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**División de Estudios de Posgrado**

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**Facultad de Biología**

**Programa Institucional de Maestría en Ciencias Biológicas**

**Área Temática: Ecología y Conservación**

**Estructura de la comunidad de trematodos (Platyhelminthes: Digenea) en  
seis especies de *Haemulon* (Osteichthyes: Haemulidae) en el Parque  
Nacional Arrecife de Puerto Morelos, Quintana Roo, México.**

**TESIS**

**Que presenta:**

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**Como requisito para obtener el título profesional de**

**Maestro en Ciencias Biológicas**

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## **Abstract**

Haemulids (grunts) represent one of the most conspicuous families of marine fishes. Even though haemulids are well represented in Mexico along the Pacific and Gulf of Mexico slopes, as well as in the Caribbean Sea, their trematode fauna has been scarcely studied. Here, eight species of *Haemulon* from the Puerto Morelos Reef National Park (PMRNP), in Quintana Roo, Mexico were analyzed to establish their trematode species composition and to describe the patterns of their community structure at both, infracommunity and component community levels. Eleven species of trematodes were identified, namely *Hamacreadium mutabile*, *Helicometrina nimia*, *Pycnadenoides* sp., *Homalometron* sp. 1, *Homalometron* sp. 2, *Monolecithotrema* sp., *Leurodera decora*, *Lasciotocus haemuli*, *Macradena* sp. and two species of the family Hemiuridae. Overall, 16 new host records were reported in this study. Eight of the 11 trematode species were reported in the PMRNP for the first time. All trematode species were considered rare species, with prevalence values <20%. Species accumulation curves showed that only three of the six host species, i.e., *H. flavolineatum*, *H. plumierii* and *H. sciurus*, reached an asymptote, and their trematode community structure was analyzed. Communities were species-poor and dominated by a single trematode species, with low diversity values at both, infracommunity and component community levels. Trematode communities differed among species of grunts analyzed in this study, indicating that some ecological factors such as feeding habits, geographic distribution, and vagility of the hosts play a major role structuring these communities.

*Key words:* Parasites, infracommunity, component community, grunts, diversity.

## Resumen

Los hemúlidos (roncadores) representan una de las familias de peces marinos más conspicuos en el mundo. A pesar de la alta riqueza de especies de Haemulidae en México, tanto en las costas del Pacífico y del Golfo de México, así como en el Caribe, su fauna de tremátodos ha sido escasamente estudiada. En este trabajo, se estudiaron ocho especies del género *Haemulon* en el Parque Nacional Arrecifes de Puerto Morelos (PNAPM), Quintana Roo, México para determinar la composición de la fauna de trematodos y para describir la estructura de sus comunidades a nivel de infreacomunidad y de componente de comunidad. Se reporta la presencia de 11 especies de trematodos, incluyendo a *Hamacreadium mutabile*, *Helicometrina nimia*, *Pycnadenoides* sp, *Homalometron* sp. 1, *Homalometron* sp. 2, *Monolecithotrema* sp., *Leurodera decora*, *Lasciotocus haemuli*, *Macradena* sp. y dos especies de la familia Hemiuridae. En este trabajo se presentan 16 nuevos registros de hospedero. Ocho de las 11 especies de trematodos encontradas se registran por primera vez en el PNAPM. Todos los trematodos se clasificaron como especies raras, dado que la prevalencia de infección en sus hospederos fue siempre <20%. Las curvas de acumulación de especies indicaron que solo tres de las ocho comunidades de trematodos, *H. flavolineatum*, *H. plumierii* and *H. sciurus*, alcanzaron la asíntota y por ello, solo esas tres comunidades fueron analizadas. Las comunidades resultaron ser pobres en especies y dominadas por una sola especie de trematodo, alcanzando valores bajos de diversidad tanto en las infracomunidades como en los componentes de comunidad. Estas comunidades de trematodos variaron entre las diferentes especies de roncadores, lo que indica que factores ecológicos como los hábitos alimentarios, distribución geográfica y la vagilidad de los hospederos son aquellos que determinan principalmente la estructura de sus comunidades.

*Palabras clave:* Parásitos, infracommunidad, comunidad componente, roncadore, diversidad.

