



Distribution patterns of two species of *Corynosoma* (Acanthocephala: Polymorphidae) in fishes from Southwestern Atlantic

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Abstract

Corynosoma australe and *C. cetaceum* are the most frequently reported acanthocephalans in fish from the Argentine Sea, particularly in central and northern areas. Their definitive hosts are otariids and odontocete cetaceans, respectively. The low specificity of these larvae, in combination with high infective capability and long survival periods in fish, make them potentially good biological markers for stocks and other biological features of their fish hosts. In order to determine the distribution patterns of these species and their determining factors, a large dataset composed by newly collected fish samples, published and unpublished data from previous studies by the authors in the region were analysed in relation to host and environmental variables. The complete dataset comprised a total of 5084 fish, belonging to 29 species distributed in 21 families and 9 orders. Host size and trophic habits arose as the main determinants of abundance for both species of *Corynosoma*, showing higher abundances on larger fish and on higher trophic levels, as it is usual for trophically transmitted parasites. Biogeographic province and depth (indirectly representing the temperature of water) were the main drivers of the spatial distribution, displaying a latitudinal pattern associated to the temperature clines created by the interaction of Malvinas and Brazil currents, determining a decrease in abundance southwards and towards the deeper areas. No patterns were found regarding the distribution of definitive hosts. The knowledge of these distribution patterns of *Corynosoma* spp. in fish at regional scale, as well as of their causes, provides useful information to design management and conservation policies thus contributing to maintain the full and sustainable productivity of fisheries.

Keywords *Corynosoma australe* · *Corynosoma cetaceum* · Distribution · Fishes · Biological tags

Introduction

Polymorphid acanthocephalans of the genus *Corynosoma* Lühe, 1909 are common components of marine ecosystems, where they reproduce in fish-eating mammals and birds, using

amphipods and fishes as intermediate and paratenic hosts, respectively (Aznar et al. 2006). In fishes from central and northern areas of the Argentine Sea, two species, *Corynosoma australe* Johnston, 1937 and *C. cetaceum* Johnston and Best, 1942, are frequently reported (Cantatore and Timi 2015). In this region, the definitive hosts of *C. australe* are the otariids *Arctocephalus australis* Zimmermann, 1783 and *Otaria flavescens* Shaw, 1800 (George-Nascimento and Marín 1992; Sardella et al. 2005; Aznar et al. 2004, 2012), whereas the main definitive hosts of *C. cetaceum* are odontocete cetaceans *Pontoporia blainvillei* (Gervais and D'Orbigny, 1844), *Delphinus delphis* Linnaeus, 1758, *Tursiops truncatus* (Montagu, 1821) and *Phocoena spinipinnis* (Burmeister, 1865) (Hernández-Orts et al. 2015). These two larval acanthocephalans have low host specificity, being widely distributed across fish species in the southern Southwest Atlantic (Sardella et al. 2005; Santos et al. 2008; Hernández-Orts et al. 2015).

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In the Argentine Sea, juvenile *Corynosoma* have been identified among the best biological tags in diverse studies on fish stock discrimination (Cantatore and Timi 2015; Alarcos et al. 2016; Canel et al. 2019). A precise assessment of resources abundance in space and time is a prerequisite for the implementation of management and control measures, to restore stocks and to maintain the full and sustainable productivity of fisheries (Begg and Waldman 1999). *Corynosoma australe* and *C. cetaceum* share a combination of desirable characteristics as biological tags that make them excellent candidates for further studies to distinguish fish stocks in the region. First, they appear as larval stages of long permanence in fishes (Lester and MacKenzie 2009). Second, they have low specificity, which makes them potential markers for any fishery resource and, third, they show recurrent distribution patterns in different fish species in the Argentine Sea, such as a decrease in parasite burdens with increasing latitude (Cantatore and Timi 2015). Both acanthocephalans have also contributed to the identification of zoogeographical regions in the Southwest Atlantic in multivariate analyses of fish parasite assemblages (Lanfranchi et al. 2016; Braicovich et al. 2017; Soares et al. 2018). Such distribution patterns are congruent with the environmental conditions of the study region, mostly related with the temperature cline characteristic of the region (decreasing southwards) (Hoffmann et al. 1997; Piola et al. 2010), although water temperature also decreases with depth at lower latitudes (Acha et al. 2004; Piola et al. 2010). However, a combination of several interacting variables, environmental and those related to the biology of the hosts, could affect the distribution of *Corynosoma* spp., as been recorded for other parasites in the region (Irigoitia et al. 2018). The identification of these variables, and the resulting distribution patterns of *Corynosoma* spp., will help improving the knowledge of host population structure for many valuable resources under exploitation, and will provide predictive power to their use as biological tags.

In this work, we analyse a large database composed by newly collected *Corynosoma* spp. from several fish species at different spatial scales, complemented by unpublished data from studies carried out previously and those published by the authors in the region. Therefore, the aim of this work is to determine the spatial distribution patterns of *Corynosoma* spp. across fish species in the Argentine Sea and their main drivers.

Materials and methods

General procedures

A total of 1675 fish belonging to 12 species, 10 families and 6 orders were examined for juvenile acanthocephalans (Table 1). This included 32 samples, of at least 20 specimens

each, from different localities of the Argentine Sea, ranging from the Argentine-Uruguayan Common Fishing zone to central Patagonian waters (35.00–49.25° S), caught between 1990 and 2018. Fishes were either kept fresh or deep frozen in plastic bags at $-18\text{ }^{\circ}\text{C}$ until examination. After thawing, each fish was measured for total length (TL), dissected and examined for parasites. Body cavity, musculature and viscera (stomach, intestine, liver, swim bladder, spleen, heart, gonads and mesenteries) were examined with the aid of a stereoscopic microscope. Juvenile acanthocephalans were recorded and identified.

