RESEARCH NOTE

Sighting of the rare Poey's scabbardfish, *Evoxymetopon poeyi*, in the Polynesian triangle

Avistamiento del escaso Poey's scabbardfish, *Evoxymetopon poeyi*, en el triángulo Polinésico

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Abstract.- Rapa Nui only allows artisanal fishery activities, but these often go unaware. The market is centralized on Pacific chub, snoek and yellowfin tuna, all common pelagic fish. On September 2016, one un-identified specimen was caught off-shore as by-catch, and left on the main port at Hanga Piko. The objective of this study was to identify the specimen to a species level, using a morphological, meristic and molecular approach. All analyses suggest that the specimen belongs to a Poey's scabbardfish, *Evoxymetopon poeyi*. Concluding that the rare Poey's scabbardfish, has an oceanic distribution through seamounts as a mid-water migrator.

Key words: Mesopelagic fauna, Salas y Gómez Ridge, Trichiuridae

INTRODUCTION

Rapa Nui (Easter Island) is a small remote Polynesian Island located at the southeastern corner of the Polynesian triangle. It has an area of 160 km², and it is located in the middle of the Pacific Ocean, 3,500 km away from the nearest landmass, South America. This oceanic island was discovered by natives from the Marquesas Islands during the Christian era (Arana 2014), and as many other Polynesians islands, has a volcanic origin. Currently, Rapa Nui, along with the uninhabited Salas y Gómez Island, belong to the Easter Island Province and Ecoregion (EIE) (Spalding *et al*. 2007) (Fig. 1).

The marine biodiversity of Rapa Nui has evolved under a complex geological history, and it is more closely related to the Indo-Pacific biota, than to the Eastern Pacific. There is a total of 178 described fish species for Rapa Nui, 145 are shore fishes, and 26% are endemic (Randall & Cea 2011, Easton *et al*. 2017). The low number of described fish species (N= 178), make this island the most impoverished island in fish fauna of the Indo-Pacific region. Randall & Cea (2011), have suggested that this impoverishment could be a consequence of the small size of the island, the presence of few marine habitats, the age of the island, 2.5 million years (considered young), and the oligotrophic conditions surrounding the island (Easton *et al*. 2017). Despite of this described impoverishment,

recent expeditions on the surrounding seamounts of Rapa Nui have discovered new species, suggesting that the EIE might not be as impoverished of fish fauna as previously thought (Parin *et al*. 1997, Friedlander *et al*. 2013, Easton *et al*. 2017, 2018).

Since 2018, the Chilean government declared the EIE as a Multiple Use Coastal and Marine Protected Area (AMCP-MU), benefiting small artisanal fisheries with an exclusive zone of 200 km around the island. Today, all fishing activities in Rapa Nui are controlled by the Servicio Nacional de Pesca y Acuicultura (SERNAPESCA)[1]. The main port is Hanga Piko, here, two types of fisheries take place: first, coastal artisanal fisheries that mainly catch Pacific chub, commonly known as *Nanue* (*Kyphosus sandwicensis*), and snoek, commonly known as *Sierra* (*Thyrsites atun*); and second, offshore artisanal fisheries that mainly center in the capture of yellowfin tuna, locally known as *Toremo* (*Thunnus albacares*) (Zylich *et al*. 2014). Although, SERNAPESCA keeps a record of artisanal fisheries disembarkation (species and tons extracted), there are still a number of bycatch species that remain unidentified. In the years 2000 to 2010, Zylich *et al*. (2014) recognized that 11.5% of the total biomass of fish caught by offshore artisanal fisheries in Hanga Piko, corresponded to unidentified species.

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[1]Servicio Nacional de Pesca y Acuicultura (SERNAPESCA) under the Law Nº 18,892. Valparaíso, Chile. <http://bcn.cl/2lmjx>

On September 14, 2016 one unidentified fish specimen was caught as bycatch, and thrown away at the main port, at Hanga Piko. Morphologically, it was thought to belong to the Family Trichiuridae, which has 11 recognized genera, known as cutlassfishes, hairtails, scabbardfishes and frostfishes (Nakamura & Parin 1993). These species are benthopelagic voracious predators that inhabit the continental shelf, slope and rise, from the surface to about 2,000 m deep. Therefore, the main objective of this study was to identify the specimen to a species level, using a morphological, meristic and molecular approach.