## Introduction

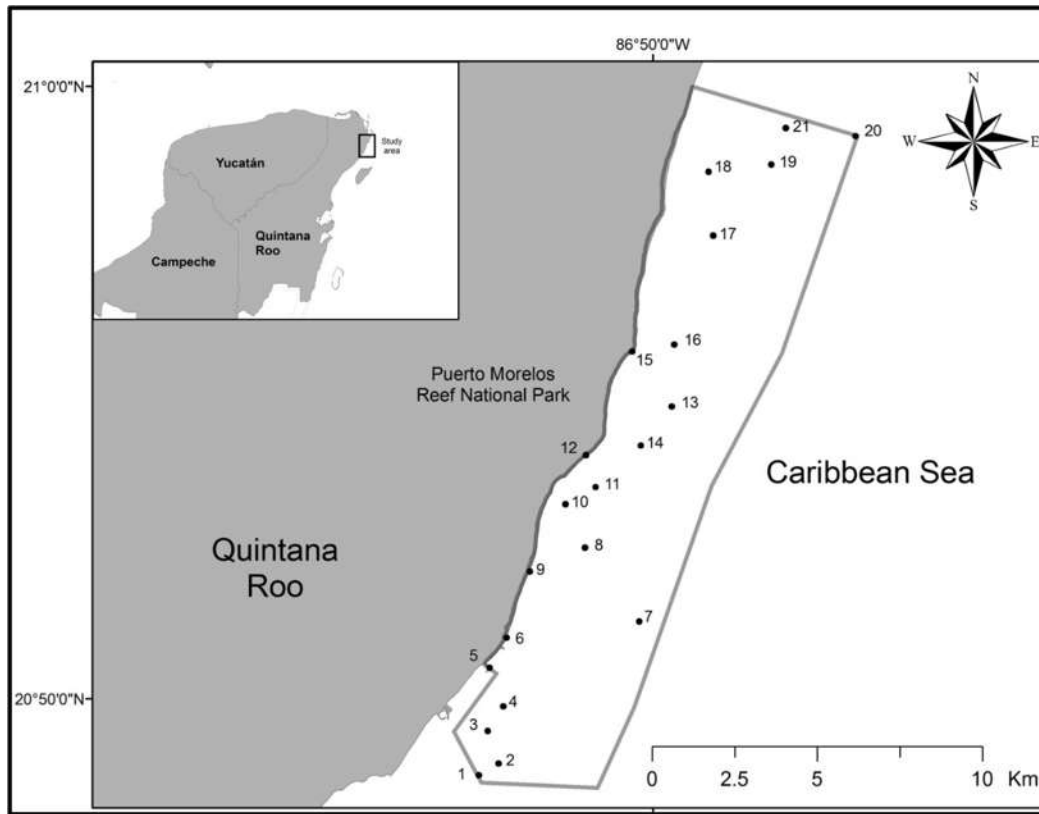
The family Haemulidae is one of the most conspicuous groups of marine fishes within the order Perciformes. Currently, this family contains 150 species included in 17 genera distributed worldwide (Froese & Pauly 2019). In particular, the Neotropical genus *Haemulon* Cuvier is one of the most species-rich, with 145 species (Tavera et al. 2012). In Mexico, species of the genus are distributed in the Pacific and Gulf of Mexico slopes, as well as in the Caribbean Sea. The genus is represented by 21 species of which 14 are exclusively found in the West Atlantic and Caribbean (Froese & Pauly, 2019). The genus *Haemulon* is one of the most well-represented in coral reefs of the New World. Few studies have documented the helminth parasite fauna of haemulids. Paschoal et al. (2015) reported 147 species of helminths (plus 37 undetermined taxa) infecting 48 species of grunts in a checklist of the metazoan parasites of Haemulidae in the Americas; trematodes were the most diverse, with 83 species. Centeno & Bashirullah (2003) compared the helminth parasite communities of eight species of *Haemulon* in the Golfo de Cariaco, Venezuela. Later, Bashirullah & Díaz (2015) determined the infracommunity structure of the helminth parasite fauna of *H. aurolineatum* in the same locality. In Mexico, species of trematodes in grunts have been documented mostly as isolated reports (see Pérez-Ponce de León et al., 2007 and references therein); however, no studies have been conducted to evaluate the parasite community structure of haemulids.

The Puerto Morelos Reef National Park (PMRNP) is located in the Mexican state of Quintana Roo, and is part of the second largest barrier reef coral on the world (Carabias et al., 2000); the natural protected area is characterized by a large species diversity of fish and many invertebrate groups. Winfield et al. (2017) reported 19 species of tanaidaceans

(Crustacea); Hernández & Alvarez (2019) reported 120 species of mollusks; interestingly, the large diversity of crustaceans and mollusks show the availability of intermediate hosts for trematodes in the study area. The Puerto Morelos reef also holds a diverse fish fauna, with 254 species, 13 of which belong to the family Haemulidae (Domínguez-Domínguez et al. 2016). However, only four studies have documented the presence of marine fish trematodes in the area (Rufino-González, 1989; Caballero, 1990; Pérez-Ponce de León, 1992; and Pérez-Ponce de León & Hernández-Mena, 2019), accounting for 17 species of trematodes in 11 host species. This contrast with the trematode diversity that has been documented in other reef systems. For instance, Cribb et al. (2014) reported 240 species of trematodes described from marine fishes in the Great Barrier Reef, Australia. Considering the large fish species richness in the reef, it is clear that very few trematode species have been recorded in the study area. Moreover, no studies on the patterns and structuring processes of parasites operating at different scales in the PMRNP have been addressed. The aim of this paper was to report the trematode diversity in six species of grunts, and to describe their patterns of community structure, at the infracommunity and component community levels.