Quantitative analyses

Prevalence and mean abundance for each parasite species in each sample were calculated following Bush et al. (1997). Data on prevalence and mean abundance of juvenile acanthocephalans in fishes from the region were obtained from the literature. These were restricted to those articles published by members of the research team to ensure taxonomic consistency (Table 2). This way, by adding 63 additional samples to the unpublished data, the analysed dataset was extended to 5084 fishes belonging to 29 species, 21 families and 9 orders (Electronic supplementary table). The presence of other long-lived larval parasites (anisakids and cestodes) in the samples was also recorded in order to comparatively analyse the host range of the most common parasites in the region.

Statistical analyses

The effect of six variables on the abundance of *C. australe* and *C. cetaceum* in the Southwest Atlantic was evaluated using Generalised Linear Mixed Models (GLMMs) using a Compound Poisson distribution with log link function. The selected variables were host total length (L), biogeographic province of origin (BP)—a factor with three levels: Argentine province, Ecotonal zone and Magellanic province, trophic level (TL), diet (D)—a factor with four levels: fish, fish and invertebrates, invertebrates and plankton—depth (DE) and habitat (H)—a factor with three levels: pelagic, demersal and benthic. These variables were treated as fixed effects while host species (HS) was incorporated as a random effect. Treating host species as random effect introduces a correlation structure between all observations from the same host species. Initial data exploration showed no correlation between the explanatory variables, which corresponds to the independent variables assumption (Zuur et al. 2009). For these analyses, migratory fish species alternating between different regions or masses of water were excluded to avoid misinterpretation of results by assigning to a given locality, parasite loads acquired in other region, with different environmental and ecological conditions. Species identified as migratory were *Engraulis anchoita* Hubbs and Marini, 1935, that

Table 1 Composition of samples of fish hosts in the Argentine Sea, along with data on parasite loads

Host species	NHE	L (cm)	BP	DE (m)	H	D	TL	<i>Corynosoma australe</i>		<i>Corynosoma cetaceum</i>	
								P	MA ± SD	P	MA ± SD
<i>Anchoa maringii</i> 1	136	9.8	A	10	Pel	P	3.4	0.0	0.0	0.0	0.0
<i>Anchoa maringii</i> 2	23	9.5	A	20	Pel	P	3.4	0.0	0.0	0.0	0.0
<i>Bassanago albescens</i>	27	65.3	A	200	Ben	I	3.9	22.2	0.3 ± 0.9	11.1	0.1 ± 0.3
<i>Odontesthes argentinensis</i>	26	29.1	A	10	Pel	P	3.7	80.8	7.0 ± 6.7	0.0	0.0
<i>Odontesthes incisa</i>	66	8.9	A	50	Pel	P	3.4	3.0	0.1 ± 0.6	0.0	0.0
<i>Patagonotothem ramsayi</i>	48	25.6	E	60	Dem	I	3.5	35.4	0.8 ± 1.5	0.0	0.0
<i>Percophis brasiliensis</i> 1	23	54.7	M	50	Dem	F	4.2	73.9	3.6 ± 4.5	0.0	0.0
<i>Percophis brasiliensis</i> 2	47	37.3	A	40	Dem	F	4.2	89.4	8.8 ± 12.7	59.6	1.9 ± 3.6
<i>Pomatomus saltatrix</i>	41	42.4	A	25	Pel	F	4.5	85.4	17.3 ± 39.2	12.2	0.2 ± 0.5
<i>Cynoscion guatucupa</i> 1	57	7.0	A	20	Dem	P	3.3	3.5	0.04 ± 0.2	0.0	0.0
<i>Cynoscion guatucupa</i> 2	61	45.5	A	20	Dem	FI	4.2	83.6	33.7 ± 98.2	52.5	3.03 ± 8.8
<i>Cynoscion guatucupa</i> 3	121	8.4	A	20	Dem	P	3.3	2.5	0.03 ± 0.2	0.0	0.0
<i>Cynoscion guatucupa</i> 4	25	44.3	A	115	Dem	FI	4.2	100	15.0 ± 13.3	24	0.48 ± 1.1
<i>Cynoscion guatucupa</i> 5	154	22.7	A	115	Dem	I	3.5	25.9	0.6 ± 1.3	5.2	0.05 ± 0.2
<i>Cynoscion guatucupa</i> 6	54	20.9	A	110	Dem	I	3.5	9.3	0.1 ± 0.3	0.0	0.0
<i>Cynoscion guatucupa</i> 7	37	46.8	A	20	Dem	FI	4.2	100	22.0 ± 20.4	37.8	0.62 ± 1.1
<i>Cynoscion guatucupa</i> 8	34	9.2	A	20	Dem	P	3.3	0.0	0.0	0.0	0.0
<i>Cynoscion guatucupa</i> 9	59	14.8	A	20	Dem	I	3.5	52.5	1.6 ± 2.4	10.2	0.1 ± 0.3
<i>Cynoscion guatucupa</i> 10	60	11.5	A	20	Dem	I	3.3	5.0	0.05 ± 0.2	1.7	0.02 ± 0.1
<i>Cynoscion guatucupa</i> 11	77	18.4	A	20	Dem	I	3.5	27.3	0.7 ± 1.5	12.9	0.2 ± 0.6
<i>Cynoscion guatucupa</i> 12	36	49.0	A	20	Dem	FI	4.2	100	86.1 ± 82.0	69.4	5.6 ± 8.8
<i>Cynoscion guatucupa</i> 13	55	35.2	A	20	Dem	FI	3.7	78.2	5.9 ± 16.6	0.0	0.0
<i>Cynoscion guatucupa</i> 14	70	21.4	A	20	Dem	I	3.5	35.7	0.8 ± 1.45	12.9	0.2 ± 0.5
<i>Cynoscion guatucupa</i> 15	20	34.8	A	20	Dem	FI	4.2	85	4.45	50	0.65
<i>Pagrus pagrus</i>	26	27.9	A	75	Dem	FI	3.9	84.6	29.8 ± 36.5	3.9	0.04 ± 0.2
<i>Congiopodus peruvianus</i> 1	30	21.8	M	157	Dem	I	3.3	0.0	0.0	0.0	0.0
<i>Congiopodus peruvianus</i> 2	26	24.9	M	114	Dem	I	3.3	0.0	0.0	0.0	0.0
<i>Helicolenus lahillei</i> 1	44	19.0	E	64	Ben	I	4.2	43.2	0.8 ± 1.2	0.0	0.0
<i>Helicolenus lahillei</i> 2	79	17.5	E	89	Ben	I	4.2	41.8	0.7 ± 1.1	0.0	0.0
<i>Merluccius hubbsi</i> 1	50	41.8	M	80	Dem	F	4.2	42.6	0.7 ± 1.3	0.0	0.0
<i>Merluccius hubbsi</i> 2	31	44.7	M	80	Dem	F	4.2	16.1	0.2 ± 0.4	0.0	0.0
<i>Merluccius hubbsi</i> 3	32	40.5	M	80	Dem	F	4.2	12.2	0.2 ± 0.5	0.0	0.0

