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Helminth parasite communities of spotted rose snapper *Lutjanus guttatus* from the Mexican Pacific

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Summary

The helminth communities of *L. guttatus* from Mazatlan Bay (MB) and Banderas Bay (BB), on the Pacific coast of Mexico, were studied during two consecutive years. A total of 536 fish were collected and 19 parasite taxa registered (six digeneans, two cestodes, nine nematodes, and two monogeneans). Infection levels of common helminth species (*Helicometrina nimia*, *Siphodera vinaledwardsii*, Tetraphyllidea gen. sp., *Pseudoterranova* sp., Ancyrocephalidae gen. sp. and *Microcotyloides incisa*) as well as the infracommunity indices varied significantly between MB and BB, and among dry and rainy seasons; however, no clear seasonal patterns were observed. *Pseudoterranova* larvae appeared frequently in MB, possibly because of the presence of the California sea lion in this locality. Similarity analysis did not show a clear separation of parasite species composition between both localities, which suggest that fish samples came from a single population of *L. guttatus*.

Keywords: parasitic worms; fishery; marine ecology; Gulf of California

Introduction

Fishes of the family Lutjanidae, commonly known as snappers, are generally piscivores or planktivores distributed worldwide in tropical and subtropical waters. These fishes are targets of subsistence, commercial, and recreational fisheries. The spotted rose snapper *Lutjanus guttatus* inhabits coastal ecosystems, including reefs and estuaries, along the Eastern Pacific from Mexico to Peru. In Mexico, *L. guttatus* is one of the most economically important fish species, which has caused its exploitation above optimum levels (Amezcuca *et al.*, 2006). In addition, this fish is considered as one of the best candidates for commercial aquaculture in the region (Alvarez-Lajonchère *et al.*, 2012; Hernández *et al.*, 2016). As far as we are aware 16 species of helminths (*Anisakis* sp., *Hamacredium lariosi*, *Helicometrina nimia*, *Lecithochirium microstomum*, *Maculifer japonicus*, *Microcotyloides incisa*, *Neobivagina aniversaria*, *Polycryptocylis leonilae*, *Polymicrocotyle manteri*,

Pseudoterranova sp., *Siphodera vinaledwardsii*, *Euryhaliotrema mehen*, *E. perezponcei*, *Haliotrematoides guttati*, *H. plectridium* and *H. spinatus*) are known from *L. guttatus* (Lamothe-Argumedo *et al.*, 1997; Pérez-Ponce de León *et al.*, 1999; García-Vargas *et al.*, 2008; Soler-Jiménez & Fajer-Ávila, 2012; Soler-Jiménez *et al.*, 2012). Given the importance of *L. guttatus* for fisheries and aquaculture, it is necessary to improve our knowledge about its parasite diversity and infection levels on wild fish populations. In fish parasite ecology, there has been some evidence for an increase in parasite diversity with host size (Lo *et al.*, 1998); however, in many cases the correlation between those factors may be weak and non-significant (Poulin, 2000). Other ecological processes may occur at spatial scale. For instance, similarity in parasite communities may decay with increasing distance between localities which could be related to discontinuities in the landscape or the probability that parasites species disperse among localities via host movements (Poulin, 2003; Timi *et al.*, 2010). Such variation

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in composition and abundance of parasites provides information about the host population movements and structure which can be useful for the efficient and sustainable management of a commercially exploited marine fish species (MacKenzie, 2005; Moore *et al.*, 2011; Baldwin *et al.*, 2012); however, this biological tool has received limited use in Mexican fisheries (Violante-González *et al.*, 2016).

Therefore, the aim of this study was 2-fold: (1) to analyse the temporal and spatial variation of fish parasite populations and infracommunities of *L. guttatus* from two important fishing localities in the Mexican Pacific; and (2) to evaluate the relationship between parasite load and fish body length. This information may be useful for strategies of management and protection of local fishery resources.

Materials and Methods

A total of 536 specimens of *L. guttatus* were collected between April 2004 and February 2006 from two important fishing localities in the Mexican Pacific: Mazatlan Bay (MB, 23°12'N, 106°26'W) and Banderas Bay (BB, 20°44'N, 105°26'W) which are approximately 300 km apart. The study area experiences two contrasting

seasons, dry from December to May, and rainy from June to November. Thus, we performed comparisons of parasitological data between localities, and among climatic seasons (dry 2004, rainy 2004, dry 2005, rainy 2005, and dry 2006).

Each fish was measured for standard length (cm) and a complete necropsy was done with the aid of a dissection microscope. The fish length was compared between both localities with Mann-Whitney test with SigmaStat 3.5 software. All helminths collected were counted and processed according to Lamothe-Argumedo (1997). For each season and locality, prevalence and mean intensity (*sensu* Bush *et al.*, 1997) with their respective 95 % confidence interval were calculated for each parasite species or taxon identified using Quantitative Parasitology on the Web (QPweb) software (Rozsa *et al.*, 2000; Reiczigel *et al.*, 2013). This software was also used to compare prevalence and mean intensity of the commonest species (prevalence > 10 %) among all samples. Specifically, prevalence was compared using Fisher's exact test and intensity using Mood's median test. A posteriori pairwise comparisons of prevalence and intensity were performed, respectively, with Fisher's exact test and bootstrap *t*-test with 1,000 replications.

