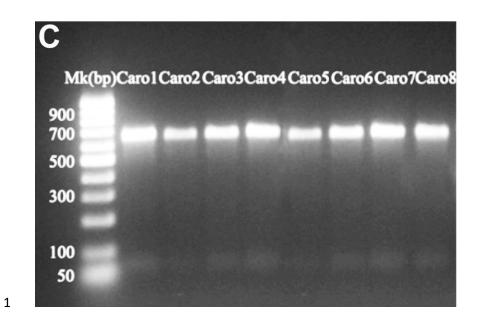
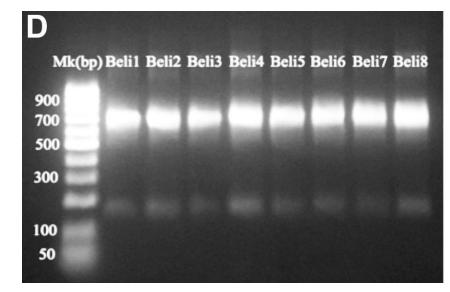
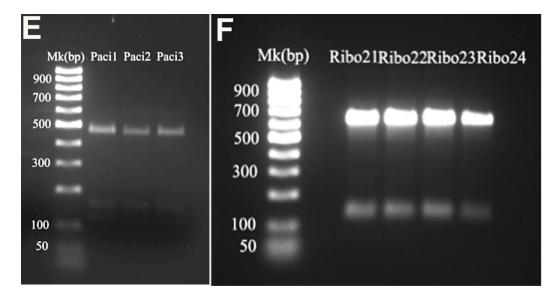


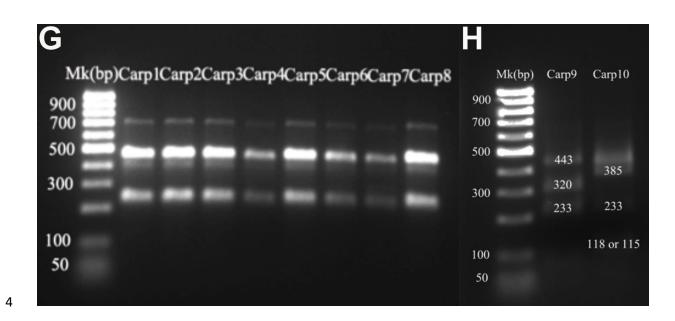
Figure 2. RFLP profiles of LSU rDNA (D1-D2 hypervariable regions) of conspecific strains. A: G. caribaeus from Caribbean Sea (Cari1~7), B: G. caribaeus from French Polynesia (Cari8~9), C: G. carolinianus (Caro1~8), D: G. belizeanus (Beli1~8), E: G. pacificus (Paci1~3), F: Gambierdiscus ribotype 2 (Ribo21~4), G: G. carpenteri from the Caribbean Sea (Carp1~8), H: Pseudogene-containing G. carpenteri from French Polynesia (Carp9 and 10), I: G. australes (Aust1~6), J: G. polynesiensis (Poly1~4), K: G. toxicus (Toxi1~3), L: G. silvae (Silv1~4). See Table 1 for additional information regarding the isolates used in each assay, including the isolate abbreviations above each lane.

