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First Report with Molecular Confirmation of the Colonial Sphenopid *Palythoa mutuki* (Cnidaria: Anthozoa: Zoantharia: Sphenopidae) Forming Massive Colonies in Southern Jeju Island, Korea

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Abstract: As the global sea surface water temperature increases due to climate change, some zooxanthellate species have extended their habitat range to higher latitudes. *Palythoa* species, a colonial zooxanthellate cnidarian, is one such example of a range-extending animal. Recently, massive colonies of zoantharians that appeared to be of *Palythoa* spp. were discovered in a subtidal area of southern Jeju Island. Because a zoantharian-dominated ecosystem could indicate an unhealthy status, the documentation of its occurrence and species identification are crucial for subsequent studies. In this study, we report and confirm the presence of massive *Palythoa* colonies in Taeheung and Topyeong, off the southern coast of Jeju Island, using in situ underwater images and identify the species by sequencing the internal transcribed spacer rDNA. The resulting Bayesian inference tree clearly demonstrates that the massive colonies consist of *Palythoa mutuki* and are closely related to *P. mutuki* collected from the Ryukyu Archipelago in southern Japan. These records provide evidence of the northward expansion of subtropical and tropical marine organisms.

Keywords: climate change; zooxanthellate species; zoantharian-dominant ecosystem; internal transcribed spacer rDNA; habitat expansion

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1. Introduction

Range shifts and/or the expansion of marine organisms poleward have occurred due to the effects of global climate change, such as increasing seawater temperatures [1–5]. Most zooxanthellate scleractinian corals are typical organisms living in tropical regions, and coral reefs live in shallow waters with sea surface temperatures higher than 18 °C [6]. These organisms are sensitive to climate change, and their habitats are threatened by global warming [5]. The rapid poleward range expansion of tropical coral-reef-associated organisms can also occur in temperate areas owing to increasing temperatures [1,7]. Zooxanthellate corals play a fundamental role in the primary production and habitat formation of numerous marine organisms in tropical and subtropical regions. In relation to climate warming, poleward range shifts for some zooxanthellate species have already been observed in temperate areas, such as southern Australia and Korea [8,9].

Zoantharians (Cnidaria: Anthozoa: Hexacorallia: Zoantharia) are a common component of the benthic ecosystem in coral reefs, with many zooxanthellate species in subtropical and tropical regions [10–12]. Recently, they have been reported to live in India, the Gulf of Thailand, the South China Sea, and Caribbean waters [13–17]. Zoantharians are benthic organisms with two rows of tentacles, usually covered by sand and other debris, on their body wall [18]. Zoantharians are difficult to classify at the species level because they have large amounts of intraspecific variation related to various morphological characteristics, including cnidae, polyps, and colony shape, size, and color [19–21]. Recently, new species, genera, and families have been used to identify zoantharians using molecular biological methods [19,20,22–24], and a large diversity of unknown zoantharian fauna has been identified [24–27].

Jeju Island is strongly influenced by the Kuroshio warm current, which transports warm water northward from tropical areas [28]. Jeju Island is a high-latitude marginal distribution zone of corals in the Asia Pacific region, and their habitat range is gradually expanding owing to the continuous increase in the winter average water temperature [29,30]. Recently, large-scale areas of *Palythoa* sp. were observed on the Topyeong (southeastern coast) and Taeheung (southern coasts) area of Jeju Island. These areas were known as typical algae communities [31], but the spread of scleractinian coral *Alveopora japonica* and zoantharians in the barren subtidal hard bottom has recently been observed [32]. *Palythoa* sp. is a zoantharians species generally found in the Indo-Pacific Ocean at depths ranging from intertidal to >35 m [11,33]. The few studies on zoantharians in Korea have only included Reimer et al.'s reports from Jeju Island [9,34]. This study is the first to report the presence of a mass colony of a *Palythoa* community in Jeju waters with molecular confirmation.