## Material and methods

A total of 213 specimens of grunts were collected using a fishing hawaiian sling in 21 sampling sites of the Puerto Morelos Reef National Park (Fig. 1), between January and May 2015. The total sample consisted of: *Haemulon aurolineatum* Cuvier (n=36), *H. chrysargyreum* Günther (n=10), *H. flavolineatum* (Desmarest) (n=80), *H. plumierii* (Lacepède) (n=30), *H. sciurus* (Shaw) (n=36) and *H. carbonarium* Poey (n=21). Collected fish were placed on ice, transported to the laboratory, and examined a few hours after capture. Each individual fish was necropsied and all internal organs were separated and placed in Petri dishes with saline 8.5%, and observed under the stereomicroscope. Trematodes were separated from the organs and fixed in hot (steaming) 70% EtOH (Lamothe, 1997). Trematodes were stained with Mayer's paracarmine and Gomori's thrichrome, cleared in methyl salicylate and mounted on permanent slides using Canada balsam (Lamothe, 1997). For the identification of trematodes, the Keys to the Trematoda (Gibson et al., 2002; Jones et al., 2005; Bray et al., 2008) were used, as well as specialized literature. All the trematode specimens were deposited in the Colección Nacional de Helminthos (CNHE) Biology Institute, UNAM, Mexico City (Table 1). Fishes were deposited in the Colección de Peces, Universidad Michoacana (CPUM) Morelia, Michoacan.



**Figure 1.** Map of the Puerto Morelos Reef National Park, Quintana Roo, México, showing the collecting sites for this study: 1. Fish Market, 2. La Luna, 3. La Pared, 4. Jardín Frontal, 5. Muelle Fiscal, 6. Ojo de Agua, 7. Barco Hundido, 8. Rordman, 9. Muelle UNAM, 10. Ojo Norte, 11. Punta Caracol, 12. Mar casa de playa, 13. Cuevones, 14. Cazones, 15. Bahía Petempich, 16. Herradura, 17. Bonanzas Sur, 18. Punta Norte, 19. Boya Zona Norte, 20. Límite punta Norte del Parque, 21. Limones.

Infection parameters describing the populations of trematodes in their fish hosts were calculated following Bush et al. (1997). Prevalence is the number of hosts infected with one or more individuals of a particular parasite species divided by the number of hosts examined for that parasite species. Mean Intensity is the total number of parasites of a particular species found in a sample divided by the number of hosts infected with that parasite. Mean

Abundance is the average abundance of a parasite species among all members of a particular host population; these parameters were calculated using the statistics software Quantitative Parasitology v. 1.0.14 with 95% of confidence limits (Reiczigel et al., 2019).

To determine if the sampling effort was sufficient to recover the majority of existent species in the trematode community of each *Haemulon* species in the study area, accumulation curves of species were carried out using Estimates v. 8.20 (Colwell, 2016), with the data of the accumulated trematode richness (X axis), and the sampled individuals (Y axis), randomized 100 times. A comparison was made between the accumulated wealth observed and the estimator Chao 2 to decide the accuracy of sampling effort; only hosts with a representative sampling effort greater than 50% representing the majority of the trematodes in the community were considered in further community analyzes.

Analyses were made at the infracommunity (all trematodes in each individual host, representing a subset of the parasite fauna of the host species) and component community (all trematodes in all hosts collected, i.e., the parasites found in a host population) (Holmes and Price, 1986, Poulin, 1997). Component community parameters included the total number of parasite species, total number of individual parasites, the Shannon–Wiener Index (H) as a measure of diversity (Krebs, 1999), and the Berger–Parker Index (BPI) as a measure of numerical dominance (Magurran, 1998).

Taking into account the difficulties that arise when trying to compare the different diversity indices, mainly because they significantly affect the units (Simpson index, Shannon-Wiener index), these are mathematical transformations to the indices, where each species weighted by its abundance, obtaining the Hill numbers where  $N_0$  the ‘total number

of species' in the sample; N1 is the 'number of the abundant species' and N2 is the 'number of the very abundant species' in the sample (Magurran, 1988). Additionally, to show the relative abundance of species and dominance in the communities, a curve range-abundance was performed.

The  $\beta$ -diversity of the infracommunities and component components were calculated with the Jaccard index to analyze qualitative similarity, and with the Bray Curtis index to analyze quantitative similarity (Magurran, 1998). All indices were calculated using PAST 2.01 (Hammer et al., 2001).