Analyses were made at the infracommunity (all the helminth parasites in an individual fish) level (Bush *et al.*, 1997) using the num-

Table 1. Overall prevalence (P), mean intensity (MI) and infection site of helminth parasites in *Lutjanus guttatus* from two localities in the Mexican Pacific. Values in parentheses are 95 % confidence intervals.

| Parasite | Infection site | Locality | | | |
|--|---|------------------------|--------------------|------------------------|------------------|
| | | Mazatlan Bay (n = 283) | | Banderas Bay (n = 253) | |
| | | P % | MI | P % | MI |
| Digenea | | | | | |
| <i>Stephanostomun casum</i> (A) | Intestine and stomach | 1.1 (0.2 – 3.1) | 1 | 1.2 (0.2 – 3.4) | 1 |
| <i>Hamacreadium mutabile</i> (A) | Intestine and stomach | 6.4 (3.8 – 9.9) | 1.9 (1.3 – 2.8) | 0.4 (0 – 2.2) | 13 |
| <i>Helicometrina nimia</i> (A) | Intestine and stomach | 2.8 (1.2 – 5.5) | 2.6 (1.2 – 5) | 42.3 (3.6 – 48.6) | 4.6 (3.7 – 6.3) |
| <i>Siphodera vinaledwardsii</i> (A) | Intestine and stomach | 0.4 (0.0 – 2.0) | 3 | 36.8 (30.8 – 43) | 6 (4.6 – 8.2) |
| <i>Torticaecum</i> sp. (L) | Gills | 1.4 (0.4 – 3.6) | 1.2 (1 – 1.5) | 0.0 | 0.0 |
| <i>Parahemiurus merus</i> (A) | Intestine and stomach | 0.7 (0.1 – 2.5) | 1.5 (1 – 1.5) | 0.8 (0.1 – 2.8) | 2 (1 – 2) |
| Cestoda | | | | | |
| Trypanorhyncha (L) | Intestinal lumen | 0.4 (0.0 – 2) | 1 | 0.0 | 0.0 |
| Tetraphyllidea (L) | Intestinal wall and stomach | 36.4 (30.8 – 42.3) | 18.3 (11.4 – 39.9) | 29.6 (24.1 – 35.7) | 157 (72.3 – 426) |
| Nematoda | | | | | |
| Capillariidae (A) | Intestine and stomach | 1.1 (0.2 – 3.1) | 1 | 1.6 (0.4 – 4) | 1 |
| <i>Anisakis</i> sp. (L) | Mesenteries | 0.7 (0.1 – 2.5) | 1 | 1.6 (0.4 – 4) | 1.5 (1 – 2) |
| <i>Pseudoterranova</i> sp. (L) | Mesenteries, liver, intestinal wall and stomach | 42.8 (36.9 – 48.7) | 5.2 (4.3 – 6.5) | 2.4 (0.9 – 5.1) | 1.2 (1 – 1.5) |
| <i>Hysterothylacium</i> sp. (L) | Mesenteries and intestinal lumen | 0.0 | 0.0 | 9.9 (6.5 – 14.2) | 2.2 (1.5 – 3.3) |
| <i>Goezia</i> sp. (L) | Intestine and stomach | 1.8 (0.6 – 4.1) | 2.4 (1 – 3.2) | 1.2 (0.2 – 3.4) | 4.3 (1 – 6.7) |
| <i>Ascarophis</i> sp. (A) | Stomach | 5.3 (3.0 – 8.6) | 1.9 (1.1 – 3.4) | 1.2 (0.2 – 3.4) | 1 |
| <i>Spinitectus</i> sp. (L) | Intestinal lumen | 0.0 | 0.0 | 0.8 (0.1 – 2.8) | 1.5 (1 – 1.5) |
| <i>Procamallanus</i> (Spirocamallanus) sp. (L) | Intestine and stomach | 2.5 (1.0 – 5.0) | 1.3 (1 – 1.9) | 0.8 (0.1 – 2.8) | 5.5 (1 – 5.5) |
| <i>Philometra</i> sp. (A) | Gonads | 1.1 (0.2 – 3.1) | 1.3 (1 – 1.7) | 1.6 (0.4 – 4) | 1.2 (1 – 1.5) |
| Monogenea | | | | | |
| Ancyrocephalidae | Gills | 80.6 (75.5 – 85.0) | 68 (55.2 – 82.8) | 92.5 (88.5 – 95.4) | 53.4 (47 – 61.6) |
| <i>Microcotyloides incisa</i> | Gills | 10.2 (7 – 14.4) | 2.1 (1.6 – 3.2) | 34 (28.2 – 40.2) | 3.1 (2.5 – 4.4) |

A = adult; L = larvae

ber of species (S), number of individuals (N), Brillouin's index of diversity (HB) and Berger-Parker's index of dominance (BP) (Magurran, 1988). Mann-Whitney and Kruskal-Wallis tests were used to determine, respectively, significant differences in infracommunity indices between localities (MB and BB) and between climatic seasons. Possible significant correlation between infracommunity indices and fish body length were detected with Spearman's rank test. Only correlations of $r > 0.4$ were considered significant. Uninfected fish were excluded from analyses at the infracommunity level, except for correlation analyses.