NHE, number of hosts examined; L, total length; BP, biogeographic province (argentine (A), ecotonal (E), Magellanic (M)); DE, depth; H, habitat (pelagic (Pel), demersal (Dem), benthic (Ben)); D, diet (fish (F), fish and invertebrates (FI), invertebrates (I), plankton (P)); TL, trophic level; P prevalence; MA ± SD, mean abundance ± standard deviation

alternates between coastal and slope (subantarctic) waters (Angelescu 1982); *Trachurus lathami* Nichols, 1920, *Umbrina canosai*, Berg, 1895 and *Pomatomus saltatrix* Linnaeus, 1766 which migrate from southern Brazil during warmer seasons (Saccardo and Katsuragawa 1995; Haimovici and Krug 1996; Haimovici et al. 2006) and *Odontesthes smitti* that moves from north Patagonian gulfs to the north of the Argentine Sea during winter (Carballo et al. 2012).

Trophic level was obtained from Froese and Pauly (2018) for each host species. Data on biogeographic province (as

latitude and longitude) and depth were recorded for those specimens caught during research cruises; in the case of commercial catches, the depth was estimated from the region of capture in a bathymetric map. For those samples composed by fish caught in more than one trawl at sites close to each other, averaged depth values were used. Data on host habitat and diet were obtained from Cousseau and Perrotta (2004).

For each parasite species—*C. australe* and *C. cetaceum*—a global model, containing all explanatory variables to be evaluated, and a set of alternative candidate models, considered a priori biologically meaningful, was selected among all

Table 2 Composition of samples of fish hosts in the Argentine Sea, along with data on parasite loads from previously published studies in the Southwestern Atlantic