## Results

### *Trematode species composition in Haemulon spp.*

Eleven species of trematodes allocated in six families were identified as parasites of the six species of *Haemulon* in the Puerto Morelos Reef National Park, including three species of Opecoelidae (*Hamacreadium mutabile* Linton, 1910, *Helicometrina nimia* Linton, 1910, and *Pycnadenoides* sp.), two species of Apocreadiidae (*Homalometron* sp. 1 and *Homalometron* sp. 2), three species of Hemiuridae (*Monolecithotrema* sp. and two of Hemiuridae gen. sp.), one of Derogenidae (*Leurodera decora* Linton, 1910), one of Monorchhiidae (*Lasciotocus haemulid* Overstreet, 1969), and one of Lecithasteridae (*Macradena* sp.). Some species were not determined up to species level because of the low number of sampled specimens required for the taxonomic identification, or due to the poor quality of the fixed specimens. However, we are certain that two species of *Homalometron* were collected. They can be easily differentiated by the anterior distribution of the vitelline follicles, and the position of testes along the body. In *Homalometron* sp. 1, vitelline follicles reach anteriorly the ventral sucker, testes are postequatorial, and both testes and ovary are lobulated. The two hemiurids were not identified due to the low number of sampled specimens (three and one, respectively), although they can be differentiated as separate species. Hemiuridae gen. sp. 1 possesses a uterus occupying most of hindbody, from the caecal bifurcation to the posterior end of body and rounded and relatively small eggs (150 $\mu$  long); instead, in Hemiuridae gen. sp. 2 the uterus is postequatorial and eggs are ovoid and large (300 $\mu$  long).

The most frequent trematode species in grunts was *Leudorera decora* since it was found in four of the six fish species, followed by *Lasiotocus haemuli* and *Hamacreadium mutabile*, found in three species. Each host species harbored between one and eight trematode species. The French grunt (*H. flavolineatum*) reached the highest trematode species richness with eight species, followed by the White grunt (*H. plumierii*) and the Bluestriped grunt (*H. sciurus*) with four species each. The other three haemulids (*H. aurolineatum*, *H. carbonarium* and *H. chrysargyreum*) were infected by two or only one species of trematode (Table 1).

**Table 1.** Trematodes of six species of *Haemulon* from the Puerto Morelos Reef National Park, Quintana Roo, México.

<b>Taxa</b>	<b>HAURO</b>	<b>HCARB</b>	<b>HCHRY</b>	<b>HFLAV</b>	<b>HPLUMI</b>	<b>HSCIU</b>	<b>CNHE</b>
<b>Apocreadiidae</b>							
<i>Homalometron</i> sp.1				X			
<i>Homalometron</i> sp. 2				X		X	
<b>Derogenidae</b>							
<i>Leurodera decora</i>	X			X	X	X	1947,11221,11222, 11223, 11219, 11220
<b>Hemiuridae</b>							
Hemiuridae gen. sp. 1					X		

Hemiuridae gen. sp. 2			X			1951,1949
<i>Monolecithotrema</i> sp.	X					11218
<b>Lecithasteridae</b>						
<i>Macradena</i> sp.					X	
<b>Monorchiiidae</b>						
<i>Lasiotocus haemuli</i>		X	X	X		1972, 11225
<b>Opecoelidae</b>						
<i>Hamacreadium mutabile</i>			X	X	X	11224
<i>Pycnadenoides</i> sp.		X	X			11226
<i>Helicometrina nimia</i>			X			

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*HAURO*: *H. aurolineatum*; *HCARB*: *H. carborinarium*; *HCHRY*: *H. chrysargyreum*; *HFLAV*: *H. flavolineatum*; *HPLUMI*: *H. plumierii*;  
*HSCIU*: *H. sciurus*; CNHE: Colección Nacional de Helmintos (UNAM, Mexico City).

### *Characterization of infrapopulations*

In total, 101 trematode specimens were collected in 42 of the 213 analyzed fish, corresponding to six species of *Haemulon*. The values of prevalence for each trematode species did not yield either dominant species (prevalence >40%) nor common species (prevalence 20-40%); in consequence, all trematodes are considered rare species (prevalence <20%). The trematodes that reached the highest prevalence of infection were *Lasiotocus haemuli* in *H. plumierii* (15.6%), and *Leurodera decora* in two hosts, *H. sciurus* (15.2%), and *H. flavolineatum* (11.2%) (Table 2). All other trematodes reached prevalence values of less than 10% in all the fish species analyzed. The mean abundance was relatively low, with the highest value recorded for *L. decora* with 0.48 individuals per analyzed host (*H. sciurus*). Mean intensity values varied between 1 and 143 trematodes per infected host.

**Table 2.** Ecological parameters of the infection of trematodes in six *Haemulon* spp. of the Puerto Morelos Reef National Park, Quintana, Roo, México.

<b>Host species</b>	<b>Digenean species</b>	<b>NR</b>	<b>NI</b>	<b>TP</b>	<b>P (%)</b>	<b>AB</b>	<b>M.I</b>
<i>H. aurolineatum</i>	<i>Monolecithotrema</i> sp.	36	1	1	2.8	0.03	1.0
	<i>Leurodera decora</i>		1	2	2.8	0.06	2.0
<i>H. carbonarium</i>	<i>Pycnadenoides</i> sp.	19	2	3	10.5	0.16	1.5
<i>H. chrysargyreum</i>	<i>Lasiotocus haemuli</i>	10	1	1	10.0	0.10	1.0
<i>H. flavolineatum</i>	<i>Homalometron</i> sp. 1	80	5	6	6.2	0.06	-----
	<i>Homalometron</i> sp. 2		1	2	1.2	0.03	2.0
	<i>Leurodera decora</i>		9	14	<b>11.2</b>	0.18	1.5
	<i>Hamacreadium mutabile</i>		1	3	1.2	0.04	3.0
	Hemiuridae gen. sp. 2		2	3	2.5	0.04	1.5
	<i>Helicometrina nimia</i>		1	1	1.2	0.01	1.0
	<i>Lasiotocus haemuli</i>		1	14	1.2	0.18	14
<i>H. plumierii</i>	<i>Leurodera decora</i>	30	2	4	6.2	0.13	2.0