A non-metric multidimensional scaling (MDS) plot was performed to analyse differences in the composition of helminth infracommunities between MB and BB. The magnitude of such differences was tested with a one-way analysis of similarity (ANOSIM). Similarity percentages (SIMPER) were calculated to identify the helminth parasite species driving the differences between communities at different localities. These multivariate analyses were performed in PRIMER v6 (Clarke & Warwick, 2001; Clarke & Gorley, 2006) based on standardised abundance data and Bray-Curtis distances.

Results

Fish body length (mean \pm standard deviation) from BB (24.7 ± 5.8 cm) was significantly larger than that from MB (20.8 ± 4.3 cm) when data from all seasons were pooled ($U = 19528.0$, $P < 0.001$). In the total sample ($n = 536$), 19 helminth species (six digeneans, two cestodes, nine nematodes, and two monogeneans) were found (Table 1). Of these, 15 were present in both localities and only six (*Helicometrina nimia*, *Siphodera vinaledwardsii*, Tetraphyllidea gen. sp., *Pseudoterranova* sp., Ancyrocephalidae gen. sp., and *Microcotyloides incisa*) can be considered the commonest as they reached prevalences $> 10\%$ in fish from one or both localities. The monogenean Ancyrocephalidae gen. sp. was by far the dominant species. This species as well as *Helicometrina nimia*, *S. vinaledwardsii*, and *M. incisa* were significantly more prevalent in BB than in MB (all $P < 0.0001$) but their intensity did not vary between both localities (all $P > 0.05$). For Tetraphyllidea gen. sp. there were no differences in prevalence and intensity between both localities ($P > 0.05$) while *Pseudoterranova* sp. showed significantly higher prevalence ($P < 0.0001$) and intensity ($P < 0.05$) in MB than in BB.

In each locality, the helminth species showed an unequal distribution between climatic seasons (Tables 2 and 3), which was confirmed by significant differences in prevalence and intensity of the commonest species ($P < 0.05$). However, no clear seasonal patterns could be detected according to the posteriori pairwise comparisons (data not shown).

Considering pooled samples from each locality, all infracommunity indices were significantly higher in BB than in MB (S: $U = 23845.5$, $P < 0.001$; N: $U = 25396$, $P < 0.001$; HB: $U = 27013.5$, $P < 0.001$; BP: $U = 26199$, $P = 0.001$) (Fig. 1). In each locality, all infracommunity indices varied significantly between dry and rainy seasons

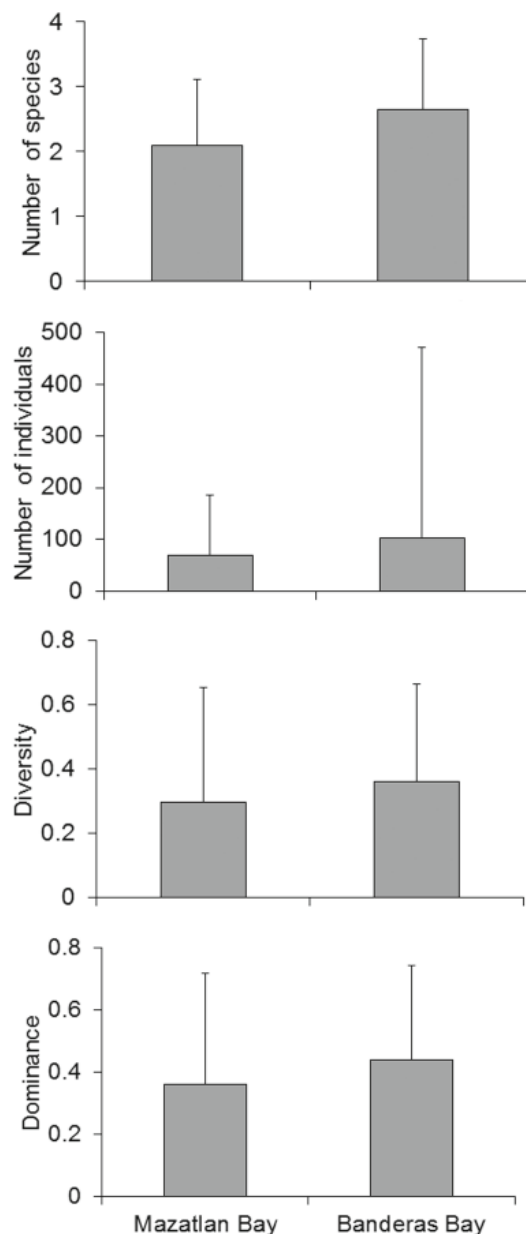


Fig. 1. Overall mean infracommunity descriptors \pm standard deviation of *Lufjanus guttatus* collected in Mazatlan Bay and Banderas Bay.