2. Materials and Methods

2.1. Sample Collection

The study site included Taeheung (TH, 33°17′24″ N, 126°45′40″ E) and Topyeong (TP, 33°14′22″ N, 126°34′54″ E) along the southern coast of Jeju Island (Figure 1). Colonies of zoantharians that appeared to be *Palythoa* sp. were collected from the rocky subtidal bottom during scuba diving at depths of 5–10 m in October 2017 and June 2018 from TH and February 2020 from TP. In situ underwater images were captured in each study area and morphologically identified as described by Mizuyama et al. [35]. For DNA analysis, approximately 20–25 specimens of *Palythoa* species were collected thrice at TH and TP, separately. A total of 18 individuals were used for DNA extraction and PCR after selecting 3 individuals from the samples collected at each site. For molecular identification, specimens from TH (collected in June 2018) and TP (collected in February 2020) were preserved in absolute ethanol until further analysis. The collected samples were deposited in the Library of Marine Samples at the Korea Institute of Ocean Science & Technology (KIOST; Busan, Republic of Korea) under specimen number B_S_MA_00014120.

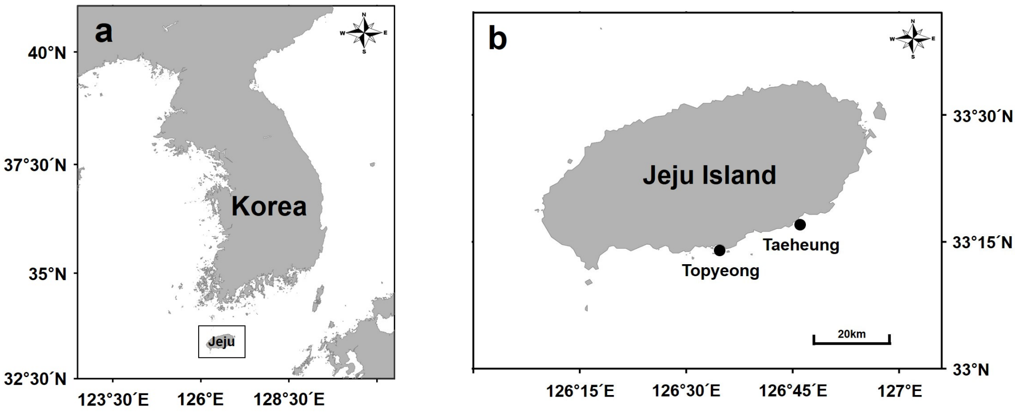

Figure 1. Map of the study area. The black dot indicates the two sampling sites, Taeheung (TH) and Topyeong (TP), off the southern coast of Jeju Island, Republic of Korea.

2.2. DNA Extraction and PCR

Total DNA was extracted from approximately 15 mg of soft tissue from each specimen using a DNeasy Blood and Tissue Kit (Qiagen, Hilden, Germany). We used the internal transcribed spacer region of nuclear ribosomal DNA (ITS rDNA) as a molecular marker because this region was proven to be inappropriate for species differentiation among the genus *Palythoa* [36]. ITS rDNA containing the ITS1, 5.8S, and ITS2 regions was amplified via PCR using a zoantharia-specific primer set (Zoan-f/Zoan-r [37]). Amplicons were visualized by performing 1.5% agarose gel electrophoresis, and positive PCR products from each locality were ligated into the cloning vector pUC118. Following cloning, nine positive recombinant clones from each locality were sequenced using a 3730xl DNA analyzer.

2.3. Phylogenetic Analyses

In total, 18 sequences were registered in GenBank under accession numbers OP896949–OP896966. Considering the relative geographical proximity and the morphological similarity of our specimen to *Palythoa* sp. reported from Japan, we decided to reference the *Palythoa* sp. ITS rDNA sequences from Japan to contrast the results. The sequences obtained in this study were aligned using Clustal W [38] with 21 ITS rDNA sequences of *Palythoa* sp. (Table 1). Once the aligned sequences were manually trimmed by removing terminal gaps, Bayesian inference (BI) phylogenetic analysis was performed using BEAST v2.7.1 [39] under the GTR substitution model. The Bayesian Markov Chain Monte Carlo was run for 2 million generations, and the first 25% of the trees was discarded. A consensus tree with Bayesian posterior probabilities was visualized using FigTree v1.4.4.