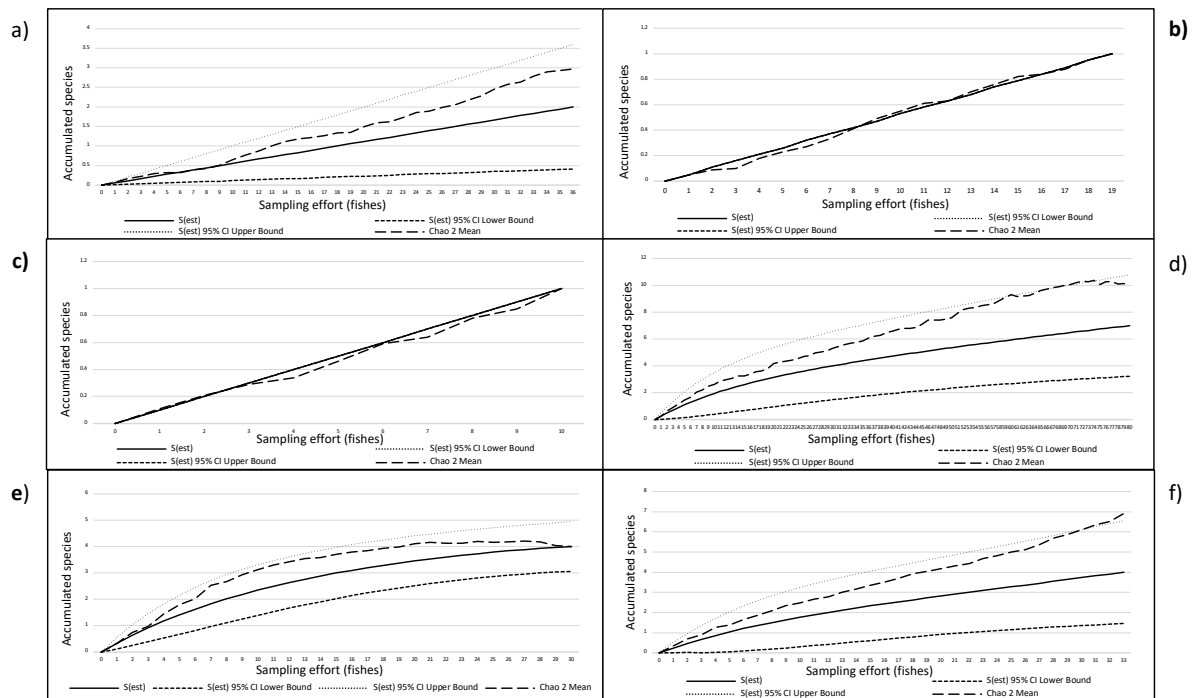
	<i>Lasiotocus haemuli</i>		5	15	<b>15.6</b>	0.47	3.0
	<i>Hamacreadium mutabile</i>		2	3	6.2	0.09	1.5
	Hemiuridae gen. sp. 1		1	1	3.1	0.03	1.0
<i>H. sciurus</i>	<i>Leurodera decora</i>	33	5	16	<b>15.2</b>	0.49	3.2
	<i>Hamacreadium mutabile</i>		1	9	3.0	0.27	9.0
	<i>Homalometron</i> sp. 2		1	2	3.0	0.06	2.0
	<i>Macradena</i> sp.		1	1	3.0	0.03	1.0

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NR= Number of revised individual fishes, NI= Number of infected individual fishes, TP= Total parasites per individual fishes, P (%)= Prevalence, AB= Abundance, M.I= Mean Intensity. In bold the highest values are presented.

## Species accumulation curves

Species accumulation curves showed that only three of the six host species, that is, *H. flavolineatum*, *H. plumierii* and *H. sciurus*, presented more than half of the expected trematode species. The values for the non-parametric species richness estimator (Chao2) for these three species showed that three missing species remain to be found, except for the curve of *H. plumierii* where Chao2 does not predict that more species will be found (Fig. 2). Based on the latter result, the analysis of the trematode community structure we present next only includes these three host species. Species accumulation curves showed that only three of the six host species, that is, *H. flavolineatum*, *H. plumierii* and *H. sciurus*, presented more than half of the expected trematode species.



**Figure 2.** Species accumulation curves in six *Haemulon* species of the Reef National Park of Puerto Morelos Quintana Roo. a) *H. aurolineatum*, b) *H. carbonarium*, c) *H. chrysargyreum*, d) *H. flavolineatum*, e) *H. plumierii* and f) *H. sciurus*.