MATERIALS AND METHODS

SPECIMEN HISTORY

During offshore artisanal pole fishing in Rapa Nui (27º9'S, 109º26'W) (Fig. 1), an unidentified fish specimen was caught by local island fishermen. Their target catch was yellowfin tuna, but as an incidental catch they caught this specimen (Alverson *et al*. 1994). The specimen was brought to shore dead, and discarded at the main port of Hanga Piko. None of the fishermen present at Hanga Piko were able to identify the specimen. The specimen was frozen and shipped to Santiago de Chile by plane for scientific determination. Upon arrival the specimen was frozen at -20 °C for storage, but during the trip the specimen lost the first dorsal spine.

Only one specimen was caught due to the limitations of pole fishing, and the artisanal boat infrastructure. The pole fishing lines for tuna were designed to reach an maximum depth of 100 m, limiting the maximum depth while fishing. Additionally, the artisanal boats in Rapa Nui are 7.1 m long and 1.89 m wide fiber glass boats that have a weight limitation of 50 tons (Acuña *et al*. 2018), which limits the amount of weight they could safely carry on an expedition.

MORPHOLOGY AND MERISTIC

To study the external and internal anatomy, the specimen was first thawed, and taken to a radiology center. Here, five x-ray photographs were taken to cover the whole length of the fish with an x-ray SUMMIT LX125V. All x-rays were assembled with Adobe® Illustrator CC v. 2017. The internal image of the specimen was used for a morphological and meristic analysis, following Burhanuddin *et al*. (2002) and Nakamura & Parin (1993). All measurements were made to the nearest 0.1 mm, and proportional measurements were rounded off to the first decimal place.
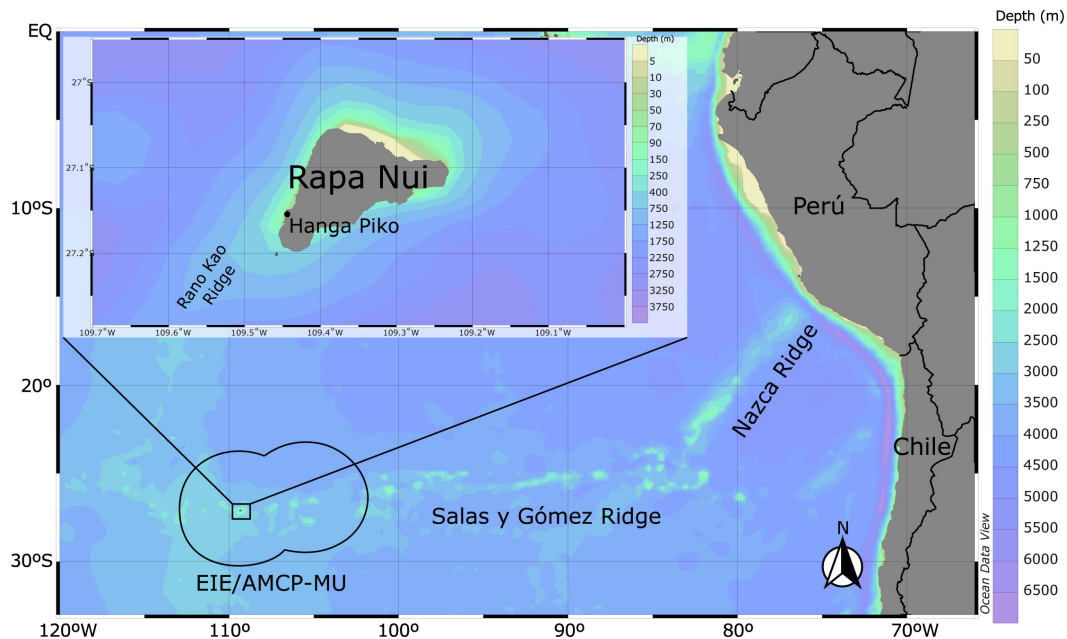