($P < 0.05$); however, no clear seasonal patterns could be detected (Fig. 2). There was no significant correlation between infracommunity indices and fish body length, neither when samples were pooled nor when analysed separately.

Multidimensional scaling (Fig. 3) and global ANOSIM (Global $R = 0.042$, $P = 0.01$) showed little but significant separation of parasite species composition between both localities. SIMPER was low in MB (55) and BB (61) with Ancyrocephalidae gen. sp. being the main responsible ($> 90\%$) to similarity within samples of each locality. Average dissimilarity (44) between MB and BB was also

Table 2. Prevalence (P) and mean intensity (MI) of helminth parasites in *Lutjanus guttatus* from Mazatlan Bay during dry and rainy seasons. Values in parentheses are 95 % confidence intervals.

| | Dry 2004 n = 53 | | | Rainy 2004 n = 65 | | | Dry 2005 n = 90 | | | Rainy 2005 n = 25 | | | Dry 2006 n = 50 | | |
|---|--------------------|--------------|--|----------------------|-------------|--|--------------------|--------------|--|----------------------|---------------|--|--------------------|--------------|--|
| | P% | MI | | P% | MI | | P% | MI | | P | MI | | P% | MI | |
| Digenea | | | | | | | | | | | | | | | |
| <i>Stephanostomum casum</i> | 0 | 0 | | 4.6 (1–13) | 1 | | 0 | 0 | | 0 | 0 | | 0 | 0 | |
| <i>Hamacreadium mutabile</i> | 0 | 0 | | 21 (12–33) | 2.1 (1–3.4) | | 4.4 (1.2–11) | 1 | | 0 | 0 | | 0 | 0 | |
| <i>Helicometina nimia</i> | 3.8 (0.5–13) | 4.5 (1–8) | | 6.2 (1–15) | 2 (1–3) | | 1 (0–6) | 2 | | 4 (0–20) | 2 | | 0 | 0 | |
| <i>Siphodera vinaledwardsii</i> | 0 | 0 | | 1.5 (0–8.3) | 3 | | 0 | 0 | | 0 | 0 | | 0 | 0 | |
| <i>Torticaecum</i> sp. | 0 | 0 | | 3.1 (0–10) | 1 | | 1 (0–6) | 2 | | 0 | 0 | | 2 (0–10) | 1 | |
| <i>Parahemirius merus</i> | 0 | 0 | | 1.5 (0–8) | 2 | | 1 (0–6) | 1 | | 0 | 0 | | 0 | 0 | |
| Cestoda | | | | | | | | | | | | | | | |
| <i>Trypanorhyncha</i> | 1.9 (0–10) | 1 | | 0 | 0 | | 0 | 0 | | 0 | 0 | | 0 | 0 | |
| <i>Tetraphylidea</i> | 45 (32–59) | 13.6 (4–50) | | 60 (47–72) | 14 (10–21) | | 26 (18–37) | 11 (7.5–16) | | 24 (9.4–45) | 2.2 (2–2.3) | | 20 (10–33) | 73 (17–282) | |
| Nematoda | | | | | | | | | | | | | | | |
| <i>Capillariidae</i> | 5.7 (1.2–16) | 1 | | 0 | 0 | | 0 | 0 | | 0 | 0 | | 0 | 0 | |
| <i>Anisakis</i> sp. | 0 | 0 | | 0 | 0 | | 0 | 0 | | 4 (0–20) | 1 | | 2 (0–10) | 1 | |
| <i>Pseudoterranova</i> sp. | 39 (26–54) | 6.67 (5–9.4) | | 75 (63–85) | 3.5 (3–4.3) | | 36 (27–47) | 6.9 (4.5–11) | | 16 (4.5–36) | 6 (2–10.5) | | 28 (16–42) | 4.6 (2–10.7) | |
| <i>Hysterothylacium</i> sp. | 0 | 0 | | 0 | 0 | | 0 | 0 | | 0 | 0 | | 0 | 0 | |
| <i>Goezia</i> sp. | 3.8 (0.5–13) | 3.5 (3–3.5) | | 0 | 0 | | 0 | 0 | | 12 (2.5–31) | 1.7 (1–2.3) | | 0 | 0 | |
| <i>Ascarophis</i> sp. | 11.3 (4–23) | 3 (1–5.3) | | 9.2 (3.5–19) | 1.3 (1–1.7) | | 1 (0–6) | 1 | | 4 (0–20) | 1 | | 2 (0–10) | 1 | |
| <i>Spiritectus</i> sp. | 0 | 0 | | 0 | 0 | | 0 | 0 | | 0 | 0 | | 0 | 0 | |
| <i>Procamallanus</i> (<i>Spirocamallanus</i>) sp. | 0 | 0 | | 4.6 (1–13) | 1.7 (1–2.3) | | 3.3 (1–9) | 1 | | 4 (0–20) | 1 | | 0 | 0 | |
| <i>Philometra</i> sp. | 0 | 0 | | 0 | 0 | | 2 (0–7) | 1.5 (1–1.5) | | 4 (0–20) | 1 | | 0 | 0 | |
| Monogenea | | | | | | | | | | | | | | | |
| <i>Ancyrocephalidae</i> | 92 (82–98) | 23 (19–28) | | 81 (70–90) | 16 (12–23) | | 65 (55–75) | 72 (51–104) | | 84 (64–95) | 184 (118–271) | | 92 (81–98) | 116 (85–165) | |
| <i>Microcotyloides incisa</i> | 3.8 (0.5–13) | 2 (1–2) | | 1.5 (0–8) | 1 | | 14 (7.9–23) | 1.8 (1–2.3) | | 16 (4.5–36) | 1.2 (1–1.5) | | 18 (8–31.4) | 3 (1.4–5) | |

