Molecular diversity of *Symbiodinium* spp. within six coral species in Larak Island, the Persian Gulf

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Abstract

Reef-building coral harbor communities of photosynthetic taxa of the genus Symbiodinium (zooxanthellae). The genus Symbiodinium is currently classified into nine genetic clades (A-I). Various corals harbor different Symbiodinium clades; some show specificity to a single strain. Coral and their zooxanthellae are sensitive to environmental stresses. In the Persian Gulf, coral reefs are subject to harsh environmental conditions including extreme temperatures and high salinity. This is the first study to use clade specific primers to clarify the diversity of Symbiodinium in each coral species of Larak Island. For this purpose six coral species were collected at two different locations in Larak Island. After DNA extraction, PCR amplification was performed using clade specific primers. The results showed that multiple Symbiodinium clades are hosted by most coral species. In addition, among thirteen obtained Symbiodinium sequences, the frequency of either tree clades, A, C and D was almost the same. Corals species may contain different clades of Symbiodinium depending on the region and on the tolerance characteristics of each clade. Thus, knowledge of zooxanthellae diversity associated with scleractinian can contribute to a better understanding of the sensitivity of corals to environmental conditions.

Keywords: Persian Gulf, Symbiodinium, Clade A, Clade C, Clade D.

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Introduction

Reef corals are hosts to a group of exceptionally diverse dinoflagellate symbionts of the genus Symbiodinium (commonly referred to as zooxanthellae) (Pochon and Gates. 2010). The high productivity and diversity of coral reefs is largely due to this mutualistic symbiosis (Silverstein et al., 2012). The Symbiodinium transports newly fixed organic carbon to the coral and, in return, receive inorganic waste metabolites from host respiration and an environment free from predators (Davy, 2012).

Symbiodinium are morphologically most species cryptic and are morphologically similar (Baker, 2003). Therefore, their identification must be done on molecular methods. It has been established that there are at least nine major clades of this dinoflagellate genus (Pochon and Gates, 2010). Numerous sub-clades and types have also been identified within each Symbiodinium clade, most commonly using the internal transcribed spacer-2 (ITS-2) marker (LaJeunesse, 2002).

Scleractinian coral and their endosymbiont are sensitive to environmental stresses that include high salinity (Reimer. 1971). temperatures (Hoegh-Guldberg and Smith, 1989), low temperatures (Steen and Muscatine, 1987), ultraviolet radiation (Gleason and Wellington, 1993) and turbidity (Trench, 1986). The physiological responses of Symbiodinium vary greatly among phylogenetic types; for example, among

the known clades, Symbiodinium clade D has a higher thermal tolerance than other clades, and clade D increases the resistance of corals that harbor them to elevated sea surface temperatures (Rowan, 2004: Berkelmans and van Oppen. thermal 2006). The and flexibility physiological of *Symbiodinium* may provide mechanisms for scleractinian corals to survive under unfavorable conditions (Berkelmans and van Oppen, 2006).

The previous studies have shown that corals associate with different *Symbiodinium* clades or types depending on local environmental conditions (Baker, 2003). The Persian Gulf. located in the northwest of the Indian Ocean, is known as one of the most extreme environments for coral reefs with high temperature fluctuations. high salinity, high turbidity and low depth (Sheppard et al., 1992; Baker, 2004). Research conducted on northern Persian Gulf zooxanthellae since 2005 demonstrates the occurrence of Symbiodinium clades D, C and A in the shallow waters of the world's hottest sea (Mostafavi et al., 2005, 2014; Shahhosseiny et al., 2011). The present study aims to investigate the diversity of Symbiodinium in coral species of Larak Island, one of the seventeen islands in the northern Persian Gulf. Individual colonies can with associate several genetically symbionts distinct simultaneously. Corals of the same species may vary in depending their symbionts on environmental characteristics (van Oppen *et al.*, 2001). Therefore, the results of this survey will provide a valuable insight to the survival of Iranian coral reefs in the unfavorable environment of the Persian Gulf.