Table 1. List of GenBank accession numbers of internal transcribed spacer region (ITS) rDNA sequences of the genus *Palythoa* used in this study.

Species	Accession Number	Locality	Sampling Date	Sequence Code	Sequence Length *	Reference
P. mutuki	OP896949	Taeheung, Jeju, Korea	Jun 2018	TH1-1	639	This study
P. mutuki	OP896950	Taeheung, Jeju, Korea	Jun 2018	TH1-2	639	This study
P. mutuki	OP896951	Taeheung, Jeju, Korea	Jun 2018	TH1-3	639	This study
P. mutuki	OP896952	Taeheung, Jeju, Korea	Jun 2018	TH2-1	639	This study
P. mutuki	OP896953	Taeheung, Jeju, Korea	Jun 2018	TH2-2	653	This study
P. mutuki	OP896954	Taeheung, Jeju, Korea	Jun 2018	TH2-3	653	This study
P. mutuki	OP896955	Taeheung, Jeju, Korea	Jun 2018	TH3-1	653	This study
P. mutuki	OP896956	Taeheung, Jeju, Korea	Jun 2018	TH3-2	639	This study
P. mutuki	OP896957	Taeheung, Jeju, Korea	Jun 2018	TH3-3	639	This study
P. mutuki	OP896958	Topyeong, Jeju, Korea	Feb 2020	TP1-1	648	This study
P. mutuki	OP896959	Topyeong, Jeju, Korea	Feb 2020	TP1-2	648	This study
P. mutuki	OP896960	Topyeong, Jeju, Korea	Feb 2020	TP1-3	654	This study
P. mutuki	OP896961	Topyeong, Jeju, Korea	Feb 2020	TP2-1	652	This study
P. mutuki	OP896962	Topyeong, Jeju, Korea	Feb 2020	TP2-2	652	This study
P. mutuki	OP896963	Topyeong, Jeju, Korea	Feb 2020	TP2-3	652	This study
P. mutuki	OP896964	Topyeong, Jeju, Korea	Feb 2020	TP3-1	652	This study
P. mutuki	OP896965	Topyeong, Jeju, Korea	Feb 2020	TP3-2	652	This study
P. mutuki	OP896966	Topyeong, Jeju, Korea	Feb 2020	TP3-3	652	This study
P. mutuki	DQ997889	Miyakejima, Japan	Jun 2005	PmMiI1	570	[37]
P. mutuki	DQ997894	Erabu, Japan	May 2006	PmES1	567	[37]
P. mutuki	DQ997888	Iriomote, Japan	Feb 2006	PmIrHo1	570	[37]
P. mutuki	DQ997891	Amami, Japan	Aug 2004	PmAT1	557	[37]
P. mutuki	DQ997892	Yakushima, Japan	Jul 2004	PmYS2	562	[37]
P. aff. mutuki	KX389476	Okinoerabu, Japan	Jun 2005	233PamErYa	652	[35]
P. aff. mutuki	KX389479	Okinoerabu, Japan	Jun 2011	237PamErSu	641	[35]
P. mutuki	KX389480	Okinawa, Japan	Feb 2012	316PmOkKo	615	[35]
P. mutuki	KX389481	Okinoerabu, Japan	Mar 2010	77PmErYa	630	[35]
P. mutuki	KX389482	Okinoerabu, Japan	Mar 2010	75PmErYa	658	[35]
P. mutuki	KX389483	Okinawa, Japan	May 2011	218PmOkOd	628	[35]
P. mutuki	KX389484	Okinoerabu, Japan	Mar 2010	73PmErYa	623	[35]
P. mutuki	KX389485	Okinawa, Japan	May 2011	222PmOkOd	636	[35]
P. mutuki	KX389488	Yoron, Japan	Mar 2010	42PmYoUk	606	[35]