Host species	NHE	Number	L (cm)	BP	DE (m)	H	D	TL	Source	<i>Corynosoma australe</i>		<i>Corynosoma cetaceum</i>	
										P	MA	P	MA
<i>Engraulis anchoita</i>	671	4	14.8–16.3	A-E	30–80	Pel	P	2.5	Timi (2003)	0.0–18.2	0.0–0.05	0.0	0.0
<i>Conger orbignianus</i>	50	1	80.7	A	70	Ben	F	3.7	Timi and Lanfranchi (2013)	86.0	95.4	44.0	1.1
<i>Odontesthes smitti</i>	177	5	21.7–28.3	E-A	10–30	Pel	P	3.6	Carballo et al. (2012)	3.0–54.0	0.03–1.1	0.0	0.0
<i>Merluccius hubbsi</i>	344	4	38.7–40.5	A-E-M	90–170	Dem	F	4.2	Sardella and Timi (2004)	0.0–27.3	0.0–1.4	0.0	0.0
<i>Urophycis brasiliensis</i>	62	1	36.6	A	30	Dem	I	3.9	Pereira et al. (2014)	83.9	6.6	43.6	1.6
<i>Raneya brasiliensis</i>	183	4	23.0–24.7	A-E	20–80	Dem	I	3.6	Vales et al. (2011)	86.7–100	5.1–73.5	0.0–3.9	0.0–0.04
<i>Trachurus lathami</i>	223	2	19.5–20.0	A	30–40	Pel	P	4	Braicovich et al. (2012)	88.5–91.0	8.4–8.9	9.0–9.7	0.3–0.1
<i>Nemadactylus bergi</i>	100	5	32.4–36.2	A	30	Dem	I	3.2	Rossin and Timi (2010)	93.8–100	12.0–25.5	2.9–18.8	0.03–0.2
<i>Mullus argentinae</i>	75	1	19.5	A	30	Ben	I	3.5	Lanfranchi et al. (2009)	38.7	0.67	4.00	0.05
<i>Percophis brasiliensis</i>	412	9	49.4–56.6	A-E-M	20–50	Dem	F	4.2	Braicovich and Timi (2008), Braicovich and Timi (2010) and Braicovich et al. (2017)	75.0–100	5.5–174.7	25.0–78.0	1.4–5.9
<i>Pinguipes brasilianus</i>	310	7	32.5–37.1	A-E	20–100	Dem	I	3.5	Timi et al. (2009)	50.0–100	1.6–34.1	0.0–6.7	0.0–0.1
<i>Pseudoperca semifasciata</i>	100	3	67.2–71.2	A-E	20–30	Dem	FI	3.9	Timi and Lanfranchi (2009a)	90.0–100	5.5–79.9	2.0–85.0	1.0–13.3
<i>Dules auriga</i>	178	6	10.7–13.3	A	20–60	Ben	I	3.7	Braicovich and Timi (2015)	60.0–98.1	1.8–8.3	0.0–6.7	0.0–0.1
<i>Pagrus pagrus</i>	38	1	39.1	A	80	Dem	FI	3.9	Soares et al. (2018)	100	200.1	0.0	0.0
<i>Paralichthys isosceles</i>	51	1	27.9	A	60	Ben	I	4	Alarcos and Timi (2012)	92.2	14.7	0.0	0.0
<i>Paralichthys patagonicus</i>	51	1	35.2	A	60	Ben	I	3.9	Alarcos and Timi (2012)	94.1	6.4	74.51	2.6
<i>Xystreureys rasile</i>	133	3	29.2–32.1	A	10–50	Ben	I	3.3	Alarcos and Timi (2013)	53.0–90.0	1.7–9.3	2.0–15.0	0.04–0.4
<i>Prionotus nudigula</i>	101	1	19.7	A	20	Dem	I	4.2	Timi and Lanfranchi (2009b)	85.1	9.2	10.9	0.1
<i>Zenopsis conchifer</i>	44	1	27.4	E	100	Ben	F	4.5	Lanfranchi et al. (2016)	20.4	1.5	2.3	0.02
<i>Umbrina canosai</i>	106	3	28.9–37.2	A	20–60	Dem	I	3.9	Canel et al. (2019)	100	70.9–368	22.2–35.9	0.4–1.7

NHE, number of hosts examined; N, number of samples; L, total length; BP, biogeographic province (argentine (Arg), ecotonal (Eco), Magellanic (Mag)); DE, depth; H, habitat (pelagic (Pel), demersal (Dem), benthic (Ben)); D, diet (fish (F), fish and invertebrates (FI), plankton (P)); TL, trophic level; P, prevalence; MA, mean abundance

possible models. In both cases, the response variable was the mean abundance of parasites. The fit of each global model (one for *C. australe* and one for *C. cetaceum*) was assessed graphically through quantile-quantile plots and residuals versus fitted values plots.

The information theoretic (IT) model comparison method was used, in order to select the best model of each set which allows evaluating simultaneously several competing models (Burnham and Anderson 2002). To identify the best model, it is necessary to trade off model bias against model precision; this was achieved by using Akaike Information Criterion adjusted for small samples (AIC_c) (Symonds and Moussalli 2011). The models were ranked by AIC_c , and the model with the lowest AIC_c was considered the best from each set. Then, the Δ_i were computed as the difference between the best model and each of the candidate models and the Akaike's weight (w_i) was calculated to obtain the relative likelihood, of each fitted model, of being the best among the set of candidates (Johnson and Omland 2004).

In case the best model showed a high degree of uncertainty ($w_i < 0.9$), model averaging was performed on the subset of models whose accumulated weights summed 0.9. This was made in order to estimate the magnitude of the effect of each predictor in explaining the variation of the response. The parameter estimates (β), standard errors (SE) and confidence intervals (CI) were recalculated after averaging and new Akaike's weights (w'_i) were recomputed (Burnham and Anderson 2002; Symonds and Moussalli 2011).

The relative importance of each variable was estimated adding the recomputed Akaike weights of all the models where the variable of interest occurs (Burnham and Anderson 2002).

All the statistical analyses were performed with the statistical software R, version 3.5.1 (R Development Core Team; www.r-project.org/) using the package CPLM version 0.7-7 (Zhang 2013).

Results

General results

Juvenile of both species of *Corynosoma* were found free or encapsulated in the body cavity on most fish species, being *C. australe* occasionally found in stomach and intestine serosa of some host species. No parasites were found in musculature.

C. australe showed the highest host range among long-lived parasites of fishes in the study region (Fig. 1) parasitising 28 of the 29 fish species considered, excepting *Anchoa marini* Hildebrand 1943. This species was also found in *Congiopodus peruvianus* (Cuvier, 1829) at very low abundance (a single worm in a single host) at two localities (41° 34' S–58° 32' W and 47° 13' S–63° 15' W) which were not

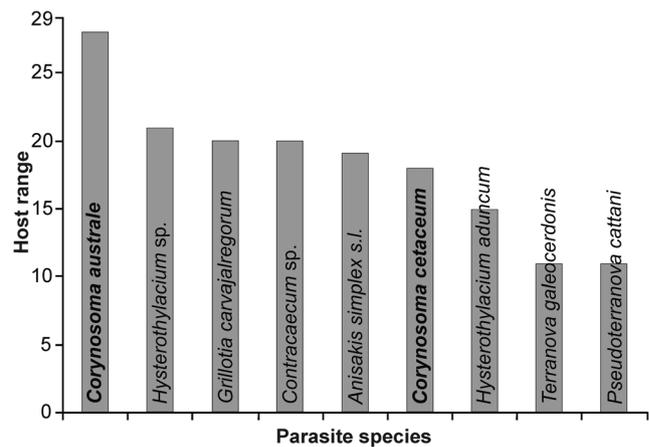


Fig. 1 Host range (number of host species) of long-lived and low specific larval parasites of fish (restricted to those with host range > 10 among the 29 considered fish species) in the Southwestern Atlantic

included in the analyses due to the small sample size. On the other hand, the distribution of *C. cetaceum* was more restricted, being present in 18 of the considered host species (Fig. 1).