### *Infracommunity*

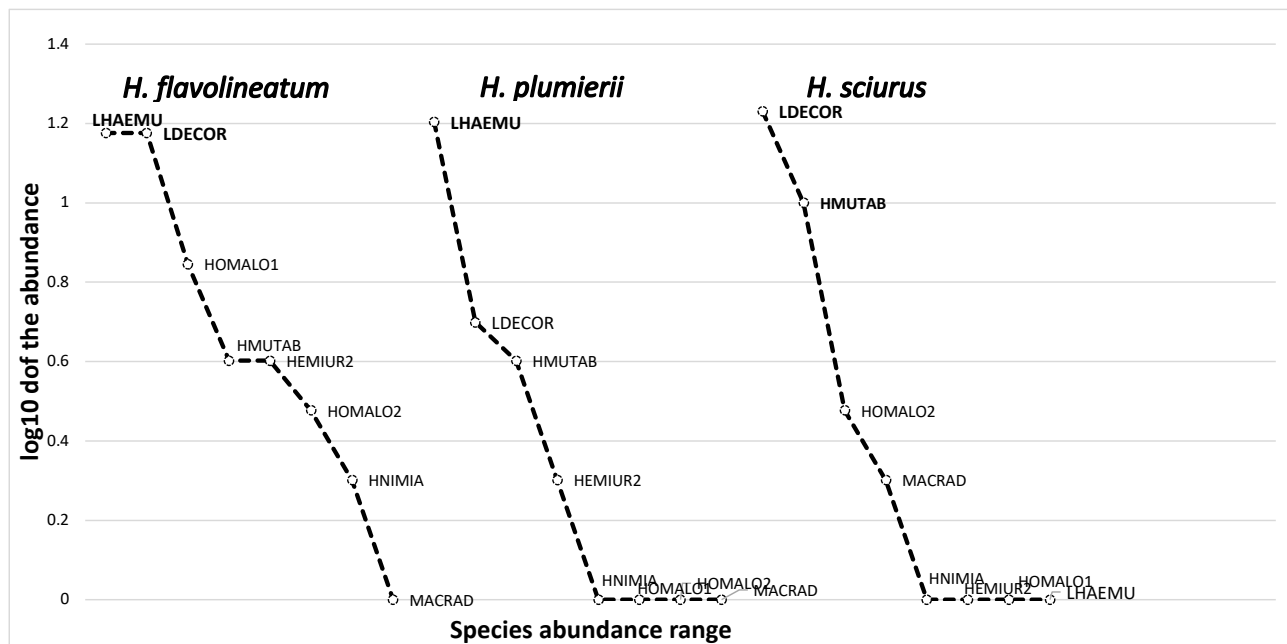
At the infracommunity level, *H. flavolineatum* reached the highest mean species richness, although *H. sciurus* exhibited the highest mean abundance with 4.67 trematodes per infected host. The Shannon-Wiener diversity index was very low and indicated that *H. flavolineatum* had the highest trematode diversity ( $0.21 \pm 0.38$ ), although the evenness was very similar among infracommunities. Using Hill's numbers, it was possible to determine the representative number of species for the diversity indices, which showed a richness represented by a species ( $N_0 = 1.33-1.42$ ), diversity by a species ( $N_1 = 1.11-1.42$ ) as well as its dominance ( $N_2 = 1.10-1.15$ ) (Table 3).

**Table 3.** Trematode infracommunities of three species of *Haemulon* in the Puerto Morelos Reef National Park, Quintana Roo, México. Values are presented as the mean  $\pm$  standard deviation.

Infracommunity										
Host	No. Host	% Infect.	MSR	MA	H'	N0	N1	N2	d	Dominant species
<i>H. flavolineatum</i>	80	17.5	1.42 $\pm$	3 $\pm$	0.21 $\pm$	1.42	1.23	1.15	0.90 $\pm$	<i>Lasiotocus</i>
			0.76	3.68	0.38				0.20	<i>haemuli</i> and <i>Leurodera decora</i>
<i>H. plumierii</i>	30	26.66	1.25 $\pm$	2.88 $\pm$	0.14 $\pm$	1.25	1.14	1.10	0.93 $\pm$	<i>Lasiotocus</i>
			0.47	2.1	0.26				0.12	<i>haemuli</i>
<i>H. sciurus</i>	33	18.18	1.33 $\pm$	4.67 $\pm$	0.16 $\pm$	1.33	1.11	1.12	0.93 $\pm$	<i>Leurodera</i>
			0.51	3.07	0.27				0.13	<i>decora</i>

No. Host= Total number of studied hosts, % Infect= Percentage of infected, MSR= Mean trematode species Richness, MA= Mean Abundance of trematodes, H'=Shannon-Wiener diversity Index, Numbers of Hill: N0= Total number of species, N1= Number of abundant species and N2=Number of most abundant species,  $d$ = Berger-Parker dominance Index.

Overall, infracommunities were highly dominated by one species, with the exception of *H. flavolineatum* which presented two dominant species, all with a Berger Parker index higher than 0.9; in the abundance range curve, *L. haemuli* and *L. decora* stand out in *H. flavolineatum*, while *L. haemuli* was the dominant species in *H. plumierii*, and *L. decora* in *H. sciurus* (Fig. 3).