Table 1. *Cont.*

Species	Accession Number	Locality	Sampling Date	Sequence Code	Sequence Length *	Reference
P. tuberculosa	KX389459	Yoron, Japan	Mar 2010	39PtYoUk	615	[35]
P. tuberculosa	DQ997921	Yoron, Japan	May 2005	PtYoS1	585	[37]
P. tuberculosa	KX389470	Yoron, Japan	Mar 2010	43PyYoUk	620	[35]
P. tuberculosa	DQ997897	Amami, Japan	Aug 2004	PtAT2	570	[37]
P. tuberculosa	KX389464	Okinoerabu, Japan	Mar 2010	83PyErYa	601	[35]
P. heliodiscus	DQ997880	Ishigaki, Japan	Dec 2005	PhIsK11	574	[37]
P. heliodiscus	DQ997883	Saipan, Japan	Dec 2004	PhSaL1	574	[37]

* All sequences listed were amplified using a Zoantharia-specific primer set (Zoan-f/Zoan-r, [37]).

3. Results and Discussions

3.1. In Situ Underwater Images and Morphology

The zoantharian community in the southern part of Jeju identified in this survey was more than 2 m wide and more than 13 m long at TH (Figure 2a,b) and 1.5 m wide and 5 m long at TP (Figure 2c). The morphological observations showed that the average number of tentacles was more than 61 (±3, n = 15), and it was identified as an independent ("liberal type" [35]) form of polyp (Figure 2d in the small box). *Palythoa* sp. have been reported to live in coral reefs in the Atlantic and in the Pacific, including Asian areas [10–17], and they are known to exhibit encrusted sand or debris around the body [40,41]. The species on the southern coast of Jeju was found to be covered with sand (Figure 2d in the small box). According to Mizuyama et al. [35], the morphological characteristics of *Palythoa tuberculosa* and *P. mutuki* of a zoantharian species are largely divided based on the number of tentacles and the independence of polyps. The average numbers of tentacles in *P. tuberculosa* and *P. mutuki* are 31.6 (±3.4) and 54.4 (±7.43), respectively; it is known that there are a greater number of tentacles in *P. mutuki* than in *P. tuberculosa*. Moreover, in terms of the polyp structure type of the two species, the polyps of *P. tuberculosa* are of the immerse type ("embedded"), whereas those of *P. mutuki* are of the liberal type ("free standing") [35]. Therefore, the species found on Jeju was similar to the *P. mutuki* species reported by Japan [35,41]. According to Shiroma and Reimer's [41] study, they measured the number of colonies of *P. mutuki* in Okinawa using a transect method. Although it was a small survey area, many huge colonies (up to 2 m × 5 m) of *P. mutuki* were found in Okinawa, Japan [41]. The zoantharian communities found in Jeju were found to be more than two times as large as those found in Okinawa, Japan. The habitats at TH and TP are the largest known zoantharian communities in terms of size reported from Korea.

3.2. Species Identification Using ITS rDNA

The lengths of the 18 sequences obtained in this study varied by clone, ranging from 639 to 654 bp. The percent similarity of ITS rDNA sequences based on pairwise distance analysis revealed that our sequences were 94.4–99.8% similar to those of *P. mutuki* collected elsewhere, indicating that intraspecific variation ranged from 0.2 to 5.6% (Table S1). The extent of the variation was lower among the 18 sequences obtained in this study (0.0–3.7%), and these variations were found exclusively in the ITS1 and ITS2 regions. It was also noticeable that the clonal variation within a single sample (intragenomic variation, 0.2–0.3%) occurred in every individual analyzed. Based on a comparison among the genus *Palythoa*, the variation in percent similarity ranged from 5.9 to 33.3%. In the BI tree, our sequences were grouped into '*P. mutuki* + *P.* aff. *mutuki*' with 100% posterior probability (Figure 3). This mixed group was paraphyletic, consisting of two well-supported clades, one containing sequences from both TP and TH and the other containing sequences from TH.