The prevalence of both species was variable across samples (Table 1); *C. australe* was absent only in samples of small coastal fishes (*A. marini* and some juvenile of *Cynoscion guatucupa* (Cuvier, 1830)) and southern samples of

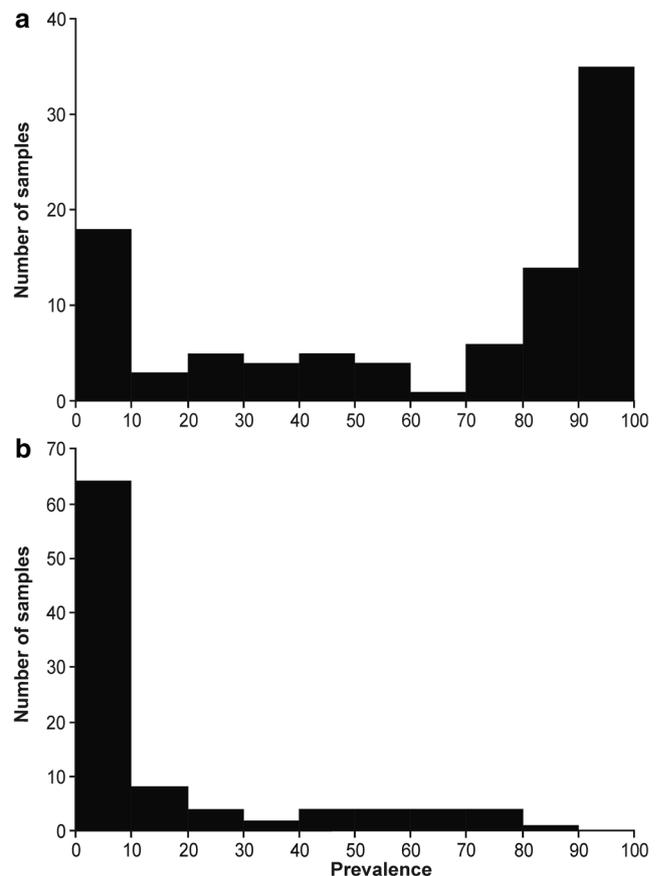


Fig. 2 Frequency of values of prevalence of *Corynosoma australe* (a) and *C. cetaceum* (b) across 95 fish samples in the Southwestern Atlantic

Merluccius hubbsi Marini, 1933 and *C. peruvianus*. Considering both, present (Table 1) and published (Table 2) data, this species was frequently present at high prevalence (Fig. 2a); whereas the prevalence of *C. cetaceum* was very low in a considerable proportion of the samples (Fig. 2b).

Corynosoma australe was present at low average abundance in most samples (Fig. 3a), although a group of them showed high values (60–200 parasites per fish) for this parameter, being represented by fish species (*Conger orbignyanus* Valenciennes, 1837, *C. guatucupa*, *Pagrus pagrus* Linnaeus, 1758, *Percophis brasiliensis* Quoy and Gaimard, 1825, *Pseudopercis semifasciata* (Cuvier, 1829), *Raneya brasiliensis* (Kaup, 1856) and *U. canosai*) with different habits, all from coastal waters in the northern region of the study area (Table 1). Finally, two samples of *U. canosai* harboured the higher values of mean abundance (297.0 and 368.6). *C. cetaceum* was comparatively much less abundant, with very low mean abundances prevailing across samples (Fig. 3b).

Distribution of *Corynosoma* spp.

Model validation plots showed no discrepancies from model theoretical assumptions (graphs not shown).

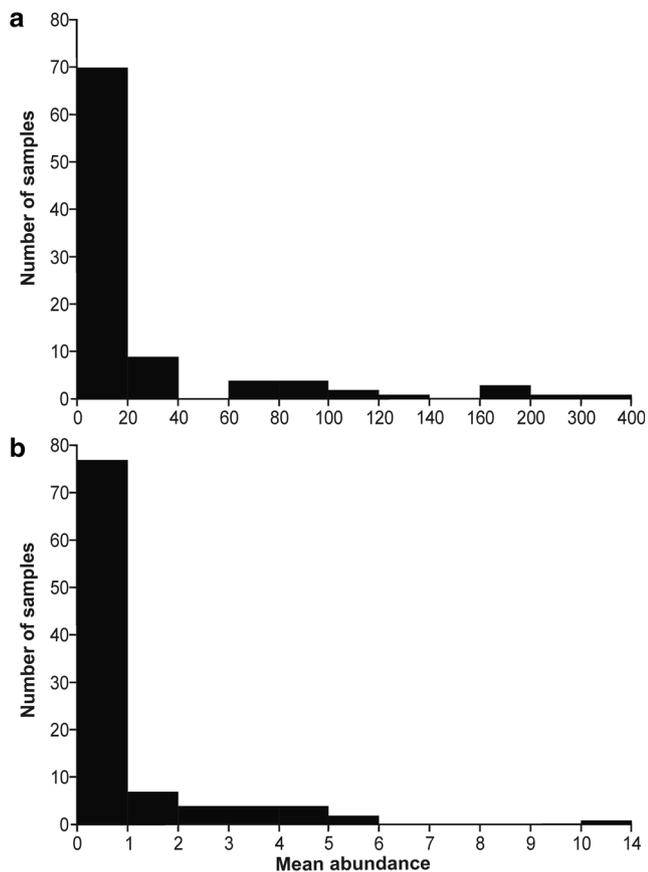


Fig. 3 Frequency of values of mean abundance of *Corynosoma australe* (a) and *C. cetaceum* (b) across 95 fish samples in the Southwestern Atlantic