**Figure 3.** Range-Abundance curves showing the trematode infracommunity. HMUTAB: *Hamacreadium mutabile*, HNIMIA: *Helicometrina nimia*, HEMIUR2: Hemiuridae sp2, HOMALO1: *Homalometron* sp1., HOMALO2: *Homalometron* sp2. LHAEMU: *Lasiotocus*

*haemuli*, LDECOR: *Leurodera decora*, MACRAD: *Macradena perfecta*. In bold type the most abundant species in the three *Haemulon* species stand out.

The results of the similarity indices determined a low beta diversity among species of *Haemulon* herein studied; these diversity values implied a low overlap of parasite species among individuals. The infracommunities of *H. flavolineatum* shared several trematode species, but the values of qualitative (0.31) and quantitative similarity were very low (0.25). Within *H. plumierii*, infracommunity similarity is even lower, and in *H. sciurus* exchange occurs in all individuals, but in low quantities (Table 4).

**Table 4.** Beta diversity in *Haemulon* infracommunity with Jaccard and Bray Curtis coefficients. Values are presented as the mean and range.

	N	Jaccard coefficient (qualitative)	Bray Curtis coefficient (quantitative)
<i>H. flavolineatum</i>	13	0.31 (0.25-0.67)	0.25 (0.11-0.67)
<i>H. plumierii</i>	8	0.43 (0.5)	0.26 (0.22-0.83)
<i>H. sciurus</i>	5	0.70 (0.33-0.5)	0.48 (0.13-0.91)

N = number of pairs of individuals compared.

#### *Component community*

At the component community level, *H. flavolineatum* was the species that reached the highest values for the descriptors of the community structure. This haemulid had the highest abundance with 43 individual trematodes, the highest diversity index (1.66), the highest species richness, with 7 species; the Shannon-Wiener diversity Index of the trematode component community in *H. flavolineatum* was 1.66 which was the highest value compared to the other component communities. The Berger Parker index did not show a marked

dominance for the hosts (Table 5). Similarity indices showed that *Haemulon* species show low beta diversity, both in composition (Jaccard index) and in structure (Bray-Curtis). The highest similarity was found between *H. flavolineatum* and *H. plumierii*, with values of 0.57 and 0.67, respectively. Instead, the lowest similarity was found between *H. plumierii* and *H. sciurus*, with 0.33 and 0.27, respectively.

**Table 5.** Trematode in component community of three species of *Haemulon* in the Puerto Morelos Reef National Park, Quintana Roo. Mexico.

	<b>Component community</b>					
	<b>A</b>	<b>H'</b>	<b>N0</b>	<b>N1</b>	<b>N2</b>	<b>d</b>
<i>H. flavolineatum</i>	43	1.66	7	4.99	4.1	0.32
<i>H. plumierii</i>	23	0.99	4	2.68	2.1	0.65
<i>H. sciurus</i>	28	1	4	2.69	2.29	0.57

A= Abundance of trematodes, H' = Shannon-Wiener diversity Index, Numbers of Hill: N0= Total number of species, N1= Number of abundant species and N2=Number of most abundant species, d= Berger-Parker dominance Index

## Discussion

In this study, 11 trematode species were identified as parasites of six species of *Haemulon* in the PMRNP area. Previous studies indicate that the trematode fauna of these species of *Haemulon*, distributed along the Western Atlantic coast, may harbor up to 173 taxa, 150 of them taxonomically determined to species level (see Paschoal et al., 2015 and references therein). Our results contrast with the records of the trematode fauna of these haemulids because they possess a higher trematode species richness, i.e., the number of species of trematodes reported for *H. aurolineatum* across its distributional range is 25, that of *H. carbonarium* is 17, 12 in *H. chrysargyreum*, 29 in *H. flavolineatum*, 36 in *H. plumierii*, and 54 in *H. sciurus* (Paschoal et al., 2015). Instead, in the PMRNP, these same species are only infected by 2, 1, 1, 8, 4 and 4 trematode species, respectively. The most striking contrast was found for the trematode fauna of *H. sciurus* that include 54 species, while in our study, only four species were reported in the same host species. Interestingly, only one of the trematode species (*L. decora*) had been previously reported in *H. sciurus* in Florida (Linton, 1910). The other three represent new host records (*Hamacreadium mutabile*, *Macradena* sp., and an unidentified and probably new species of *Homalometron*).