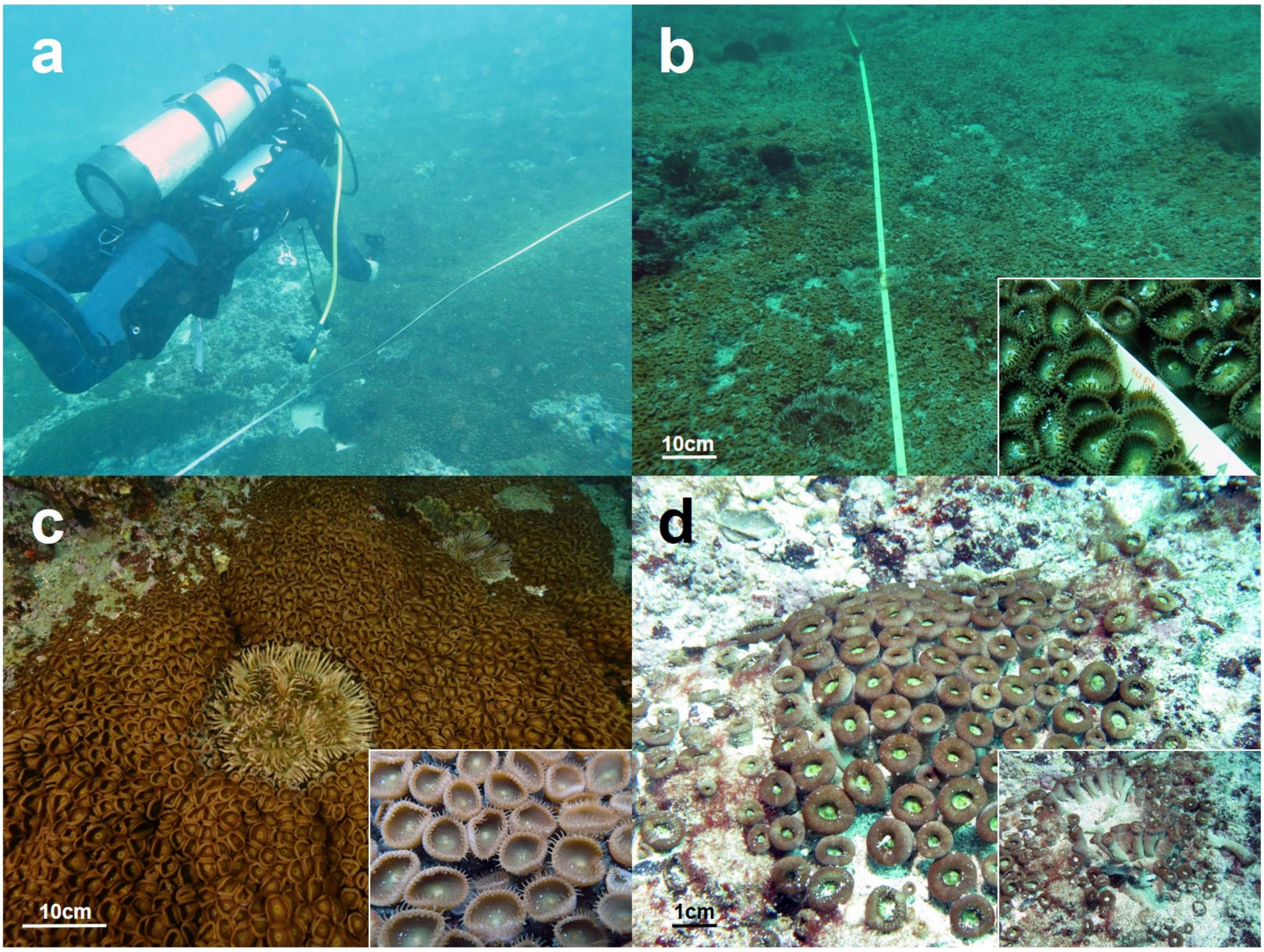

Figure 2. In situ underwater images of *Palythoa mutuki*. (**a**,**b**), Community-scale measurement at Taeheung, Jeju, Korea, in June, 2018, and (**c**), at another sampling location, Topyeong, Jeju, Korea, in February 2020; small box in (**b**,**c**); opened polyps and tentacles arranged at the edges of *P. mutuki*. (**d**), closed polyps of *P. mutuki* observed at Taeheung in October 2017.

