Patterns in deep-sea biodiversity across four Ocean Island Province sites in the Tropical Eastern Pacific

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# (Glynn, Veron, and Wellington 1996)Abstract

# Introduction

The Tropical Eastern Pacific (TEP) ocean, stretching from the Gulf of California to northern Peru, is characterized oceanographically by extensive stratification, a shallow thermocline, and very low oxygen (Fiedler and Lavín 2016; Robertson and Cramer 2009; Priede 2017). The boundaries of this biogeographic region are located northward to Magdalena Bay, Baja California (~25° N) and southward to the Gulf of Guayaquil’s southern shore (~4° S). These northern and southern boundaries are defined not by hard physical barriers, but by sharp temperature gradients between tropical and temperate conditions. The TEP can be divided into three biogeographic provinces according to shore fish (0 -100 m) assemblage similarities (Robertson and Cramer 2009). The continental coast contains two provinces; the Cortez (Gulf of California and lower Pacific Baja) and the Panamic (southward province). These two distinct areas were identified by a peak in abundance of local endemics and a peak in overall species richness. The third province within the TEP consists of five isolated ocean islands and archipelagos; the Galapagos; the Revillagigedo group, Clipperton, Cocos, and Malpelo, collectively termed the “Ocean Island Province” (Hubbs and Briggs 1974)Robertson and Cramer 2009).

Small ocean islands, such as the five in the TEP, typically support smaller faunal assemblages compared to adjacent continental areas (e.g. Robertson 2001). The fauna of these ocean islands also have different functional-group composition, including both more broad-ranging species and more localized endemics. Thus, this area is a hotspot, both for the origin and maintenance of biodiversity in the sea (Robertson and Cramer 2009). Given their smaller fauna compared to neighboring mainland areas, they are also sensitive to species extinctions (ref).

Due to the longitudinal East Pacific Rise, which limits population connectivity by creating a spatial barrier to gene flow and dispersal among marine organisms, the TEP is largely isolated from the wider Pacific (Lessios and Robertson 2006). The islands and archipelagos likely represent important stepping stones and corridors for species connectivity across the TEP and the wider Pacific (Emerson 1994, Glynn et al. 1996, Robertson and Allen 1996).

Overall, the TEP is noted for its high level of endemism (72%) and relatively diverse shore fish assemblages (Zapata and Robertson 2006). Additionally, the euthrophic mesopelagic zone (200 m – 1000 m), hosts a large proportion of endemic deep-water fish species adapted to the low oxygen in these waters (Priede 2017). However, the bathyal demersal (200 m - 3,000 m) fauna of the TEP have remained largely un-described because exploration has historically been a challenge in these remote locations. Previous research has assessed marine biodiversity at these islands and atolls (e.g.(Heller and Snodgrass 1905) , others), but focused on the shallow-water ecosystems (Bussing, Allen, and Robertson 1996; Alzate, Zapata, and Giraldo 2014)(Glynn, Veron, and Wellington 1996) (Jost and Andréfouët 2006)(Fourriére et al. 2014)The deep-sea has rarely been studied  in the TEP,   with few studies from the Ocean Island Province in particular (but see Friedlander et al. 2018, submitted (Lubetkin et al. 2018; Sánchez-Jiménez et al. 2018; Auster et al. 2016)

The objective of this research was to describe patterns in biodiversity of bathyal demersal fauna at four ocean/island archipelagos in the TEP to better understand the deep-ocean biodiversity and community composition in the region. The seascapes of the Tropical Eastern Pacific ocean generates and maintains biodiversity through its biogeographic patterning of barriers and connectivity; our study represents the first characterization of deep-sea biodiversity in response to this seascape across four islands and archipelagos in the region.

# Methods

## Data collection:

National Geographic’s Exploration Technology Lab developed Deep-Ocean Dropcams, high definition cameras encased in glass pressure housings, to observe deep-sea life *in situ* by capturing high quality imagery of the sea floor.

(I’ll add more deets on drop cams) (Turchik et al. 2015)

Using these Dropcams, we collected video footage from four ocean island/archipelago sites in the Tropical Eastern Pacific: Clipperton, Galapagos, Revillagigedos, and Malpelo, in depths ranging from 200 m to ~ 3,000 m (n= 9 - 34 drops per site).