Figure 1. World bathymetric map including Rapa Nui. The main seamount trails are indicated, and the surface area of the Multiple Use Coastal and Marine Protected Area (AMCP-MU) of Easter Island province and ecoregion EIE (map done in Ocean Data view Schlitzer R, Ocean Data View, <https://odv.awi.de>, 2018) / Mapa batimétrico mundial incluyendo a Rapa Nui. Se indican los nombres de las principales cordilleras submarinas, y el área de superficie de la Área Marina Costera Protegida de Múltiple Uso (AMCP-MU) de la Ecorregión y Provincia de Isla de Pascua (EIE) (mapa creado en Ocean Data view Schlitzer R, Ocean Data View, <https://odv.awi.de>, 2018)

A piece of muscle from the tail was cut and stored in 99% ethanol for molecular analysis, and the specimen was deposited in the ichthyology collection of the National Museum of Natural History of Chile (MNHNCL-ICT 7613). The DNA was extracted using the salting-out method (modified from Jowett 1986). A partial sequence of the mitochondrial gene encoding cytochrome oxidase subunit I (COI) was amplified using primers FishF2 and FishR2 described by Ward *et al*. (2005). The polymerase chain reaction (PCR) mixture had a total volume of 35 µl, and contained 1X PCR Buffer (200 mM Tris-HCL pH 8.4, 500 mM KCL), 2 mM $MgCl_2$, 0.2 mM of each dNTP, 0.1 µM of each forward and reverse primers, 0.3 U *Taq* DNA polymerase (Invitrogen™), and 70 ng of template DNA. The thermo-cycling conditions consisted of an initial denaturation step at 94 °C for 3 min, followed by 25 cycles of 94 °C for 30 s, 52 °C for 30 s, 72 °C for 1 min, and a final extension at 72 °C for 10 min. The PCR product was sequenced in an ABI PRISM 3100 Genetic Analyzer in the sequencing center of the Pontificia Universidad Católica de Chile. The sequence was aligned, and edited using BioEdit v7.0.5 (Hall 1999) using the option ClustalW, and later a visual inspection was done.

PHYLOGENETIC ANALYSIS

A phylogenetic analysis was done using maximum parsimony (MP), maximum likelihood (ML), and Bayesian inference (BI) methods in order to establish the phylogenetic position of the unidentified fish. The phylogenetic reconstruction was based on partial sequences of the COI gene of the Superfamily Trichiuroidea, with the following GenBank accession number: AP012507, AP012509 (Miya *et al*. 2013), JN990842, JN990843, JN990845, JN990846, JN990862, JN990868 (Tzeng & Chiu 2012), KU945006, and KU945019 (Chang *et al*. 2017). The tree was rooted using species from the Family Scombridae as outgroup, GenBank accession number HM007708 (Cawthorn *et al*. 2011), and a species of the Family Gempylidae as a sister group, GenBank accession number KU945005 (Chang *et al*. 2017). After obtaining all available sequences, they were aligned with the sequence of the unidentified fish (GenBank accession number MN052559) in BioEdit v7.05 (Hall 1999), using the option ClustalW. The MP analysis was done in PAUP* version 4a (Swofford 2002), using a heuristic search with the tree bisection-reconnection, and branch-swapping options. The ML analysis was done in RAxMLGUI v 1.5b1 (Silvestro & Michalak 2012). For the statistical support of the nodes in the MP and ML analyses, a non-parametric bootstrap of 1000 pseudoreplicates was done. The BI analysis was done in Mr. Bayes v3.2.6 x64 (Ronquist *et al*. 2012) with two independent runs of MCMC analyses with 10 million generation, each with 4 Markov chains. The MCMC analyses were sampled every 1000 generations, discarding the first 20% of trees. Convergence was considered checking the ESS (Effective Sample Size) and PSRF (Potential Scale Reduction Factor) values. For both ML and BI analysis, the GTR model (General Time Reversible) plus Invariant sites and Gamma parameter (GTR+I+G) was used, selected by JModelTest 2.0 (Darriba *et al*. 2012) under both Akaike information criterion (AIC) and Bayesian information criterion (BIC).