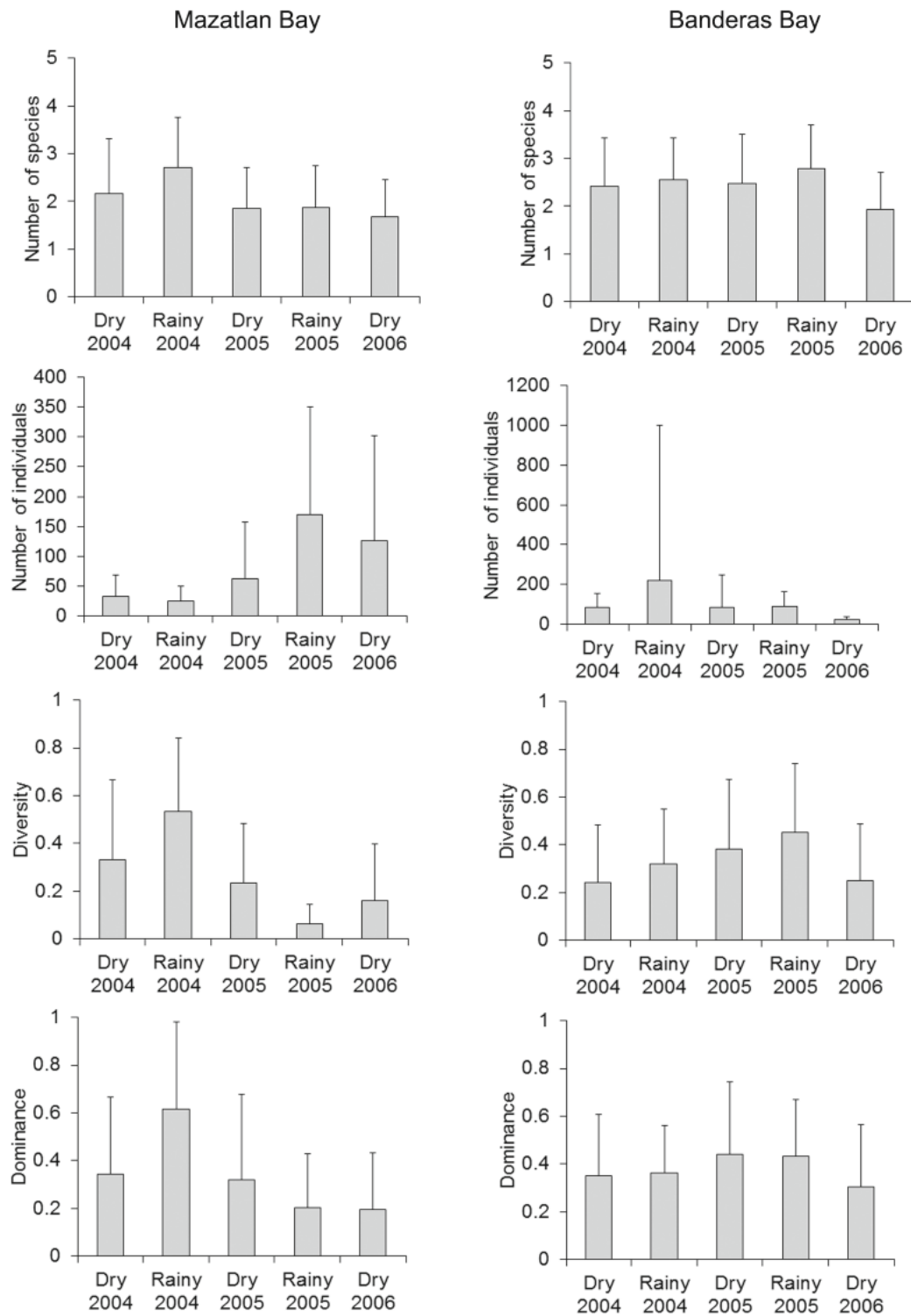


Fig. 2. Mean infracommunity descriptors \pm standard deviation of *Lutjanus guttatus* in each sampling season in Mazatlan Bay and Banderas Bay.

