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Structure of parasite communities in Procellariiformes stranded along the coast of the state of São Paulo, Brazil[1]

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ABSTRACT.- Guimarães J.P., Castro C.B.S., Ferioli R.B., Valença G., Zochio M., Maranho A., Marcondes T., Bolsoni J., Nascimento C.C. & Bertozzi C.P. 2026. **Structure of parasite communities in Procellariiformes stranded along the coast of the state of São Paulo, Brazil**. *Pesquisa Veterinária Brasileira 46:e07850, 2026.* Instituto Biopesca, R. Carlos Eduardo Conte de Castro, 93 - Canto do Forte, Praia Grande - SP, 11700-430, Brasil. E-mail: juvetpg@yahoo.com.br

Procellariiformes play a crucial ecological role in marine ecosystems and are widely regarded as sensitive indicators of environmental change. This study characterized the structure of parasite communities in stranded Procellariiformes along the coast of São Paulo State, Brazil, providing new insights into infection dynamics and their potential implications for seabird health. Data from 1,010 necropsies conducted between January 2020 and December 2024 were analyzed within the scope of the Santos Basin Beach Monitoring Project (PMP-BS). Overall, 42.3% of the examined individuals hosted at least one parasite species, with ten host species found to be parasitized. The helminths *Seuratia shipleyi*, *Renicola sloanei*, and *Contracaecum pelagicum* were the most prevalent. Species of the genus *Puffinus* displayed the greatest parasite diversity, while the stomach and kidneys were identified as the main sites of infection. Multivariate analyses revealed distinct host–parasite association patterns, with host species grouping according to the similarity of their parasitic assemblages. Notably, Northern Hemisphere migratory species exhibited higher infection prevalence (36,4%) compared to those migrating from the Southern Hemisphere (14,2%). The detection of high-intensity infections in vital organs suggests that parasitism may contribute to physiological stress and debilitation in stranded individuals, particularly during energetically demanding migratory periods. These findings highlight the value of long-term monitoring of stranded seabirds and, through the integration of five years of data, provide the first comprehensive characterization of parasite community in stranded Procellariiformes from the coast of São Paulo.

INDEX TERMS: Seabirds, helminths, parasite ecology, migration.

RESUMO.- [**Estrutura das comunidades parasitárias em Procellariiformes encalhados ao longo da costa do estado de São Paulo, Brasil.**] Os Procellariiformes desempenham um papel ecológico crucial nos ecossistemas marinhos e são amplamente considerados indicadores sensíveis de mudanças ambientais. Este

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estudo caracterizou a estrutura das comunidades parasitárias em Procellariiformes encalhados ao longo da costa do estado de São Paulo, Brasil, fornecendo novos insights sobre a dinâmica das infecções e suas potenciais implicações para a saúde das aves marinhas. Foram analisados dados de 1.010 necropsias realizadas entre janeiro de 2020 e dezembro de 2024, no âmbito do Projeto de Monitoramento de Praias da Bacia de Santos (PMP-BS). No total, 42,3% dos indivíduos examinados apresentaram pelo menos uma espécie de parasito, sendo dez espécies hospedeiras encontradas parasitadas. Os helmintos *Seuratia shipleyi, Renicola sloanei* e *Contracaecum pelagicum* foram os mais prevalentes. Espécies do gênero *Puffinus* apresentaram a maior diversidade parasitária, enquanto o estômago e os rins foram identificados como os principais sítios de infecção. As análises multivariadas revelaram padrões distintos de associação parasito–hospedeiro, com agrupamento das espécies hospedeiras de acordo com a similaridade de seus conjuntos parasitários. Notavelmente, espécies migratórias do Hemisfério Norte apresentaram maior prevalência de infecção (36,4%) em comparação com aquelas migratórias do Hemisfério Sul (14,2%). A detecção de infecções de alta intensidade em órgãos vitais sugere que o parasitismo pode contribuir para estresse fisiológico e debilitação em indivíduos encalhados, particularmente durante períodos migratórios de alta demanda energética. Esses achados destacam a importância do monitoramento a longo prazo de aves marinhas encalhadas e, por meio da integração de cinco anos de dados, fornecem a primeira caracterização abrangente da comunidade de parasitas em Procellariiformes encalhados no litoral de São Paulo.