Table 3 Alternative candidate GLMMs ranked according to their AIC_c to evaluate the effect of different predictor variables on the abundance of *Corynosoma australe* and *Corynosoma cetaceum*

Model	Predictors	AIC_c	ΔAIC_c	W_i
<i>Corynosoma australe</i>				
M3	<i>L + PB + DE + TL</i>	507.4	0.00	0.719
M4	<i>L + PB + DE + D</i>	510	2.56	0.200
MG	L + BP + DE + TL + D + H	512.4	4.98	0.060
M2	L + BP + TL	515.3	7.84	0.014
M1	L + BP + D	516.9	9.44	0.006
M7	L + BP	521.1	13.7	0.001
M15	BP + DE + TL + D	525.6	18.19	0.00
M19	BP + DE + D + H	527.7	20.24	0.00
M6	BP + D	529.2	21.78	0.00
M9	L + D + DE	541.8	34.42	0.00
M16	L + DE + TL + D	542.5	35.05	0.00
M18	L + DE + TL + H	545.6	38.15	0.00
M5	L + D	559	51.62	0.00
M10	L + TL	559.5	52.1	0.00
M8	L	561.2	53.75	0.00
M13	D	567	59.59	0.00
M14	TL	576.8	69.37	0.00
M11	BP	580.8	73.4	0.00
M12	DE	598.1	90.68	0.00
M0	–	605.9	98.44	0.00
M17	H	606.9	99.22	0.00
<i>Corynosoma cetaceum</i>				
M4'	<i>L + BP + DE + D</i>	117.2	0.00	0.651
M3'	<i>L + BP + DE + TL</i>	119.5	2.35	0.201
MG'	<i>L + BP + DE + TL + D + H</i>	120.5	3.39	0.120
M15'	BP + DE + TL + D	124.1	6.97	0.020
M1'	L + BP + D	126.9	9.79	0.005
M2'	L + BP + TL	130.2	13.01	0.001
M19'	BP + DE + D + H	130.3	13.16	0.001
M6'	BP + D	130.9	13.79	0.001
M7'	L + BP	134.9	17.72	0.00
M9'	L + DE + D	138.8	21.69	0.00
M18'	L + DE + TL + H	139.0	21.81	0.00
M16'	L + DE + TL + D	139.7	22.52	0.00
M5'	L + D	148.6	31.50	0.00
M13'	D	151.4	34.23	0.00
M10'	L + TL	151.4	34.25	0.00
M8'	L	152.8	35.67	0.00
M14'	TL	157.1	39.94	0.00
M11'	BP	168.3	51.19	0.00
M12'	DE	176.8	59.62	0.00
M17'	H	178.3	61.12	0.00
M0'	–	180.1	62.98	0.00

Models used for averaging are set in italics

AIC_c , Akaike Information Criterion adjusted for small samples; ΔAIC_c , AIC_c (best)– $AIC_c(i)$; W_i , Akaike weight; *L*, host total length; *TL*, trophic level; *BP*, biogeographic province; *DE*, depth; *D*, diet; *H*, habitat

All models considered biologically meaningful for both *Corynosoma* species are shown in Table 3. In the case of *C. australe*, two models were well supported (accumulating a $w_i > 0.9$), consequently a model-averaging procedure was performed in order to estimate the relative importance of the variables included in those models (Fig. 4) and to estimate parameter coefficients and standard errors (Table 4). The same procedure was applied to *C. cetaceum*, but in this case, by averaging three models (accumulating $w_i > 0.9$) (Table 3). For both parasite species, the most relevant variables were host total length (L), biogeographic province (BP) and depth (DE) (Fig. 4). Parasite abundance increased with host length while it decreased in depth and towards southern waters (understood as Magellanic province) (Table 4). In addition, variables related to trophic aspects of the hosts were included in the best models, in the case of *C. australe* as trophic level (TL) and as diet (D) for *C. cetaceum*. Parasite abundance increased with higher trophic levels and for invertebrate eating hosts (Table 4). Host habitat showed minimum effect on the determination of the abundance since it was only present in one of the significant models for *C. cetaceum* (Fig. 4).

Discussion

Corynosoma australe showed a very broad spectrum of fish hosts in the region, in agreement with previous studies on this species (Timi et al. 2010; Hernández-Orts 2013; Cantatore and Timi 2015) as well as on other congeners from different regions (Zdzitowiecki 1978, 1996; Sinisalo and Valtonen 2003), being the most widely spread parasite across fish species in the Argentine Sea. On the other hand, *C. cetaceum* showed a more restricted distribution, which, however, is not due to a higher phylogenetic specificity since it was found in fish belonging to 7 orders. This narrower host range is probably a consequence of a different set of ecological filters related to the parasite life cycle, population attributes or transmission capabilities. Indeed, the lack of effect of the fish

Fig. 4 Relative importance of variables included in the model averaging for both *Corynosoma australe* (black bars) and *Corynosoma cetaceum* (grey bars)