Table 3. Prevalence (P) and mean intensity (MI) of helminth parasites in *Lufjanus guttatus* from Banderas Bay during dry and rainy seasons. Values in parentheses are 95% confidence intervals.

| | Dry 2004 n = 45 | | | Rainy 2004 n = 53 | | | Dry 2005 n = 61 | | | Rainy 2005 n = 53 | | | Dry 2006 n = 40 | | |
|---|--------------------|--------------|--|----------------------|---------------|--|--------------------|--------------|--|----------------------|-------------|--|--------------------|-------------|--|
| | P% | MI | | P% | MI | | P% | MI | | P | MI | | P% | MI | |
| Digenea | | | | | | | | | | | | | | | |
| <i>Stephanostomum casum</i> | 0 | 0 | | 0 | 0 | | 2 (0–8) | 1 | | 4 (0–13) | 1 | | 0 | 0 | |
| <i>Hamacreadium mutabile</i> | 0 | 0 | | 2 (0–10) | 13 | | 0 | 0 | | 0 | 0 | | 0 | 0 | |
| <i>Helicometina nimia</i> | 35 (22–51) | 5.2 (2.7–10) | | 47 (33–61) | 4.8 (3–7.3) | | 62 (49–74) | 3 (2.3–3.8) | | 39 (26–54) | 8.2 (5–15) | | 17 (7–33) | 1.4 (1–1.8) | |
| <i>Siphodera vinaladwardsii</i> | 29 (16–44) | 3.9 (1.6–9) | | 17 (8–30) | 5.8 (2.8–11) | | 24 (14–37) | 3.3 (2–5.4) | | 70 (56–81) | 9.5 (7–14) | | 47 (31–64) | 2.8 (2–3.6) | |
| <i>Torticaecum</i> sp. | 0 | 0 | | 0 | 0 | | 0 | 0 | | 0 | 0 | | 0 | 0 | |
| <i>Parahemius merus</i> | 2.2 (0–11) | 3 | | 2 (0–10) | 1 | | 0 | 0 | | 0 | 0 | | 0 | 0 | |
| Cestoda | | | | | | | | | | | | | | | |
| <i>Trypanorhyncha</i> | 0 | 0 | | 0 | 0 | | 0 | 0 | | 0 | 0 | | 0 | 0 | |
| <i>Tetraphyllidea</i> | 17 (8–32) | 29 (4–128) | | 37 (25–52) | 358 (62–1460) | | 34 (23–47) | 142 (74–304) | | 30 (18–44) | 81 (46–139) | | 25 (13–41) | 5.4 (3–10) | |
| Nematoda | | | | | | | | | | | | | | | |
| <i>Capillariidae</i> | 0 | 0 | | 2 (0–10) | 1 | | 3 (0–11) | 1 | | 2 (0–10) | 1 | | 0 | 0 | |
| <i>Anisakis</i> sp. | 0 | 0 | | 3.8 (0–13) | 2 (1–2) | | 1.6 (0–9) | 1 | | 0 | 0 | | 2.5 (0–13) | 1 | |
| <i>Pseudoterranova</i> sp. | 2 (0–11) | 1 | | 0 | 0 | | 8 (3–18) | 1.2 (1–1.4) | | 0 | 0 | | 0 | 0 | |
| <i>Hysterothylacium</i> sp. | 2 (0–11) | 3 | | 2 (0–10) | 1 | | 18 (9–30) | 1.8 (1.3–3) | | 11 (4.3–23) | 4.2 (2–6.8) | | 15 (6–30) | 1 (1–1.3) | |
| <i>Goezia</i> sp. | 0 | 0 | | 0 | 0 | | 0 | 0 | | 6 (1–15) | 4.3 (1–6.6) | | 0 | 0 | |
| <i>Ascarophis</i> sp. | 0 | 0 | | 2 (0–10) | 1 | | 0 | 0 | | 2 (0–10) | 1 | | 2 (0–13.2) | 1 | |
| <i>Spiritectus</i> sp. | 0 | 0 | | 0 | 0 | | 2 (0–8) | 1 | | 2 (0–10) | 2 | | 0 | 0 | |
| <i>Procamallanus</i> (<i>Spirocamallanus</i>) sp. | 2 (0–11) | 1 | | 0 | 0 | | 0 | 0 | | 0 | 0 | | 2.5 (0–13) | 10 | |
| <i>Philometra</i> sp. | 7 (1.4–18) | 1.3 (1–1.7) | | 0 | 0 | | 0 | 0 | | 2 (0–10) | 1 | | 0 | 0 | |
| Monogenea | | | | | | | | | | | | | | | |
| <i>Ancyrocephalidae</i> | 100 (92–100) | 76 (60–94) | | 90 (79–97) | 76 (61–105) | | 85 (74–93) | 31 (24–42) | | 96 (87–99) | 56 (44–71) | | 92 (79–98) | 21 (16–27) | |
| <i>Microcotyloides incisa</i> | 58 (42–72) | 2.6 (2–3.8) | | 47 (33–61) | 4.9 (3–9) | | 23 (13–35) | 1.9 (1–3.3) | | 37 (25–52) | 2.4 (1.7–3) | | 0 | 0 | |