TERMOS DE INDEXAÇÃO: Aves marinhas, helmintos, ecologia parasitária, migração.

INTRODUCTION

Procellariiformes play a fundamental ecological role in marine ecosystems, with biological characteristics that make them key components of oceanic food chains. They are widely recognized as oceanic sentinels due to their high sensitivity to anthropogenic and environmental stressors, such as marine pollution (Clark et al. 2023, Pacyna et al. 2019, Eckbo et al. 2019, Carrasco et al. 2025) and climate change (Tavares et al. 2019, Thorne et al. 2016). Furthermore, a considerable proportion of the species in this order are currently listed in threatened categories by the International Union for Conservation of Nature (IUCN, 2025-2), highlighting the need for studies that address biological and ecological factors related to population health and vulnerability of these birds.

Due to their long lifespan, extensive migratory movements, and strong philopatry to breeding colonies, Procellariiformes exhibit a remarkable capacity to acquire, transport, and disseminate parasites and pathogens across wide geographic regions (Dietrich et al. 2011, McCoy et al. 2016). These ecological attributes expose them to diverse oceanic environments and trophic networks throughout the annual cycle, making them particularly relevant hosts for the acquisition, persistence, and dispersal of parasitic communities on a global scale (Koprivnikar et al. 2021, Hicks et al. 2021).

The diversity, abundance, and distribution of parasitic fauna in these birds are influenced by a combination of extrinsic and intrinsic factors. Among the extrinsic determinants, the availability and quality of food resources, along with habitat conditions, stand out. Since many endoparasites are transmitted through diet, their life cycles depend on the presence of intermediate hosts in the ecosystem (Lorenti et al. 2025). Consequently, spatial and temporal variations in environmental conditions can alter the structure of parasitic communities by affecting the availability of these intermediate hosts. In this context, pollution and habitat degradation can modulate both the risk of exposure and the host susceptibility, as observed in seabirds exposed to environmental contaminants (Khan et al. 2019, Clark et al. 2023).

Previous studies have demonstrated that differences in trophic ecology and habitat use are closely related to variations in parasite composition and diversity among Procellariiformes. Studies with pelagic birds, such as *Puffinus* and *Calonectris*, have shown that changes in diet and the exploitation of different oceanic niches directly affect parasite acquisition by modifying exposure to intermediate hosts and transmission routes. Host characteristics - including body condition, sex, age, and presence of comorbidities -also influence susceptibility to parasitic infection and contribute to intra- and interspecific variation in infection patterns (Marcogliese 2004, Poulin 2007, McCoy et al. 2016, Koprivnikar et al. 2021, Lorenti et al. 2025).

Parasitism can increase energy expenditure, impair locomotion, and reduce the time spent feeding. Hicks et al. (2018) demonstrated that heavily parasitized birds spend significantly less time in aerial activity compared to less infected individuals. These energy constraints can be particularly critical for migratory birds during periods of high physiological demand. Furthermore, parasitic infections can affect overall condition, alter reproductive behavior, and negatively impact survival (Wobeser 2008, Marcogliese 2004, Hicks et al. 2021).

Given the ecological relevance of Procellariiformes, concerns about the conservation of many of their species, and the still fragmented knowledge about their parasitic fauna, this study aimed to characterize the parasitic assemblages of Procellariiformes stranded along the coast of the state of São Paulo, Brazil, contributing to a broader understanding of the structure of these communities and their implications for the health and vulnerability of seabirds.

MATERIALS AND METHODS

Study Area

This study was based on records of Procellariiformes stranded along the coast of the state of São Paulo, Brazil, encompassing the coastline between the municipalities of Cananéia (25°00′S, 47°55′W) and Ubatuba (23°26′S, 45°04′W). This region extends for approximately 600 km and includes a wide variety of coastal and marine habitats, such as estuaries, oceanic islands, and open sea areas. These environments are characterized by high biological productivity and harbor important feeding and breeding areas used by various seabird species (Schaeffer-Novelli et al. 1990, Neves et al. 2006). This environmental heterogeneity promotes a diversity of trophic interactions and supports the life cycles of numerous parasite species throughout the study area.