Material and methods

Sampling

Colonies of six species of scleractinian corals, Favia pallida (DANA, 1846); Leptastrea transversa (Klunzinger, 1879); Psammocora contigua (Esper, 1794); Stylophora pistillata (Esper, 1797); Pocillopora damicornis (Linnaeus, 1758) and Acropora downingi (Wallace, 1999) were collected from two sites, S1 (latitude 26° 53' 22.39" N, longitude 56° 21' 10.44" E) and S2 (latitude 26° 52' 33.61"N, longitude 56° 20' 9.84" E), at depths 3 m (S1) and 6 m (S2) off Larak Island (Fig. 1) during March 2013. collection. After samples were preserved in DMSO buffer (20% DMSO, 0.25M EDTA, saturated with NaCl, pH=8) and transferred to the marine biology laboratory in the Islamic Azad University, Science and Research Branch.

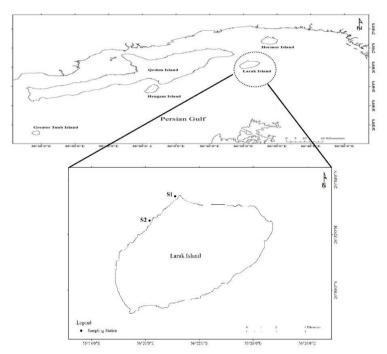


Figure 1: Map of the Larak Island showing the position of the sampling locations.

DNA extraction PCR amplification and sequencing

DNA was extracted using cetyl trimethylammonium bromide (CTAB)/Chloroform method (Baker, 1999). Polymerase Chain Reactions (PCR) assays were performed using three clade-specific primer sets targeting the ITS1-5.8S-ITS2 (for clade A) (Correa *et al.*, 2009), domain 2 of the LSU (for clade D) (Correa *et al.*, 2009) and partial ITS 1 (for clade C) (Ulstrup and van Oppen, 2003) of the nuclear rDNA of *Symbiodinium*. Each PCR reaction comprised, 1.5 mM MgCl₂, 0.2 mM dNTPs Mix, 10 pmol

of each primer, 0.3 U Taq DNA polymerase and 1 ng DNA Template for a total volume of 25 µL. Amplification was performed using a Bio-Rad PCR Thermal Cycler with the following thermal profile: 30 cycles of 30s at 94°C, 30 s at 58°C, 56°C and 60°C (for clade A, C and D, respectively), 30s at 72°C and a final extension for 5 min at 72°C. The PCR products were analyzed bv electrophoresis in 1.5% agarose gels. Thirteen PCR products obtained from this study were directly sequenced to confirm that the specific primers only recognize the target of interest. Finally, this was approved by constructing a phylogenetic tree based on sequences of each molecular marker.

Phylogenetic analyses

Sequences obtained from this study were deposited in a GenBank and their accession numbers are shown in Table 1. The new nucleotide sequences obtained during the present study were aligned with sequences available from Genbank using the software the CLUSTALW (Thompson et al., 1994). alignment datasets Three were generated (for clade A, C and D). The alignment datasets were analyzed using maximum likelihood (ML), maximum parsimony (MP) and Bayesian methods.

| Coral species | Symbiodinium | GenBank |
|------------------------|--------------|-------------------|
| | clade | accession numbers |
| Favia pallida | Clade A | KT069226 |
| Leptastrea transversa | Clade A | KT069227 |
| Stylophora pistillata | Clade A | KT069228 |
| Pocillopora damicornis | Clade A | KT069229 |
| Favia pallida | Clade C | KT069230 |
| Leptastrea transversa | Clade C | KT069231 |
| Psammocora contigua | Clade C | KT069232 |
| Stylophora pistillata | Clade C | KT069233 |
| Pocillopora damicornis | Clade C | KT069234 |
| Favia pallida | Clade D | KT069235 |
| Leptastrea transversa | Clade D | KT069236 |
| Psammocora contigua | Clade D | KT069237 |
| Acropora downingi | Clade D | KT069238 |

| Table1: Host species, Symbiodinium | n clade and GenBank accession numbers. |
|------------------------------------|--|
| | |