RESULTS AND DISCUSSION

MORPHOLOGICAL AND MERISTIC ANALYSES

Based on the external characteristics of the specimen found in Rapa Nui, it is suggested that it belongs to a cutlassfish of the genus *Evoxymetopon*. Until now, there are only four described species of the genus *Evoxymetopon*, and little information is known about their biology (Nakamura & Parin 1993, Chakraborty *et al*. 2006, Fricke *et al*. 2014). Nevertheless, as other species of the Family Trichiuridae, the species of the genus *Evoxymetopon* are described as benthopelagic species, inhabiting continental shelfs and slopes, and are described as abundant in sea mounts (Nakamura & Parin 1997). Since there are only two described species of the genus *Evoxymetopon* that have the first dorsal spine elongated, all morphological and meristic comparisons were done with *Evoxymetopon poeyi* Günther, 1887, and *Evoxymetopon macrophthalmus* Chakraborty, Yoshino & Iwatsuki, 2006.

The morphological and meristic values obtained for the specimen from Rapa Nui are shown in Table 1. Values obtained for the counts of dorsal fin elements, the origin of the first anal spine, the origin of pelvic fins, and the total number of vertebrates in the Rapa Nui specimen, correlate with the values of other *E. poeyi* from Japan and Taiwan. The only differences observed between the Rapa Nui specimen and the other *E. poeyi*, are in head length and eye diameter, with these measurements being slightly bigger in the Rapa Nui specimen Table 1. All of these measurements and counts were done on the compilation of the 5 x-rays. This x-ray compilation shows that specimen was captured with an empty stomach.

Table 1. Morphometrics and meristic data of *E. poeyi* from Rapa Nui, with comparative material from other *E. poeyi* and *E. macrophthalmus* from Chakraborty *et al.* (2006) and Koeda & Ho (2017) / Morfometría y mirística de *E. poeyi* de Rapa Nui, con material comparativo de otros *E. poeyi* y *E. macrophthalmus* de Chakraborty *et al.* (2006) and Koeda & Ho (2017)

	Evoxymetopon macrophthalmus	*Evoxymetopon poeyi*						
	Japan	Japan	Japan	Japan	Japan	Taiwan	Taiwan	Rapa Nui
	URM-P 41556	URM-P 6682	URM-P 33942	URM-P 33943	URM-P41557	TFRI (uncatalogued)	NMMB-P26093	MNHNCL ICT 7613
Total length (mm)	1682	990	1130	1401	1682	1975	1885	1580
Standard length (mm)	1615	955	1090	1345	1615	1930	1840	1506
Preanal length (mm)	825	457	640	665	825	980	910.8	801
Counts:								
Dorsal-fin elements	90	93	93	93	92	92	90	93
Origin of first anal spine (opposite dorsal-fin ray)	34th	35th	35th	35th	35th	35th	-	35th