Data Source

The analyzed dataset comprised records of necropsies performed between January 2020 and December 2024, extracted from the Aquatic Biota Monitoring Information System (SIMBA), of the Santos Basin Beach Monitoring Project (PMP-BS), developed to meet the requirements of the federal environmental licensing, conducted by IBAMA, for oil and natural gas exploration and production activities.

Each record included bird identification information (species, sex, location, and date) and parasitological data, such as parasite species, number of recovered individuals, and infected organ. Only records with complete information were used for analysis, excluding those with inconsistent or incomplete data.

The use of stranded seabirds as a source of parasitological data is widely recognized in ecological and health studies, providing valuable information on the dynamics of infections and population patterns in natural seabird assemblages (Mariani et al. 2019).

Parasite identification

Parasite identification was performed by specialized laboratories responsible for issuing parasitological reports at the institutions participating in the PMP-BS. Identifications were based on diagnostic morphological characteristics observed under optical microscopy and stereomicroscopy, following standardized laboratory procedures and using taxonomic keys and reference descriptions from literature, including Johnston and Mawson (1942), Anderson et al. (2009), Khalil et al. (1994), and specific taxonomic revisions.

Following fixation and preservation in 70% ethanol, the helminths were prepared for morphological analysis. Nematodes were cleared in Amann's lactophenol, while trematodes, cestodes, and acanthocephalans were stained with Langeron's carmine, according to the methodology described by Amato and Amato (2010).

This methodological framework, widely used in studies of parasite ecology and community structure, ensures the reliable identification of host-parasite associations and the consistent characterization of parasite assemblages in ecological contexts (Bush et al. 2017).

Statistical analyses

Parasite infection intensity was categorized into three classes — low (1), moderate (2), and high (3) — based on data distribution. Thresholds were determined using quartiles: values equal to or below the first quartile (Q1) were classified as low intensity, those between Q1 and the third quartile (Q3) as moderate, and those above Q3 as high intensity. This quartile-based approach provided an objective standardization of infection intensity, allowing consistent comparisons among parasite and host species, while accounting for the typically skewed distribution of parasitological data.

Analyses were descriptive and exploratory, designed to identify association patterns and similarities between hosts and parasites. The infection matrix was examined through multivariate visualization methods that simultaneously integrated infection intensity and parasite composition, enabling cross-species comparisons.

Infection patterns were visualized using a heatmap, where infection intensity was represented on an ordinal scale from 0 (absence) to 3 (high infection). Parasite species (rows) and host species (columns) were independently clustered using hierarchical clustering with average linkage, based on Bray–Curtis dissimilarities, to highlight similarities in infection profiles among hosts.

All statistical analyses and graphical outputs were performed in the R environment (version 4.4.1; R Core Team, 2024), using widely adopted packages in quantitative ecology for data processing, heatmap generation, dissimilarity computation, and clustering (Gu et al. 2016, Wickham and Bryan 2023, Oksanen et al. 2025). A discrete color palette (white, khaki, orange, and red) was applied to represent increasing infection intensities, ensuring straightforward interpretation of the ordinal scale.

Additionally, a bubble plot was constructed to visualize host–parasite associations and their corresponding infection intensities, allowing easy identification of dominant associations and variation among species. Bubble size was proportional to infection intensity (1–3), and fill color reflected the same intensity scale used in the heatmap. This visual approach provided an integrated depiction of host range, parasite distribution, and heterogeneity within the host-parasite assemblage.

RESULTS

During the study period, a total of 1,010 necropsies of Procellariiformes were performed, of which 42.3% presented at least one parasite species. In total, ten host species were found to be parasitized (Table 1). Among these, *Daption capense* showed the highest infection prevalence (33.3%), followed by *Puffinus puffinus* (30.9%), *Calonectris diomedea borealis* (26.6%), and *Puffinus griseus* (26.3%).