The most appropriate model selection for ML and Bayesian analyses was performed using Akaike Information Criterion (AIC) in MODELTEST 2.3 (Nylander, 2004). The general timereversible model (Rodriguez *et al.*, 1990) with gamma parameter (GTR+G) gave the best fit to the data (clade A, C and D). ML and MP analyses were conducted using the MEGA6 (Tamura *et al.*, 2013) and PAUP beta version 4.0b10 (Swofford, 2002) respectively. ML and MP clades were assessed with 1,000 bootstrap replicates. The Bayesian analysis was implemented in 2.3 **MrBayes** (Ronquist and Huelsenbeck, 2003) and was based on the model selected by MODELTEST above. Starting from random trees, four Markov chains (with one cold and three heated chains) were run simultaneously to sample trees using the Markov Chain Monte Carlo (MCMC) principle which approximates the posterior probability (PP) of trees. After the burn-in phase (the first 5 million generations was discarded), every 100th tree out of 20^6 was considered. The phylogenetic trees all analyses generated in were visualized using TREEVIEW (Page, 1996).

Results

The results showed that there are three clades of Symbiodinium from Larak Island; clade A, C and D. Symbiodinium sequences belonging to clade A were identified from F. pallida. L. S. pistillata transversa. and Р. damicornis, clade C from F. pallida, L. transversa, S. pistillata, P. damicornis, P. contigua and clade D from F. pallida, L. transversa, P. contigua and A. downingi.

Figs. 2, 3 and 4 show the ML phylogenetic tree for the aligned sequences. As the tree topologies were similar in all analyses, the bootstrap values for MP and Bayesian posterior probabilities are shown on the ML tree (Figs. 2, 3 and 4).

The phylogenetic tree of *Symbiodinium* clade A sequences is shown in Fig. 2. The clade A

Symbiodinium from four coral species strongly clustered (ML=91%. MP=90%, PP=0.9) with subclade A1 Symbiodinium that is hosted by *Cassiopea xamachana* in Jamaica (AF427466), Acropora sp. in Japan (AB849873-AB849875) and Zoanthus South sansibaricus in Africa (KM032592).

The phylogenetic tree of Symbiodinium clade C ITS -1 sequence is shown in Fig. 3. The clade C Symbiodinium sequences from five coral species together with previously reported sequences, including some sequences from zoantharians in Madagascar (KM032585), Singapore (EU333738) and South Africa (KM032562) formed a highly supported monophyly (ML= 99%, MP=100%, PP=1.0) within the Symbiodinium clade C radiation.

Phylogenetic results of large subunit ribosomal (LSU) RNA gene analyses are shown in Fig. 4. In the tree of clade D, all D-matching sequences from four coral species grouped with five previously reported sequences that belonged to clade D AB778761, AB778758. AB778750 from nudibranch and KF672733, KF030947 from stony corals in a well- supported monophyly (ML= 100%, MP=100%, PP=1.0).

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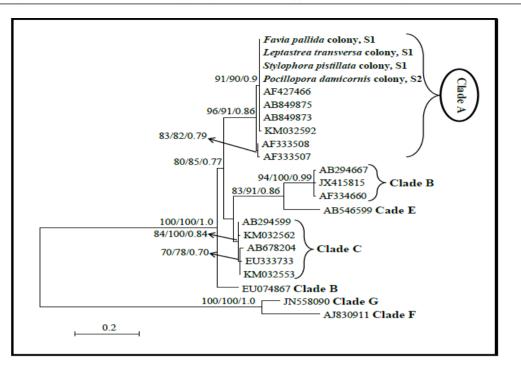


Figure 2: Maximum likelihood tree of ITS1-5.8S-ITS2 sequences for clade A. Values at branches represent maximum likelihood bootstrap percentages from 1000 trees/ maximum parsimony bootstrap percentages from 1000 trees/Bayesian posterior probabilities.

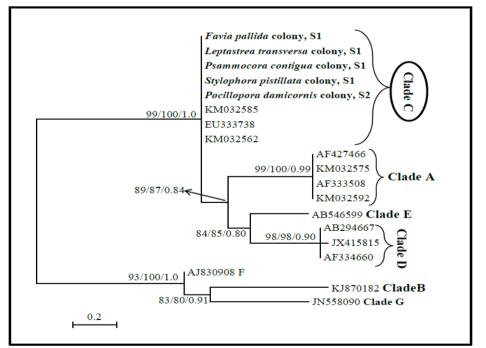


Figure 3: Maximum likelihood tree of partial ITS 1 for clade C. Values at branches represent maximum likelihood bootstrap percentages from 1000 trees/ maximum parsimony bootstrap percentages from 1000 trees /Bayesian posterior probabilities.