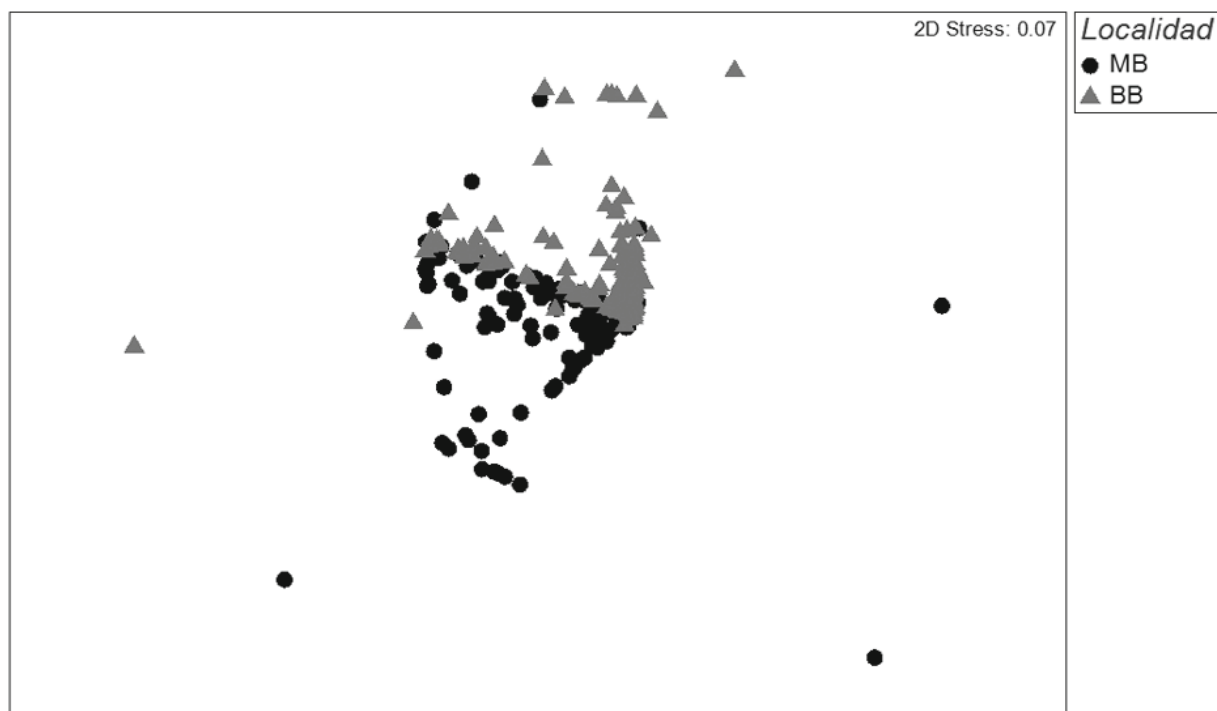


Fig. 3. Two-dimensional nonmetric MDS plot of Bray-Curtis similarity based on standardised abundance data of helminth parasites communities of *Lutjanus guttatus* collected periodically over 2 years in Mazatlan Bay (MB) and Banderas Bay (BB).

attributed to Ancyrocephalidae gen. sp. followed by Tetraphyllidae gen. sp. and *Pseudoterranova* sp. (Table 4).

Discussion

The 19 helminth species of *L. guttatus* herein reported contrast with the five helminth species found in *Caulolatilus princeps*, nine in *Sebastes miniatus*, and 14 in *Caranx caballus* from the Mexican Pacific (Rodríguez-Santiago & Rosales-Casián, 2011; Rodríguez-Santiago *et al.*, 2014; Violante-González *et al.*, 2016). Possibly, such differences would be indicating a more varied diet in *L. guttatus*. Nonetheless, several parasite species are accidental.

Our results showed a wide dominance of ancyrocephalids, followed by Tetraphyllidae. Unfortunately, at the time this survey was realized, species of ancyrocephalids were not correctly discriminated and quantified. Nowadays, based on additional studies, we know that *L. guttatus* serves as host to five ancyrocephalids species (*Euryhaliothrema mehen*, *E. perezponcei*, *Haliotrematoides guttati*, *H. plectridium* and *H. spinatus*), of which *E. perezponcei* has been the most frequent and abundant species on either wild or sea-caged fish (Soler-Jiménez & Fajer-Ávila, 2012; Soler-Jiménez *et al.*, 2015). Similarly, Montoya-Mendoza *et al.* (2014, 2016) identified 21 and 25 helminth species from *Lutjanus campechanus* and *L. synagris*, respectively, from the southern Gulf of Mexico,

Table 4. SIMPER analysis for helminth parasites of *Lutjanus guttatus* from Mazatlan Bay and Banderas Bay.