Among all the hosts analyzed, the most prevalent helminths were *Seuratia shipleyi* (10.3%), *Renicola sloanei* (6.83%), and *Contracaecum pelagicum* (4.35%). Species belonging to the genus *Puffinus* (*P. gravis, P. griseus,* and *P. puffinus*) showed the greatest parasitic diversity, with up to four parasite species recorded per host. Regarding infection sites, the stomach was the most frequently parasitized organ (13.3%), followed by the kidneys (6.8%) (Figure 1).

Analysis of the parasite community structure revealed pronounced variation in infection patterns among host species. Heatmap analysis (Figure 2) demonstrated the grouping of host species according to the similarity of their parasitic profiles, forming two large groups: one characterized by greater parasitic diversity, composed mainly of species of the genera *Puffinus* and *Calonectris*; and another with lower diversity and prevalence, including *Pterodroma*, *Daption*, and *Procellaria*. *Daption capense* showed infection exclusively by *Seuratia shipleyi.*

Nematodes *Contracaecum pelagicum* and *Seuratia shipleyi* were the most widely distributed taxa, infecting nine and seven of the ten host species analyzed, respectively. The bubble plot (Figure 3) illustrates the parasite-host associations and indicates that *C. pelagicum* showed the highest mean infection intensity in *Thalassarche chlororhynchos*, suggesting greater susceptibility of this species to the parasite. The overall mean prevalence of *C. pelagicum* was 8.3%, ranging from 2.8% in *Pterodroma mollis* to 16.0% in *Puffinus gravis*.

The most frequent and intense association was recorded between *Renicola sloanei* (Trematoda, Renicolidae) and *Puffinus puffinus.* This kidney trematode showed the highest prevalence (19.8%) and the highest mean abundance (3.77) among all identified parasites, in addition to mean infection intensity of 19.0. Of the 349 *P. puffinus* individuals examined, 69 (19.8%) were infected with *R. sloanei*, corresponding to the largest absolute number of parasites recorded in the study (Table 1).

All ten host species analyzed exhibited migratory behavior and were classified into two groups: migrants from the Northern Hemisphere (*Calonectris diomedea borealis* and *Puffinus puffinus*), representing 20.8% of the sampled individuals; and migrants from the Southern Hemisphere (*Puffinus gravis, Puffinus griseus, Procellaria aequinoctialis, Thalassarche chlororhynchos, Thalassarche melanophris, Macronectes giganteus, Daption capense,* and *Pterodroma mollis*), corresponding to 79.2% of the total. Migratory species from the Northern Hemisphere showed considerably higher average prevalence of parasitic infection (36.4%) compared to species from the Southern Hemisphere (14.2%) (Table 2).

DISCUSSION

The present study provides the first comprehensive characterization of parasite community structure in stranded Procellariiformes along the coast of São Paulo based on five consecutive years of monitoring. The results reveal a highly heterogeneous parasite community, with marked differences in prevalence, infection intensity, and abundance among host and parasite species. Although the influence of trophic ecology and migratory behavior on parasite infections has been previously suggested for Brazilian Procellariiformes (Melo et al., 2012; Schramm et al., 2018), our broader temporal coverage and multispecies approach allowed the identification of community-wide patterns that had not previously been described.

The wide distribution of *Seuratia shipleyi* among the analyzed hosts reinforces the generalist nature of this nematode in Procellariiformes. Previous reports of *S. shipleyi* infecting different seabird species along the Brazilian coast indicate low host specificity, consistent with life cycle strongly dependent on the ingestion of intermediate hosts widely available in the marine environment (Melo et al., 2012; Schramm et al., 2018). The predominance of infections in the digestive tract observed in this study supports this trophic transmission pattern. In addition, studies with stranded seabirds stranded in Northeastern Brazil have associated *S. shipleyi* with macroscopic and histological gastrointestinal lesions, such as gastritis, enteritis, and hemorrhages, suggesting that intense infections may contribute to physiological impairment in affected individuals (Mariani et al., 2019).