Origin of pelvic fin (opposite dorsal-fin spine)	9th	8th	8th	8th	8th	8th	-	8th
Pectoral-fin rays	12	12	12	12	12	12	12	12
External anal-fin rays[a]	x+15	x+20	x+20	x+20	x+20	x+20	17	15
Gill rakers (upper + middle + lower)	9+1+9	4+1+10	5+1+9	5+1+10	5+1+9	6+1+18	-	5+1+10
Precaudal vertebrae	34	35	35	35	35	-	-	36
Caudal vertebrae	60	64	64	64	64	-	-	58
Caudal peduncle vertebrae	6	7	7	7	7	-	-	5
Total vertebrae	94	99	99	99	99	-	-	99
Measurements[b]:								
Dorsal-fin base length	645.3,177.5	730.8,192.0	730.0,186.0	713.0,187.6	811.0,189.9	-	739.2,186.7	624.0, 172.7
Head length	100,27.5	100.0,26.0	100.0,25.5	100.0,26.3	100.0,23.4	100.0,24.4	100.0,25.3	100.0, 27.7
Snout length	37.0,10.0	38.3,10.0	38.6,9.8	38.6,10.2	39.0,9.1	40.8,10.0	39.2,9.9	37.5, 10.4
Postorbital length	40.0,11.0	46.6,12.3	43.0,11.0	44.7,11.8	45.3,10.6	43.3,10.6	48.8,12.3	47.8, 13.2
Preopercle length	72.7,20.0	70.3,18.5	71.7,18.3	72.2,19.0	72.7,17.0	70.8,17.3	-	70.7, 19.6
Upper jaw length	34.5,9.5	34.8,9.1	37.4,9.5	36.0,9.5	35.1,8.2	35.8,8.7	36.0,9.1	38.7, 10.7
Body depth at pectoral-fin base	55.0,15.2	59.0,15.5	62.0,15.8	60.0,15.8	60.4,14.2	63.3,15.5	63.2,16.0	62.1, 17.2
Body depth at anus	46.3,12.8	52.2,13.7	55.5,14.1	51.6,13.6	52.4,12.3	52.0,12.7	56.0,14.1	49.6, 13.7
Body width at pectoral-fin base	16.0,4.4	15.0,3.9	19.6,5.0	18.4,4.8	17.9,4.2	17.9,4.3	16.0,4.0	13.2, 3.6
Body width at anus	11.8,3.3	12.5,3.3	12.5,3.2	12.6,3.3	13.0,3.1	12.5,3.6	12.8,3.2	9.0, 2.5
First dorsal-spine length	68.4,18.8	106.9,28.1	117.1,29.8	110.0,28.9	130.3,30.5	117.2,28.2	134.4,34.0	Damaged
Second dorsal-spine length	11.4,3.1	-	8.2,2.1	-	6.8,1.6	-	-	8.1, 2.2
Dorsal-fin ray length above anus	13.4,3.7	-	15.3,3.9	12.5,3.3	13.8,3.2	-	-	14.5, 4.0
Predorsal length	75.6,21.0	72.1,18.9	78.2,19.9	76.2,20.1	77.0,18.1	75.4,18.4	76.0,19.2	60.4, 16.7
Longest pectoral-fin ray length	47.4,13.0	43.3,11.4	47.6,12.1	48.2,12.7	47.4,11.1	45.4,11.1	52.0,13.1	53.2, 14.7
Membranous interorbital width	20.0,5.5	14.6,3.9	16.6,4.2	15.7,4.1	14.7,3.5	-	13.6,3.4	15.3, 4.2
Eye diameter (bony)	22.0,6.0	18.0,4.7	17.4,4.8	17.1,4.8	17.0,4.0	17.9,4.3	18.4,4.6	23.2, 6.4
Suborbital width	9.4,2.6	8.7,2.3	7.9,2.0	8.7,2.3	9.3,2.2	7.9,1.9	7.2,1.8	7.3, 2.0
Depth below lateral line at anus	23.4,6.5	25.4,6.7	23.9,6.1	24.5,6.7	25.5,6.0	24.5,6.0	26.4,6.7	23.2, 6.4
Depth above lateral line at anus	23.9,6.6	29.1,7.7	29.2,7.3	27.7,7.7	29.3,6.9	27.0,6.6	30.4,7.8	25.1, 6.9
Pectoral-fin base	10.0,2.8	9.6,2.5	10.3,2.6	9.7,2.5	10.1,2.4	8.9,2.1	8.0,2.0	10.9, 3.0