From the video footage, fauna were classified to the lowest possible taxonomic resolution. For invertebrates, order or class were the most often identified levels, whereas for fish, family was identified in most cases. All fish observations were reclassified to family for analyses and all data were converted to incidence per deployment.

## Statistical methods:

### Biodiversity indices:

To assess biodiversity, taxon observations were converted to incidence matrices. Three Hill numbers were calculated for each site: species richness (q=0), Shannon diversity (q=1), and Simpson diversity (q=2) (Hill 1973; Chao, Chiu, and Jost 2014) in the R package iNEXT Version XX (Hsieh, Ma, and Chao 2016)

### Generalized Linear Mixed Effects Models:

We used Generalized Linear Mixed Effects Models (GLMMs) with a logit link to investigate fauna probability of occurrence according to depth, habitat, and location. Fauna observations were grouped into 20 m depth bins, and modeled as a binomial distribution with the statistical package lme4 (Bates et al. 2015). Models included a random effect to allow the relationship of the response variable (incidence) to vary by predictor variables. The magnitude of the random effect quantified the response of community composition to predictor variables. Model parameter significance was assessed using a Likelihood Ratio Test (LRT) with the statistical package LmerTest (Bates et al. 2015). All data analyses were performed in the R programing environment, Version 1.0.136 (R Core Team 2016).

# Results

XX fish unique families and XX invertebrate orders were identified across four locations in the TEP Ocean Island Province.

**Diversity:**

Invertebrates:

Fish:

**Community composition and drivers of diversity among sites:**

Invertebrates:

Fish:

# Discussion

This study represents the first assessment of bathyal demersal biodiversity across four Ocean Island Province sites in the TEP.

**Biodiversity and endemism hotspot**

*Diff between invert and fish response:*

*Fish families:* While shore and mesopelagic fish assemblages are characterized by high rates of endemism adapted to local conditions, deep-water fish assemblages would not likely hold a similar pattern. Rather, bathyal demersal fish fauna are expected to have wide distributions. Of the 284 described fish species with circumglobal distributions, more than 80% of these species are represented by deep-sea fishes (Gaither et al. 2015). Tropical Eastern Pacific deep-water fish assemblages fit the global pattern of cosmopolitan distributions. They also they share similarities with the relatively diverse shore communities, making this Ocean Island Province a unique marine biodiversity hotspot.

*Differentiation among islands/archipelagos:* A single Ocean Island Province was defined for all fish residents in assemblage similarity analysis (Robertson and Cramer 2006), but further examining endemic species only, two groups emerged: all-endemics were divided into a northern group (Revillagigedos and Clipperton) and a southern group (Cocos, Malpelo, and Galapagos). The Galapagos had the largest fauna with the greatest number of local endemics (Robertson and Cramer 2006). Ou results show XXXX

Population persistence for local endemic species depends on retained recruitment within the region (Romero-Torres et al. 2018) others). The Eastern Pacific Barrier creates separation by distance in marine populations, limiting dispersal and gene flow between the TEP and the central Pacific (Romero-Torres et al. 2018).

**Population connectivity**

Islands and archipelagos in this region may serve as step-stones to maintain population connectivity across the wider Pacific region (Romero-Torres et al. 2018). The Ocean Island Province of the TEP lies in a confluence of currents, and likely is a migration pathway for iconic species such as sharks and tunas (refs). This area likely represents a corridor for highly migratory species, within the Eastern Tropical Pacific, and across the East Pacific Barrier. Therefore, the preservation of these intact ecosystems is crucial for maintaining biodiversity both within the TEP as feedbacks to the wider Pacific region (refs).

**Marine Protected Areas in the ETP:**

This region is an oceanic biodiversity hotspot, both in terms of species richness and endemism, united by a network of step-stones and corridors for population connectivity and the persistence of marine life. Its unique configuration of isolation and connectivity forms a cradle for the genesis and maintenance of biodiversity. The marine protected areas of the TEP are in place to safeguard the entire ecosystem for shore and pelagic species. With new understanding of the deep-water communities, this enormous bathyal ecosystem might take its place within our celebrated TEP ocean heritage. As this region is unique, with high rates of endemism and biodiversity, this place warrants continued protection against the onslaught of anthropogenic pressures that threaten diversity across the planet.

# Acknowledgements

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