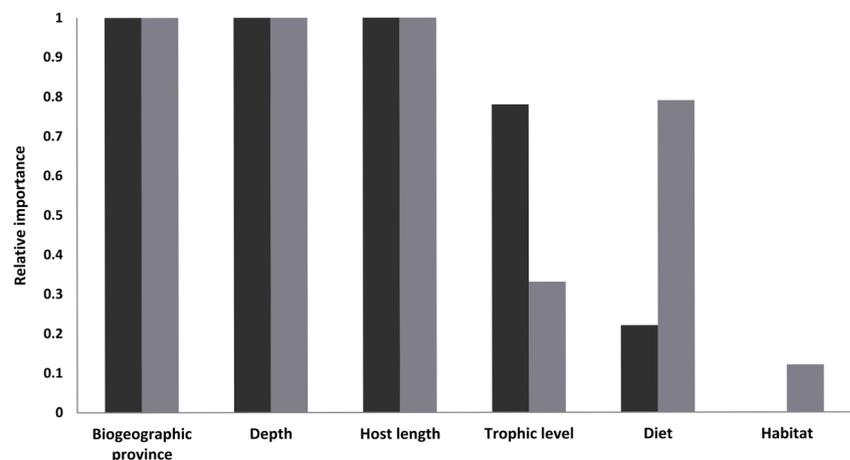


Table 4 Parameter estimates, standard errors (SE) and 95% confidence intervals (CI) of each predictor calculated after model averaging method on the abundance of *Corynosoma australe* and *Corynosoma cetaceum* in fishes from the Southwestern Atlantic

Parameter	Estimate	SE	CI
<i>Corynosoma australe</i>			
Intercept	-6.62	4.02	(-14.49, 1.25)
L	0.09	0.01	(0.06, 0.11)
TL	2.15	0.63	(0.91, 3.39)
BP (E)	-1.82	0.33	(-2.47, -1.18)
BP (M)	-3.56	0.58	(-4.70, -2.41)
DE	-0.01	0.003	(-0.02, -0.005)
D (FI)	1.55	0.56	(0.45, 2.65)
D (F)	0.34	0.69	(-1.03, 1.70)
D (P)	-2.15	0.73	(-3.58, -0.72)
<i>Corynosoma cetaceum</i>			
Intercept	-6.12	4.43	(-14.8, 2.57)
L	0.06	0.02	(0.03, 0.09)
D (FI)	1.21	0.81	(-0.38, 2.79)
D (F)	1.34	0.84	(-0.31, 2.99)
D (P)	-24.69	364.24	(-739, 689)
BP (E)	-1.59	0.49	(-2.55, -0.64)
BP (M)	-26.09	366.81	(-745, 693)
DE	-0.02	0.01	(-0.03, -0.009)
TL	2.38	0.81	(0.79, 3.96)
H (DEM)	-0.38	0.57	(-1.51, 0.74)
H (PEL)	-1.82	712.76	(-1400, 1395)

L, host total length; TL, trophic level; BP, biogeographic province (ecotonal (E), Magellanic (M)); DE, depth; D, diet (fish and invertebrates (FI), fish (F), plankton (P)); H, habitat (demersal (DEM), pelagic (PEL))

species as explanatory variable on the distribution of abundances of both helminth species is a further evidence of the low specificity of these parasites.

The differential distribution of both species is reflected also in quantitative grounds, being *C. australe* found at high prevalence and mean abundance in a considerable proportion of

samples, whereas *C. cetaceum* is much less prevalent and abundant. It is noteworthy that two samples of *U. canosai* harboured the most abundant infrapopulations of *C. australe*, being largely higher than any other species. The fact that *U. canosai* migrates from southern Brazilian waters (Haimovici et al. 2006), reaching the study zone during the warmer seasons, makes not possible to determine if these abundances are due to a specific behaviour of this host (perhaps a specialisation for preying on intermediate hosts of *C. australe*) or it reflects the structure of parasite populations from other latitudes. A combination of both factors can be also possible, since other fish with similar migratory behaviour, such as *T. lathami* and *P. saltatrix*, both pelagic (Saccardo and Katsuragawa 1995; Haimovici and Krug 1996), do not show parasite abundances notably higher than those of resident fishes.

Beyond the differences in parasite burdens displayed by both species, they share the same main determinants of their abundances: the host total length, biogeographic province of origin and depth. Regarding host length, cumulative patterns of parasite abundance as fish grow are commonly reported for trophically transmitted larval parasites (Dogiel et al. 1958; Poulin 2000, 2004; Poulin and Valtonen 2001; Timi et al. 2010; Valtonen et al. 2010; Timi and Lanfranchi 2013). Indeed, such ontogenetic changes have been previously demonstrated for *C. australe* in *P. brasiliensis* (Braicovich et al. 2016). These patterns are explained by the fact that larger hosts can ingest bigger quantities of food and display larger surface for parasites attachment, being able to sustain a greater absolute number than parasites than small ones (Guégan et al. 1992; Poulin 2000; Valtonen et al. 2010). Larger fish also can prey on larger food items, increasing the number of parasites acquired (Timi et al. 2010, 2011). All these processes, known at intraspecific level, can be extrapolated to interspecific level when unspecific parasites, such as *Corynosoma* spp., are considered. Additionally, for long-lived parasites, which remain for long periods or for the entire lifespan of their hosts, cumulative processes are expected to be more pronounced, because they depend not only on fish size, but also on age and longevity (Braicovich et al. 2016).