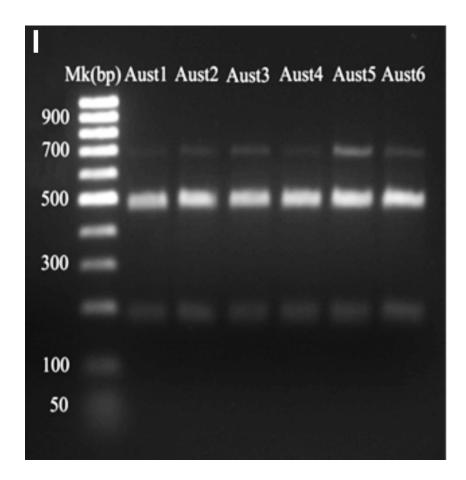


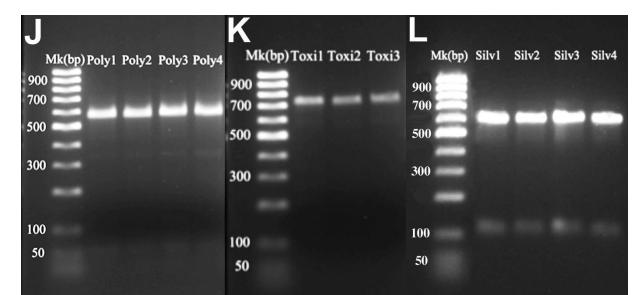




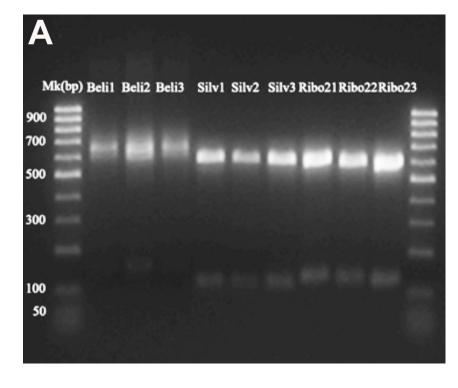




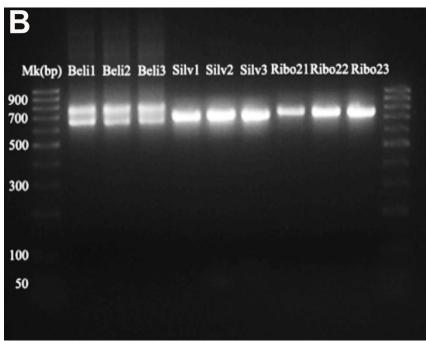




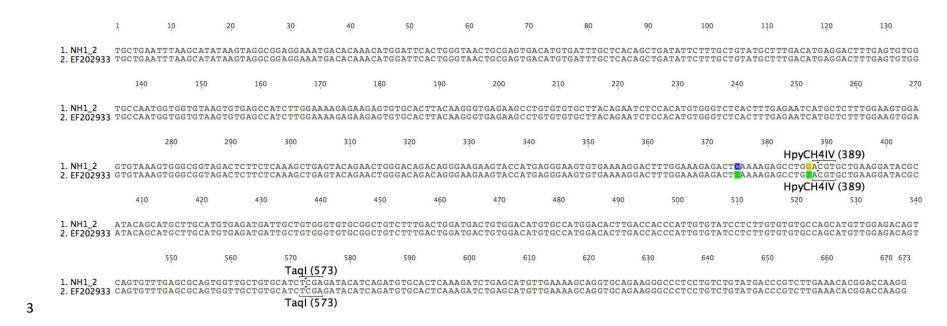
- 1 Figure 3. RFLP profiles (A) and uncut PCR product (B) of LSU rDNA (D1-D2 hypervariable
- 2 regions) from Gambierdiscus belizeanus, G. silvae, and Gambierdiscus ribotype 2. See Table 1
- 3 for additional information regarding the isolates used in each assay.







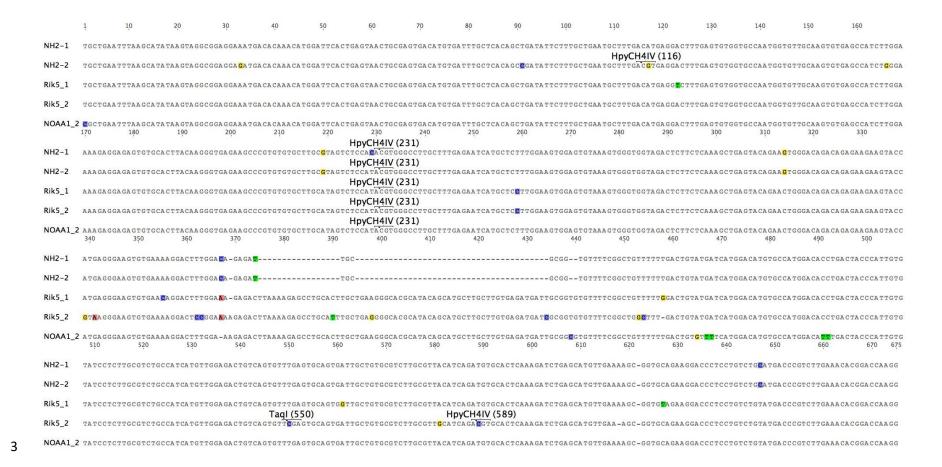
1 Supplementary Figure S1. Alignment of D1-D2 LSU rRNA gene sequence from G. caribaeus isolate NH-1 from French Polynesia,



2 along with a G. caribaeus sequence from GenBank (accession no. EF202933), annotated with known restriction sites.

1 Supplementary Figure S2. Alignment of D1-D2 LSU rRNA gene sequences from G. carpenteri isolates from French Polynesia (NH-

2 2 and Rik-5), along with a *G. carpenteri* sequence from GenBank (accession no. EF202938), annotated with known restriction sites.



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