[a]Only externally visible anal-fin ray counts are mentioned
[b]Morphometrics are expressed as percentage of head length (first) and preanal length (second)

PHYLOGENETIC ANALYSES

The total alignment of the COI gen used for the phylogenetic analyses had 651 pb. The MP analysis retained a total of 3 trees, with a tree length of 458 steps, and the consistency index was of 0.6135, the homoplasy index 0.3865, the retention index 0.6856, and the rescaled consistency index 0.4206. The ML analysis obtained a final ML optimization Likelihood of -3,003.08. The BI analyses resulted in one consensus tree, with statistical values of ESS above 200, and PSRF values with an average of one, suggesting that the analysis reached convergence.

The topology of all three trees were congruent, therefore, only the BI consensus tree is shown, with the statistical support of each node (Fig. 2). This phylogenetic reconstruction, groups the specimen found in Rapa Nui with the species *E. poeyi* in one clade, presenting only two variable sites between them. Furthermore, the genus *Evoxymetopon* is paraphyletic, resulting in a taxonomic and systematics issue that has not been addressed by

other authors. In this analysis, there was no possibility of including all four species of the genus *Evoxymetopon*, since no genetic data is available.

The morphological, meristic and molecular analyses done, suggest that the specimen found in Rapa Nui, belongs to an *E. poeyi*, commonly known as Poey's scabbardfish. This fish species was first described for the Indian Ocean in the Mauritius and in the Western North Pacific Ocean, near Japan territory (Nakamura & Parin 1993), and it has been occasionally reported in the Reunion Island (Letourneur *et al.* 2004), near Taiwan (Koeda & Ho 2017), and Cook Islands (McCormack 2007). Most of these occasional reports, state that these fish have been caught as incidental catch, or have shown up dead while pole fishing in the open ocean. As an outcome, there are only 7 individuals catalogized in museums, with published information (Chakraborty *et al.* 2006, Koeda & Ho 2017), and only 4 COI sequences in GenBank, including the one found in Rapa Nui, confirming, the rareness of this species.
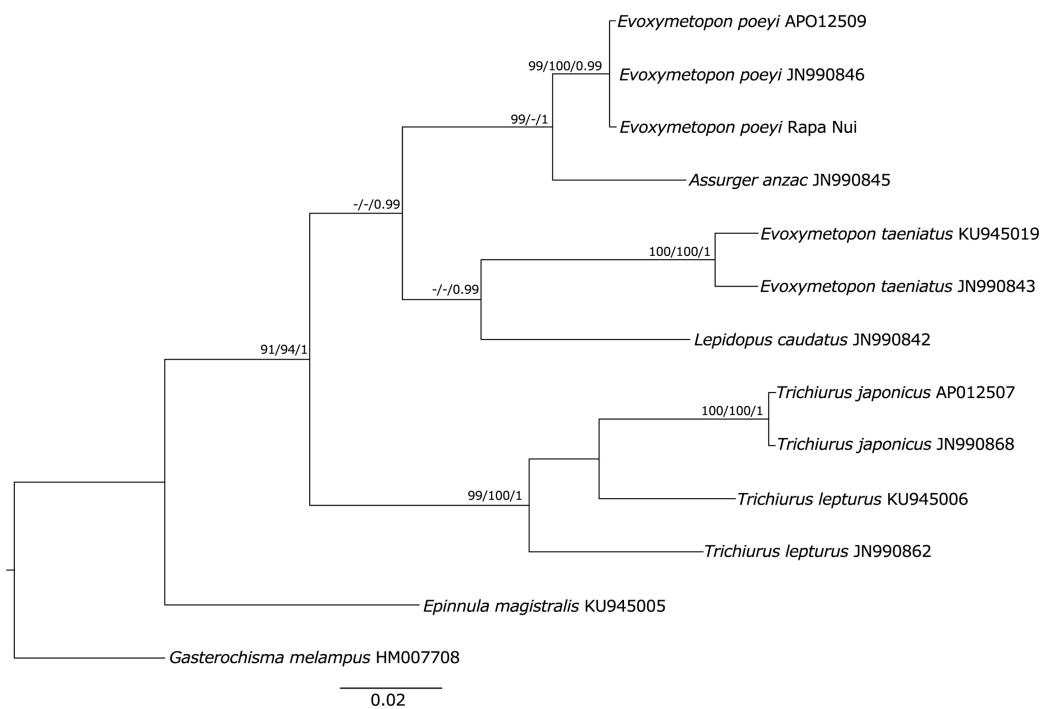

Figure 2. Consensus tree obtained using a partial sequence of the *cytochrome oxidase I* (COI) mitochondrial marker with a Bayesian inference analysis. The maximum likelihood of the tree is -3,003.08. Values above the nodes are, from left to right, the bootstrap value of maximum parsimony, maximum likelihood (above 70%) and posterior probability of the Bayesian inference (above 0.95) / Árbol de consenso del análisis bayesiano del gen *citocromo oxidasa I* (COI) marcador mitocondrial. El valor de máxima verosimilitud del árbol es -3.003,08. Valores arriba de los nodos son, desde izquierda a derecha, valor de bootstrap de máxima parsimonia, máxima verosimilitud (arriba de 70%) y el valor de probabilidad posterior obtenida del análisis bayesiana (arriba de 0,95)

This is the first record of the rare Poey's scabbardfish for the remote island Rapa Nui. It is possible that this species has been off record until now, because most offshore fishing activities focus on yellowfin tuna, that are fished at depths of 100 m, and *E. poeyi* is described inhabiting below 200 m from the surface. Additionally, most marine biodiversity expeditions at EIE are done near shore. Only recently, have there been expeditions that explore the marine fauna offshore at EIE (Parin *et al*. 1997, Friedlander *et al*. 2013, Easton *et al*. 2017, 2018). These expeditions are difficult, but crucial for the study of deep marine biodiversity, especially near Rapa Nui, because of its pristine seamount trails, and isolation. To the east of Rapa Nui, there is the Salas y Gómez ridge, to the southwest there is the Rano Kau ridge, that has the Apolo peak, and to the west, there is the Moai seamount and Pukao Seamount (Haase *et al*. 1997) (Fig. 1). Of these seamount trails, pole fishing by natives is sporadically reported in the Pukao seamount, and the Apolo surface peak (Mecho *et al*. 2019).