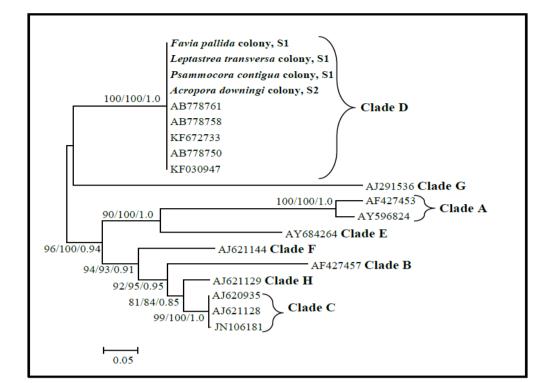


Figure 4: Maximum likelihood tree of LSU for clade D. Values at branches represent maximum likelihood bootstrap percentages from 1000 trees/ maximum parsimony bootstrap percentages from 1000 trees /Bayesian posterior probabilities

Discussion

In coral reefs off Larak Island, colonies of F. pallida and L. transversa, hosted Symbiodinium clades A, C and D simultaneously, S. pistillata and P. damicornis were associated with both Symbiodinium clades A and C, P. contigua harbored clade D and also clade C. Although the majority of coral contained species different Symbiodinium clades; Α. downingi specificity show single to Symbiodinium strain, clade D.

Several studies have shown that most coral colonies harbor multiple clade of *Symbiodinium* (Berkelmans and van Oppen , 2006; Mieog *et al.*, 2007). Therefore, in the present study PCR was performed with clade-specific primers. It appears that the occurrence of *Symbiodinium* clade in coral species is depends on a combination of factors such as symbiont availability (van Oppen *et al.*, 2001). Previous research conducted on the zooxanthellae of the Persian Gulf have demonstrated the occurrence of *Symbiodinium* clades D, C and A in this region (Baker *et al.*, 2004; Mostafavi *et al.*, 2007, 2013; Shahhosseiny *et al.*, 2011; Hume *et al.*, 2015). Consequently, three pairs of primers belonging to clade A, C and D were used to amplify the selected marker in these clades.

Most previous studies on the zooxanthellae of the Persian Gulf have shown that clade D of Symbiodinium, is of the most abundant all coral symbionts (Baker al., 2004; et

Mostafavi *et al.*, 2005, 2014; Shahhosseiny *et al.*, 2011).

Globally, clade D is common to corals from environments with high temperature and salinity (Fabricius et al., 2004), warm temperature and low light (Ulstrup and van Oppen, 2003) and high turbidity (van Oppen et al., 2001; Chen et al., 2003). Therefore, it has been concluded that the predominance of clade D in the Persian Gulf is due to the unfavorable condition of this region (Mostafavi et al., 2007). However, among the coral species collected in this study, clade D was not the most abundant symbiont. The results of the present study have shown that four colonies of the six species harbored clade A and/or D, while five of colonies six specimens were associated with clade C. The clade C dominance reported here agrees with another study of Symbiodinium from the southern Persian Gulf (Hume et al., 2015).

Although Clade C was more dominant *Symbiodinium*, other clades including A and D were commonly detected in corals off Larak Island.

Clade A of *Symbiodinium* have been found in corals inhabiting very shallow high-irradiance waters (Rowan *et al.*, 1997). It is known that only clade A of *Symbiodinium* are capable of producing considerable amounts of mycosporinelike amino acids (MAAs) (Banaszak *et al.*, 2000), compounds that help to protect against damage from UV radiation (Neale *et al.*, 1998). On the other hand, clade D of *Symbiodinium* is thermally tolerant and increases the resistance of corals that harbor them to elevated sea surface temperature. Furthermore, the thermally resistance of clade C has been reported previously (Mostafavi *et al.*, 2013). It can therefore be concluded that the simultaneous presence of these clades in common coral species of the Persian Gulf may impart some protection from future stresses that lead to coral bleaching.

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