Concerning spatial variables, such as biogeographic province and depth, in the southern Southwest Atlantic, both region and depth are closely related to water temperature, due to the effect of subantarctic waters of the Malvinas current (cold and low-salinity water) flowing northwards along the continental slope and the Brazil current (warm and saline water) flowing from its origin in lower latitudes to near 38°S. Both currents determine temperature clines (decreasing southwards and with increasing depth) on shelf waters (Hoffmann et al. 1997; Acha et al. 2004; Piola et al. 2010) and contribute to delimit the two biogeographic provinces: the Argentinian and the Magellanic (Miloslavich et al. 2011). The ecotonal zone between both assemblages takes place around 43°–44° S, near Valdés Peninsula (Miloslavich et al. 2011). Water temperature,

therefore, can have a direct effect on both acanthocephalans, whose development or transmission seems to be favoured in warmer environments. An indirect effect of temperature, through its influence on the distribution of different hosts involved in the life cycles of parasites is also possible. Unfortunately, the first intermediate hosts, known to be benthic amphipods for several species of *Corynosoma* (Zdzitowiecki and Presler 2001; Sinisalo and Valtonen 2003; Laskowski et al. 2010) are unknown in the region and no inferences can be made at this level of the life cycle.

Regarding definitive hosts, the distribution of *A. australis* and *O. flavescens* extends along all the study area, with higher concentrations of both species in Patagonian coasts (Crespo et al. 2015; Grandi et al. 2015) where *C. australe* is less abundant; consequently the density of sea lion populations is not a determinant of the observed clines in parasite abundance. On the other hand, the southern distribution limit of *P. blainvillei* is the San Matías Gulf (~42°S) in north Patagonian coasts (Crespo et al. 1998) and, although other known or potential cetacean hosts reach higher latitudes, *C. cetaceum* has been only recorded in the vicinity of San Matías Gulf, but not in southern regions (Hernández-Orts et al. 2015). This indicates that, variables other than availability of suitable definitive hosts also determine the distribution of *C. cetaceum*. Although vagility and migratory movements of some fish hosts may expand the distribution of both acanthocephalans, water temperature arose as the most probable driver of the distribution of both species, with *C. australe* displaying wider latitudinal and bathymetric ranges. High temperatures usually lead to an increase in the metabolic rates of ectothermic organisms (Schmidt-Nielsen 1997). According to it, several studies have reported a rise in parasite development rates with increasing temperatures in aquatic environments, especially for infective stages (e.g. Paull and Johnson 2011, 2014), such as it has been shown for cystacanths of polymorphid acanthocephalans in their amphipod host (Tokeson and Holmes 1982). Similar processes could be responsible of the apparent preference of both *Corynosoma* species for northern waters in the region. Warmer environments can lead to increasing levels of parasitism in two additional ways: affecting the ability of the infective stages to get to their host or affecting the capability of the host of resist the infection (Barber et al. 2016). Moreover, a modification in the metabolic rates of hosts due to the temperature shift may lead to a change in their rate of food consumption which can enhance exposure to trophically-transmitted parasites.

Depth itself is also recognised as a factor influencing the distribution of parasites with complex life cycle. In fact, parasite abundance declines with depth due to their dependence of the abundance of free-living fauna (Marcogliese 2002).

Many parasites with complex life cycles track food web interactions to propagate and maintain themselves in the marine realm (Marcogliese and Cone 1997). The results show that trophic habits are indeed a driving factor of *Corynosoma* spp. abundance,

as trophic level and diet composition determine the range of prey a predator can consume, having a direct influence on the abundance and composition of parasite communities (George-Nascimento 1987; Marcogliese 2002; Chen et al. 2008). Also, Timi et al. (2010) demonstrated a strong influence of trophic level on the structure of parasite assemblages, including *C. australe* and *C. cetaceum*, of several fish species in the region, showing that the parasite abundance increases with trophic level.

Besides the relevance of the knowledge on the distribution of larval *Corynosoma* due to their value as tags of host population structure and zoogeography, another aspect to consider for the genus *Corynosoma* is their zoonotic potential, since human infestations have been occasionally recorded (Schmidt 1971; Takahashi et al. 2016; Fujita et al. 2016) besides infestation in birds and terrestrial mammals (Machado-Filho 1970; Schmidt 1971; Richardson and Cole 1997; Cabrera et al. 1999; Tantaleán et al. 2007; Hernández-Orts et al. 2017). High infective capability, long survival periods and low specificity make infestation by *Corynosoma* spp. a potential hazard for human health, transmissible by the consumption of raw or undercooked fish (Tantaleán et al. 2007; Fujita et al. 2016). Even though the risk of infestation seems to be low due to the microhabitat of the parasites, the high abundance in some fish species makes the contamination of fillets with infective stages probable. Therefore, a precise knowledge of the distribution across host species and localities acquires relevance.

In summary, ontogenetic, latitudinal and bathymetric effects over parasite abundance have been previously observed in several fish-parasite systems in the study area (Cantatore and Timi 2015; Braicovich et al. 2016; Irigoitia et al. 2018). However, the present findings show that host size and trophic habits are the main determinants of abundances for both species of *Corynosoma*, while biogeographic province of origin and depth (both indirectly representing the temperature of water) would be the main drivers of their spatial distribution. Knowing these host and environmental characteristics will allow to propose testable hypotheses on the burdens of *C. australe* and *C. cetaceum* to be found in any fish species inhabiting different regions of the Southwest Atlantic, as well as to better perform sampling designs to use parasite tags in further studies on host population structure and zoogeography.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

Ethical statement All fishes used in this work were obtained from commercial catches or research cruises. Therefore, no ethical statement is needed regarding use of animals for scientific purposes.

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