The resulting sequence similarity and BI tree clearly revealed that our samples belonged to *P. mutuki*, supporting the morphological observations. However, it should also be noted that our samples could consist of two different species (i.e., *P. mutuki* and *P.* aff. *mutuki*), as shown in the BI tree. According to Mizuyama et al. [35], despite the close relationship between *P. mutuki* and *P.* aff. *mutuki* in molecular analyses, they could be two different species based on their reproductive characteristics and morphology.

In this study, we found both intraspecific variation (~5.6%) and intragenomic variations (5.9–33.3%) in the ITS rDNA. These results provide clues as to the extent to which variations should be considered when distinguishing between species. Intragenomic variations in the length and sequence of the ITS rDNA region were also observed, as reported previously [42]. In such studies, this variation was described as the potential result of "hybridization" or "reticulate evolution", possibly caused by mass spawning [35,43] and the altered distribution of zoantharians. Indeed, as shown in the BI tree, even clonal sequences derived from one *P. mutuki* individual (e.g., TH2-1, TH2-2, and TH2-3) could be divided into two well-supported *P. mutuki* clades. Although we could not find any polymorphism and haplotype variants owing to the low sample number, we could at least conclude that the *P. mutuki* inhabiting the rocky shores in southern Jeju Island is closely related to the *P. mutuki* from the Ryukyu Archipelago of southern Japan.