The presence of *E. poeyi* in Rapa Nui, is a sign of how unexplored seamounts are in general and in the Pacific Ocean. Additionally, the geographical distribution of *E. poeyi* is extended from the Indian Ocean to the whole Pacific Ocean, including the North and Southern hemisphere. So, it is suggested that *E. poeyi* inhabits seamounts, and that it is a possible mid-water migrator, since the specimen found had no stomach content. Therefore, the report of the rare *E. poeyi* in Rapa Nui, enlighten new information about the biology, ecology, habitat, and distribution of this species.

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LITERATURE CITED

Acuña E, C Gaymer, I Hinojosa, J Aburto, A Cortés, R Sfeir, I Petit, C Véliz, M Hey, M García, P Arana, C Canales, N Adasme, A Friedlander, A Palma & C Tapia. 2018. Estudio biológico-pesquero y evaluación del estado de situación de las pesquerías costeras de importancia para la Isla de Pascua. Informe Final Proyecto FIPA N°2016-35: 1-337. <http://www.subpesca.cl/fipa/613/articles-102957_ archivo_01.pdf>

Alverson DL, MH Freeberg, SA Murawski & JG Pope. 1994. A global assessment of fisheries bycatch and discards. FAO Fisheries Technical Paper 339: 1-233.

Arana PM. 2014. Ancient fishing activities developed in Easter Island. Latin American Journal of Aquatic Research 42(4): 673-689.

Burhanuddin AI, Y Iwatsuki, T Yoshino & S Kimura. 2002. Small and valid species of *Trichiurus brevis* Wang and You, 1992 and *T. russelli* Dutt and Thankam, 1966, defined as the "*T. russelli* complex" (Perciformes: Trichiuridae). Ichthyological Research 49(3): 211-223.

Cawthorn DM, HA Steinman & RC Witthuhn. 2011. Establishment of a mitochondrial DNA sequence database for the identification of fish species commercially available in South Africa. Molecular Ecology Resources 11(6): 979-991.

Chakraborty A, T Yoshino & Y Iwatsuki. 2006. A new species of scabbardfish, *Evoxymetopon macrophthalmus* (Scombroidei: Trichiuridae), from Okinawa, Japan. Ichthyological Research 53(2): 137-142.

Chang CH, KT Shao, HY Lin, YC Chiu, M Lee, SH Liu & PL Lin. 2017. DNA barcodes of the native ray-finned fishes in Taiwan. Molecular Ecology Resources 17(4): 796-805.

Darriba D, GL Taboada, R Doallo & D Posada. 2012. jModelTest 2: more models, new heuristics and parallel computing. Nature Methods 9(8): 772. <https://doi. org/10.1038/nmeth.2109>

Easton EE, J Sellanes, CF Gaymer, N Morales, M Gorny & E Berkenpas. 2017. Diversity of deep-sea fishes of the Easter Island Ecoregion. Deep-Sea Research Part II: Topical Studies in Oceanography 137: 78-88.

Easton EE, J Sellanes & M Gorny. 2018. First record of the yellowfin soldierfish, *Myripristis chryseres*, in the Easter Island Ecoregion. Pacific Science 72(1): 143-148.

Fricke R, D Golani & B Appelbaum-Golani. 2014. *Evoxymetopon moricheni*, a new cutlassfish from the northern Red Sea (Teleostei: Trichiuridae). Ichthyological Research 61(3): 293-297.

Friedlander AM, E Ballesteros, J Beets, E Berkenpas, CF Gaymer, M Gorny & E Sala. 2013. Effects of isolation and fishing on the marine ecosystems of Easter Island and Salas y Gómez, Chile. Aquatic Conservation: Marine and Freshwater Ecosystems 23(4): 515-531.