| Parasite | Mazatlan | Banderas | AD | D/SD | % | C % |
|-------------------------------|----------|----------|-------|------|-------|-------|
| | AA | AA | | | | |
| Ancyrocephalidae | 68.94 | 73.22 | 17.83 | 1.11 | 40.29 | 40.29 |
| Tetraphyllidae | 13.68 | 11.86 | 10.49 | 0.72 | 23.69 | 63.98 |
| <i>Pseudoterranova</i> sp. | 12.43 | 0.07 | 6.23 | 0.52 | 14.07 | 78.05 |
| <i>Helicometrina nimia</i> | 0.40 | 5.39 | 2.83 | 0.42 | 6.39 | 84.44 |
| <i>Siphodera vinalwardsii</i> | 0.04 | 4.71 | 2.36 | 0.44 | 5.34 | 89.78 |
| <i>Microcotyloides incisa</i> | 1.07 | 2.13 | 1.51 | 0.31 | 3.40 | 93.18 |

AA average abundance; AD average dissimilarity; D/SD dissimilarity/standard deviation; % and C % respectively percentage of total and cumulative dissimilarity contributed by each parasite species

with ancyrocephalids (*Euryhaliootrema tubocirrus* and *Haliotrema toides cornigerum*) being the most prevalent parasites, followed by Tetraphyllidea. These findings fit with the idea that snappers are highly suitable host for ancyrocephalids worldwide (Kritsky, 2012). The tetraphyllid life cycle is poorly known (Jensen & Bullard, 2010), but at least three hosts are involved: copepods, euphausiid shrimps or occasionally a pelecypod mollusk as first intermediate hosts; teleost fishes, decapods or cephalopods as second intermediate hosts; and elasmobranchs as definitive hosts (Caira & Reyda, 2005). In this study, the higher prevalence and abundance of tetraphyllid larvae with respect to other helminths could be associated to the feeding habits of *L. guttatus*. This fish is an active predator and opportunistic carnivorous with a diet composed mostly of crustaceans, fish and mollusks (Rojas-Herrera *et al.*, 2003), which together with potential elasmobranchs hosts are well represented in the sampling areas (van der Heiden & Hendrickx, 1982; Espinosa-Pérez *et al.*, 2004; Hendrickx *et al.*, 2005).

In MB, *Pseudoterranova* larvae appeared in all sampling months with relatively high prevalence and intensity. In contrast, this parasite was almost absent in BB. *Pseudoterranova* nematodes adults are common parasites of marine mammals. We suppose that the occurrence of *Pseudoterranova* larvae in *L. guttatus* from MB is associated to the presence of the California sea lion (*Zalophus californianus*) that may serve as final host. The main rookeries of *Z. californianus* are distributed from California islands to Baja California and the Gulf of California, with the southernmost rest rookery located in MB (Hoyos-Padilla & Gallo-Reynoso, 2015). This pinniped feed on a variety of fish species and its diet may vary among rookeries within the Gulf of California (García-Rodríguez & Auriol-Gamboa, 2004); however, its feeding habits in MB are unknown. Our study suggests that *L. guttatus* forms part of *Z. californianus* diet.

In this study, the lack of association between fish length and parasite load suggests that other local ecological factors may be more influential in regulating the parasite community of *L. guttatus*. It could be a biased analysis since our sampling effort just comprised a portion of the entire range of fish length. Nonetheless, a meta-analysis performed by Poulin (2000) indicated that the overall, mean correlation between fish length and intensity of infection, weighted for sample size, was not significantly different from zero, independent of mode of infection.

In the overall samples, metrics of most component species and infracommunities were higher in BB than in MB. Given that helminths usually have indirect life cycles that require a variety of invertebrate and vertebrate hosts, a community of these parasites within a host organism reflects the presence in the ecosystem of any other organism involved in the various parasite life cycles (Marcogliese, 2005). Thus, it is possible that the relatively low diversity of helminths in MB is a result of the absence of some intermediate or final hosts.

Despite the economic importance of *L. guttatus*, its stock structure along the Mexican Pacific remains unknown. Recently, García-

Vásquez *et al.* (2015), based on the molecular similarity between individuals of *E. perezponcei* from two distant localities (MB and Chamela Bay), suggested that populations of *L. guttatus* move along the Pacific coast of Mexico. Molecular markers may be used for population structure analysis in parasites and hosts. However, it is possible that the sole examination of organisms at genetic level is not sufficient to discriminate fish stocks. In the present study, there were not notable differences of parasite communities between MB and BB, which could suggest that specimens of *L. guttatus* caught in those localities belong to the same fish population. It was confirmed by the Global *R* from ANOSIM which was close to 0, indicating that differences in parasite species composition between both sites were small. As mentioned earlier, ancyrocephalids dominated largely the samples in terms of prevalence and intensity of infection. Also, these monogeneans were the main responsible of dissimilarity between both localities. Grutter (1998) argued that monogeneans may be useful as biological tags, since they do not leave their host, differences in abundance of these parasites between localities would be indicating different fish stocks. On other hand, Lester and MacKenzie (2009) pointed out that monogeneans seem to be short-lived, surviving on fish for less than a year, which make them of little value for stock discrimination since fish acquire and lose these parasites during their geographic move.

In conclusion, *L. guttatus* harbored helminth parasite communities which showed stability over space but no over time in terms of composition and infection levels. We consider that our data analyses provide some evidence to claim that fish samples came from a single population of *L. guttatus*.

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