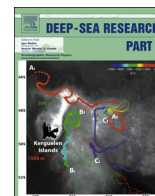




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# Metazoan parasites of deep-sea fishes from the South Eastern Pacific: Exploring the role of ecology and host phylogeny

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## ARTICLE INFO

## Article history:

Received 11 February 2016

Received in revised form

8 June 2016

Accepted 14 June 2016

Available online 15 June 2016

## Keywords:

Deep-sea fish

Metazoan parasites

Diversity

South Eastern Pacific

## ABSTRACT

We studied the parasite fauna of five deep-sea fish species (> 1000 m depth), Three members of Macrouridae (*Macrourus holotrachys*, *Coryphaenoides ariommus* and *Coelorhynchus* sp.), the Morid *Antimora rostrata* and the Synphobranchidae *Diaptobranchius capensis* caught as by-catch of the Patagonian toothfish (*Dissostichus eleginoides*) from central and northern Chile at depths between 1000 and 2000 m. The parasite fauna of *M. holotrachys* was the most diverse, with 32 species (The higher reported for *Macrourus* spp.) and the lower occur in the basketwork eel *D. capensis* (one species). Trophically transmitted parasites, mainly Digenea and Nematoda explain 59.1% of the total number of species obtained (44 species) and the 81.1% of the 1020 specimens collected. Similarity analysis based on prevalence as well as a Correspondence analysis shows that higher similitude in parasite fauna occurs in members of Macrouridae. The importance of diet and phylogeny is discussed as forces behind the characteristics of the endoparasite and ectoparasite communities found in the studied fish species.

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## 1. Introduction

As noted by Klimpel et al. (2006), the oceans are the largest ecosystems on earth. More than two-thirds of the world's surface is covered by seawater, to an average depth of 3800 m. Waters between the depths of 200–1000 m (Mesopelagic) are characterized by diffuse light and scarce nutrient conditions, whereas waters between the depths of 1000–4000 m (Bathypelagic) are completely dark and characterized by food shortage (Castro and Huber, 1997). Jointly, these layers represent the largest area of the deep sea (Bray et al., 1999). According to Froese and Pauly (2015), there are approximately 33,200 species of fish worldwide, of which perhaps 10–15% inhabit the deep sea (Klimpel et al., 2006). Given that approximately 1030 fish species are found in the waters off of the coast of Chile (Pequeño, 1989; Kong and Meléndez 1991), and following Klimpel et al. (2006) proportional estimates, then 100–150 of these Chilean fish species are deep-sea inhabitants.

The Atacama Trench (20–30°S), which runs along the Pacific coast of South America, is the deepest trench in the South Pacific Ocean, extending to a depth of more than 8000 m (Danovaro,

et al., 2002; Gambi, et al., 2003). Because of its great depths, information concerning species diversity in this trench is scarce; Kong and Meléndez (1991) identified 67 teleost fish species caught at depths of 350–1100 m between the latitudes of 18°19'S to 38°30' S. Only four articles (Rodríguez and George-Nascimento, 1996; Oliva et al., 2008; Pardo-Gandarillas et al., 2008; and Salinas et al., 2008) have been published in the scientific literature about the parasite fauna of deep-sea fishes (> 300 m) that inhabit the waters of the Southeastern Pacific.

The study of the parasites of deep-sea fishes began with Manter (1934), who analyzed 721 specimens of teleost fish collected from Dry Tortugas (Florida), and Noble (1973), who studied the parasites of *Macrourus rupestris* collected from Korsfjorden (Norway). Additional studies in the North Atlantic have been conducted by Wilhelm et al. (2008), Kellermanns et al. (2009) and Klimpel et al. (2006, 2008, 2010), among others. Parasite assemblages of deep-sea fishes collected from the Antarctic Ocean have been studied by Walter et al. (2002), whereas Brickle et al. (2005), Dallarés et al. (2014), Mateu et al. (2015) and Constenla et al. (2015) analyzed the parasite fauna of Mediterranean deep-sea fishes. Klimpel et al. (2009) presented a comprehensive list of metazoan parasites of deep-sea fishes (> 200 m).

The evolutionary history and ecology of the host species influences the composition of its parasite communities (Poulin, 1995; Chavéz et al., 2012). Over the course of their evolutionary history, hosts can lose and acquire new parasite species through

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the evolution of native parasites, or they may acquire new parasite species from other hosts (Poulin and Rohde, 1997).

Brook (1980) noted that studies of parasite communities that fail to account for phylogeny may provide inaccurate results and obscure the real relationship between host ecology and parasite richness (Poulin and Rohde, 1997). Moreover, Chávez et al. (2012) noted that few studies have simultaneously evaluated the determinant roles played by ecological and phylogenetic factors in parasite community formation, and those that have evaluated determinant roles show contradictory results.

With regard to the parasites of deep-sea fishes, Campbell et al. (1980) suggested that the parasite community of Macrouridae exhibits a high degree of similarity as a consequence of a similar diet. It is clear that ecology influences the characteristics of the parasite community of a given host in addition to host phylogeny but in different ways (Morand et al., 2002). Janovy et al. (1992), for instance, demonstrated that ecological variables have a strong influence on parasite population structure (i.e., quantitative characteristics such as prevalence, abundance and intensity), whereas the evolutionary history of the host species should only affect the evolutionary processes of their parasites.