Haase KM, P Stoffers & CD Garbe-Schönberg. 1997. The petrogenetic evolution of lavas from Easter Island and neighboring seamounts, near-ridge hotspot volcanoes in the SE pacific. Journal of Petrology 38(6): 785-813.

Hall T. 1999. Bioedit: A user-friendly biological sequence alignment editor and analysis program for windows 95/98/ NT. Version 5.0.9. Nucleic Acids Symposium Series 41: 95-98.

Jowett T. 1986. Preparation of nucleic acids. In: Roberts DB (ed). Drosophila: A practical approach, pp. 275-286. IRL Press, Oxford.

Koeda K & HC Ho. 2017. Records of rare scabbardfish (Perciformes: Trichiuridae) from southern Taiwan. Platax 14: 96-102.

Letourneur Y, P Chabanet, P Durville, M Taquet, E Teissier, M Parmentier, JC Quéro & K Pothin. 2004. An updated checklist of the marine fish fauna of Reunion Island, South-Western Indian Ocean. Cybium 28(3): 199-216.

McCormack G. 2007. Cook Islands biodiversity database, version 2007.2. Cook Islands Natural Heritage Trust, Rarotonga. <http://cookislands.bishopmuseum.org>

Mecho A, EE Easton, J Sellanes, M Gorny & C Mah. 2019. Unexplored diversity of the mesophotic echinoderm fauna of the Easter Island ecoregion. Marine Biology 166: 91. <https://doi.org/10.1007/s00227-019-3537-x>

Miya M, M Friedman, TP Satoh, H Takeshima, T Sado, W Iwasaki, Y Yamanoue, M Nakatani, K Mabuchi, JG Inoue, JY Poulsen, T Fukunaga, Y Sato & M Nishida. 2013. Evolutionary origin of the Scombridae (Tunas and Mackerels): members of a paleogene adaptive radiation with 14 other pelagic fish families. PLoS ONE 8(9): e73535. <https://doi.org/10.1371/journal.pone.0073535>

Nakamura I & NV Parin. 1993. FAO species catalogue. Vol 15. Snake mackerels and cutlassfishes of the world (Families Gempylidae and Trichiuridae). An annotated and illustrated catalogue of the snake mackerels, snoeks, escolars, gemfishes, sackfishes, domine, oilfish, cutlassfishes, scabbardfishes, hairtails and frostfishes known to date. FAO Fisheries Synopsis 125(15): 1-136.

Parin NV, AN Mironov & KM Nesis. 1997. Biology of the Nazca and Sala y Gómez submarine ridges, an outpost of the Indo-West pacific fauna in the Eastern Pacific Ocean: composition and distribution of the fauna, its communities and history. Advances in Marine Biology 32: 145-242.

Randall JE & A Cea. 2011. Shore fishes of Easter Island, 164 pp. University of Hawai'i Press, Hawaii.

Ronquist F, M Teslenko, P van der Mark, DL Ayres, A Darling, S Höhna, B Larget, L Liu, MA Suchard & JP Huelsenbeck. 2012. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61(3): 539-542.

Silvestro D & I Michalak. 2012. raxmlGUI: A graphical front-end for RAxML. Organisms Diversity & Evolution 12: 335-337.

Spalding MD, HE Fox, GR Allen, N Davidson, ZA Ferdaña, M Finlayson, BS Halpern, MA Jorge, A Lombana, SA Lourie, KD Martin, E McManus, J Molnar, CA Recchia & J Robertson. 2007. Marine ecoregions of the world: a bioregionalization of coastal and shelf areas. BioScience 57(7): 573-583.

Swofford DL. 2002. PAUP*. Phylogenetic Analysis Using Parsimony (*and other methods). Version 4. Sinauer Associates, Sunderland.

Tzeng CH & TS Chiu. 2012. DNA barcode-based identification of commercially caught cutlassfishes (Family: Trichiuridae) with a phylogenetic assessment. Fisheries Research 127/128: 176-181.

Ward RD, TS Zemlak, BH Innes, PR Last & PDN Hebert. 2005. DNA barcoding Australia's fish species. Philosophical Transactions of the Royal Society B: Biological Sciences 360(1462): 1847-1857.

Zylich K, S Harper, R Lidandeo, R Vega, D Zeller & D Pauly. 2014. Fishing in Easter Island, a recent history (1950-2010). Latin American Journal of Aquatic Research 42(4): 845-856.