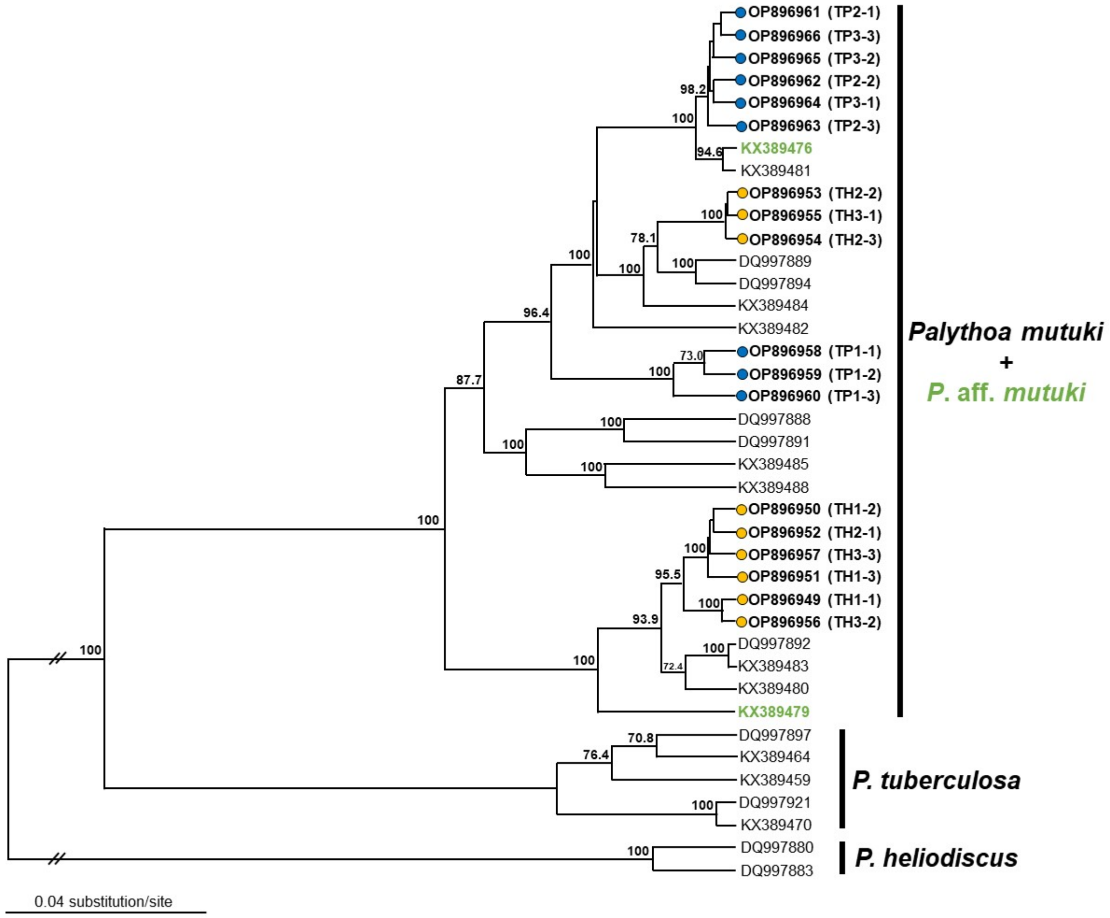

Figure 3. Bayesian inference tree based on internal transcribed spacer (ITS) rDNA of the genus *Palythoa*. Posterior probabilities are shown at each branch. Note that GenBank accession numbers of *P. mutuki* and *P.* aff. *mutuki* are indicated with different colors.

4. Conclusions

Because of the influence of climate change, the water temperature in the waters around Jeju Island is increasing, and the coral habitat is gradually increasing [9,44]. Environmental factors such as water temperature affect the distribution of zooxanthellate zoantharians [3,16,45]. The *Zoanthus sansibaricus* (zooxanthellate species) found in Jeju were also reported to be closely related to the rise in water temperature in the winter [9]. In this study, species identification was performed through the morphological and genetic analyses of a large-scale zoantharian population living in the southern waters of Jeju. Thus, we confirmed the presence of *P. mutuki*. This large-scale *P. mutuki* habitat at TH and TP on Jeju is the first to be reported with molecular confirmation. Reimer et al. [34] showed that zoantharian habitat changes in coral- and algae-dominated ecosystems are due to increased water temperature and stress caused by environmental changes, resulting in a decrease in coral and algae and a replacement with zoantharian species. This influx of subtropical organisms due to climate change can significantly impact existing ecosystems [34,46], and the changes in the Jeju marine ecosystem from an algae-based ecosystem to a coral-based ecosystem are expected to accelerate [47]. Kelp forests are economically important as well as reservoirs of high biodiversity [48,49]. In Australia, which has a temperate climate in the southern hemisphere, coral habitats are expanding at high latitudes due to global warming, resulting in a decline in kelp forests [50]. In Jeju, the production of algae is decreasing due to the expansion of corals and climate change [51]. Jeju Island has a globally important agricultural heritage system, including the *Haenyeo* (female divers) [52]. Jeju *Haenyeo* are engaged in fishing activities to collect various gastropods (i.e., abalone and topshell) and seaweeds (i.e., *Sargassum* and *Ulva*) [52]. The expansion of the *P. mutuki* habitat identified in this study might affect not only biodiversity changes in Jeju waters but also the fishing patterns of the *Haenyeo*; therefore, continuous monitoring is needed in the future.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/jmse11030574/s1; Table S1: Comparison of ITS rDNA region sequences among the genus Palythoa. Percent similarity was calculated based on pairwise distance analysis.

Author Contributions: Conceptualization, H.-S.Y.; methodology, validation, and formal analysis, H.-S.Y. and Y.-G.C.; investigation and resources, H.-S.Y., T.K. and S.-J.H.; writing and visualization, H.-S.Y. and Y.-G.C.; review and editing, H.-S.Y.; project administration and funding acquisition, H.-S.Y. and S.-J.H. We confirm that this manuscript and data are original and have not been previously published or considered elsewhere. All authors have read and agreed to the published version of the manuscript.

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