Overall, 16 new host records are reported in this study. Eight of the 11 trematode species are reported in the PMRNP for the first time. Only the opecoeliids *Helicometrina nimia*, and *Hamacreadium mutabile*, and the derogenid *Leurodera decora* were previously reported in the area, although in different host groups the first two species (see Caballero, 1990; Pérez-Ponce de León, 1992); *L. decora* was found in *H. sciurus* (Rufino-Gonzalez, 1989). The species *Pycnadenoides* sp., *Monolecithotrema* sp. and *Macradena* sp., as well as the two species of *Homalometron* represent new taxa for the family Haemulidae (see

Paschoal et al. 2015). Furthermore, the two unidentified species of *Homalometron* reported in our study are new host records. According with Paschoal et al. (2015), three species of *Homalometron* have been reported in haemulids along the Western Atlantic coast, namely *H. cryptum* (Overstreet, 1969), *H. dowgialloi* Dyer, William and Bunckley-Williams, 1992, and *H. foliatum* Siddiqi and Cable, 1960 (Siddiqi and Cable, 1960; Overstreet, 1969; Dyer et al., 1992). However, our specimens (which represent to two separate species) are morphologically very different to the species previously reported, and they can represent new species. Unfortunately, the specimens collected are in poor condition to accomplish the proper species description.

Parasite infrapopulation parameters exhibited variable values; only two parasite species reached a prevalence of 15% (*Lasiotocus haemuli* in *H. plumierii* and *Leurodera decora* in *H. sciurus*); Bashirullah & Díaz (2015) recorded prevalence values higher than 30% in *H. aurolineatum* studied off the coast of Venezuela; in our study, in the same host species the highest prevalence value reached only 2.8%. This difference can be attributed to the environmental and biological conditions of the sampling site, even if it is the same host species (Scoot, 1982; Holmes, 1990; Violante-González et al. 2010); the variation between habitats affects the composition of parasite species; therefore, the variation in spatial distribution of different taxa of local benthic invertebrates can be expected to reflect the distribution of parasites that use them as intermediate hosts (Marcogliese, 2002).

At the component community and infracommunity levels, trematodes of *Haemulon* spp. exhibited a similar pattern, with low species richness and abundance, as well as low diversity values, and having communities dominated by a single species of trematode. This overall pattern has been found in other studies, where the feeding habits and the differential

availability of the intermediate hosts harboring metacercarial stages of the parasites have been discussed as the main factors structuring parasite communities. (e.g., Violante-González et al. 2008a). The low diversity of the trematode communities analyzed in this study at both levels indicate that *Haemulon* species are not top predators in the food web in the study area; high values of parasite diversity indicate that their hosts occupy such position in the food web (Poulin, 2007; Bush et al., 2001). The low species richness values of the trematode grunt infracommunity at the PMRNP in comparison to the parameter at the component community shows that each infracommunity simply represents a subset of the species present in the component community; instead, the component community reflects a subset of a larger collection of species that represent the entire trematode fauna of these host species along its distributional range (Poulin, 1997).

Moreover, patterns of similarity were very similar at both scale levels of our study; this indicates a low beta diversity which can be the result of high dispersion rates (vagility), which acts to homogenize communities (Moos et al. 2020). At the infracommunity level, a low exchange of trematode species was shown, indicating that not all the species occur in all individual hosts; meanwhile, the  $\beta$ -diversity of the component community, despite being low, presented some species that are shared among host species e.g., *L. decora* and *H. mutabile*, as well as other species that exhibited some level of host specificity for some of species of *Haemulon*; that is the case for *Homalometron* sp. 1, Hemiuridae gen. sp. 1, Hemiuridae sp. 2, and *Macradena* sp., indicating a particular parasite structure for each *Haemulon* species.

The food preference of each host species explains the parasitic structure of each *Haemulon* species, for example, *H. flavolineatum* mainly feeds on amphipods and

scaphopods, *H. plumierii* on brachyura and caprellidae, while *H. sciurus* on ascidians; in addition, the three hosts share other food items represented by taxonomic groups such as Anthozoa, Decapoda, Foraminifera, Gastropoda, Asteroidea, Holoturioidea and Ophiuroidea (Cipresso-Pereira et al. 2015, Froese & Pauly, 2019). The hosts diet is known to be among one of the most influential factors structuring the parasite fauna (Prasanna et al., 2011; Carvallho et al. 2015); changes in prey availability and host-parasite compatibility have been also described as important factors (Ojaveer et al. 2020). Further, Esch et al. (1990) and Violante-González et al. (2008b) argued that infracommunities are separated by guild, through feeding and microhabitat mechanisms of the host; the variation in diet and the amount of food items eaten by hosts is related to the dynamics of the parasite population, and their community structure; differences in the assemblages of parasites among marine fish species are usually explained by these ecological characteristics of the host (Timi & Lanfranchi, 2009).

In conclusion, the trematode communities of the species of *Haemulon* analyzed in this study at both, infracommunity and component community levels, were characterized by presenting low diversity indices, placing them as predators at a low trophic level. Furthermore, trematode communities differed among species of grunts, indicating that ecological factors such as feeding habits, geographic distribution, and vagility of the hosts play a major role structuring these communities. In general, our results are consistent with several studies that indicate that ecological selection can strongly structure parasite communities (Moos et al. 2020). Clearly, more studies are required to fully understand the parasite community structure of marine fishes in the PMRNP, considering the inclusion of other fish species since the species richness is very high in the area (Domínguez-Domínguez et al., 2016), as well as

the entire helminth parasite community. This information will contribute to generate the necessary information to address aspects of conservation in an important area of the Mexican Caribbean Sea.

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