Although many studies suggest the importance of host phylogeny, few have integrated this information into parasite-community analyses (Poulin, 1995; Morand et al., 2000). The importance of ecological and phylogenetic factors, when analyzed simultaneously, have been explored by Bush et al. (1990), Poulin (1996, 2010), Muñoz et al., (2006) and Chávez et al. (2012), among a handful of others, but to our knowledge, no study has applied such an approach to deep-sea fish species. Our primary goal here is to identify the metazoan parasites of five deep-sea host fish species in the southeastern Pacific and to examine the relative influence of ecology and host phylogeny in determining parasite composition.

## 2. Materials and methods

### 2.1. Sampling area and parasite collection

A total of 87 deep-sea fish specimens were obtained over the period of February–March 2015 and in October 2015 from the by-

catch of artisanal fisheries and from a mark–recapture experiment of the Patagonian toothfish (*Dissostichus eleginoides* Smitt, 1898) in northern (22°16'S 70°38'W–23°26'S 70°43'W) and central (35°5'S–72°53'W) Chile at depths ranging between 1000–2200 m. (Fig. 1) using a deep-sea longline. Fish specimens belonged to 5 species: bigeye grenadier (*Macrourus holotrachys* Günther, 1878; n=30), Humboldt grenadier (*Coryphaenoides ariommus* Gilbert and Thompson, 1916; n=7), *Coelorhynchus* sp. (n=3), blue Antimora (*Antimora rostrata* Günther, 1878; n=39) and basketwork eel (*Diastobranchus capensis* Barnard, 1923; n=8). Size, weight, order and Family of the fish species are given in Table 1. Fish were immediately frozen (−18 °C) aboard the fishing vessels and transported to the laboratory for parasitological analyses. After thawing, fish were measured (total length to nearest cm), weighed, dissected and examined for metazoan parasites (both ectoparasites and endoparasites). Parasites were recorded by species and abundance for each fish, fixed in AFA (alcohol:formalin:acetic acid), and then preserved in 70° alcohol. Nematoda and Acanthocephala were cleared with Amann lactophenol. Digenea, Monogenea and Cestoda were stained (Acetic Carmin) and cleared with Oil of Clove® (Sigma-Aldrich, Madagascar), then mounted in Eukitt® (O. Kindler GmbH, Germany).

### 2.2. Data analysis

Parasites were identified to the lowest taxonomic level possible. The prevalence and mean intensity of infection were calculated based on procedures described by Bush et al. (1997). Cluster analyses (based on the Bray–Curtis similarity index and simple linkage algorithm) were used to determine whether endoparasitic composition (prevalence and intensity of infection) was similar among hosts. Correspondence analyses were then employed to assess host–parasite associations; only parasites with a prevalence ≥ 10% were included in this analysis. Due to the absence of copepods in four of the five analyzed hosts, and as all monogeneans were specific to a single host species, multivariate analyses were performed only for endoparasites. All multivariate analyses were performed using Statistica 10.0 software (StatSoft Inc., Tulsa, Oklahoma, USA).

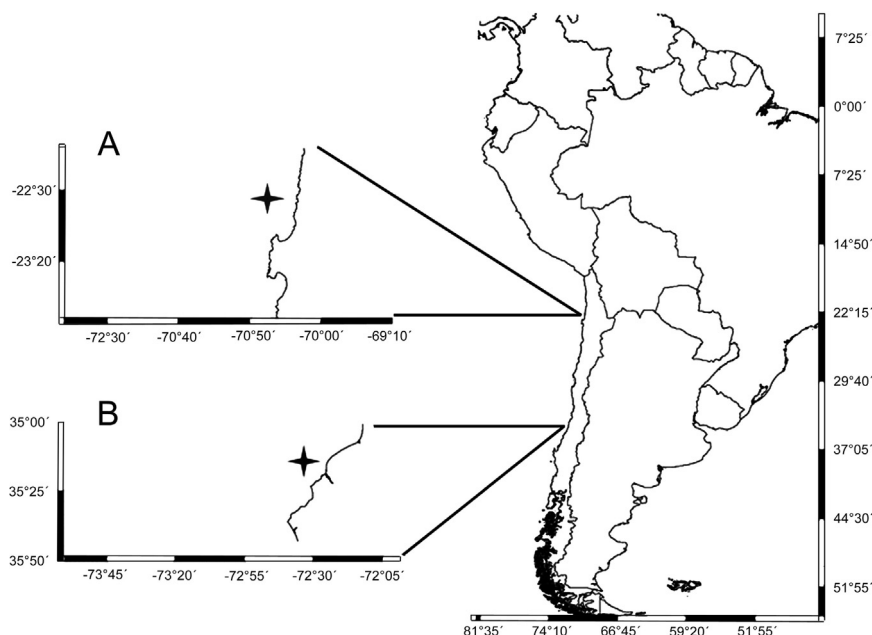


Fig. 1. Stars indicated the approximate position of localities where samples of deep sea fishes were caught. A = Northern Chile (by catch samples as well mark-recapture experiment), B =(mark-recapture experiment).

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