Stegophorus diomedeae showed low prevalence but high infection intensity in certain hosts, a characteristic pattern of aggregated distributions commonly observed among helminths and other macroparasites in natural populations (Schramm et al., 2018). This behavior reflects the variability among individuals regarding exposure and susceptibility to infection (Shaw and Dobson, 1995; Bush et al., 1997; Poulin, 2007) and has important implications for the persistence and transmission dynamics of parasites, since a small number of highly infected individuals can sustain the life cycle even when the overall prevalence remains low (McCoy et al., 2016; Tinsley et al., 2019).

Among the identified parasites, *Contracaecum pelagicum* stood out for its wide host range, being recorded in most of the species analyzed. This finding is consistent with the generalist character attributed to anisakid nematodes in seabirds. Although the overall prevalence was moderate, the high infection intensities observed in *Thalassarche chlororhynchos, Macronectes giganteus,* and *Puffinus gravis* suggest an aggregated distribution, as previously described for the genus. Intense *Contracaecum* infections have been associated with severe gastritis and enteritis in stranded seabirds, indicating that high parasite loads may contribute to physiological debilitation and increased vulnerability to stranding events (Melo et al., 2012; Mariani et al., 2019).

The exclusive association between *Renicola sloanei* (Trematoda, Renicolidae) and *Puffinus puffinus,* along with the high prevalence, infection intensity, and abundance recorded, indicates high degree of specificity both in relation to the host and the infection site, restricted to the kidneys. Although this parasite-host relationship has not been consistently reported in previous studies, the results of this study reinforce the role of *P. puffinus* as a key host in the maintenance of *R. sloanei*. In contrast, a recent study that showed *R. sloanei* on *Fratercula arctica* during a mass stranding event in the Canary Islands also reported significantly lower prevalence (5%) (Pino-Vera et al., 2024). Despite partial overlap in marine habitats and trophic niches between these species, infection levels appear substantially different. These differences may reflect the influence of host ecology and migratory behavior on exposure and susceptibility to infection, suggesting that *R. sloanei* may occur opportunistically in some seabirds, while exhibiting greater specificity in others. The marked tropism of this species for renal tissue, associated with lesions described in previous studies, suggests that intense infections can compromise renal function — especially in individuals already exposed to other environmental stressors (Matos et al., 2019).

Parasites such as *Corynosoma australe* and *Cyathostoma phenisci* showed low prevalence and average abundance, with restricted occurrence among hosts. This pattern reflects the behavior of helminths with more restricted ecological niches in Procellariiformes and may be related to the occasional ingestion of specific intermediate hosts or their low availability in the marine environment (Schramm et al., 2018).

The differences observed between migratory species from the Northern and Southern Hemispheres demonstrate that migratory patterns influence both the risk of exposure and the structure of parasitic communities. Migratory species from the Northern Hemisphere showed higher prevalence and greater parasitic diversity, possibly reflecting longer periods of stay in the South Atlantic, differences in reproductive cycles, and migratory routes that cross distinct oceanographic regions, with different sets of intermediate hosts (Dias et al., 2006; Paiva et al., 2010; Bray et al., 2008). On a global scale, migratory seabirds are recognized as important reservoirs and dispersers of parasites, contributing to their transmission and maintenance on broad spatial scales (McCoy et al., 2016).

Beyond confirming previously reported parasite-host associations, this study substantially expands current knowledge of parasite ecology in Procellariiformes from the southwestern Atlantic. By integrating five consecutive years of monitoring data from 1,010 necropsied individuals representing ten seabird species, we were able to characterize parasite community structure at a broader temporal and taxonomic scale than previous studies conducted in Brazil. This approach revealed host-specific patterns of parasite diversity, infection intensity, and community composition, as well as differences associated with migratory origin, providing a more comprehensive understanding of parasite–host interactions in stranded seabirds from the coast of São Paulo.

Finally, the similarity in parasitic profiles observed among species of the genus *Puffinus* supports the hypothesis that phylogenetically close hosts tend to share similar parasitic assemblages. This pattern reflects the combined effects of shared evolutionary history and ecological overlap - especially in diet and foraging behavior - on the organization of parasitic communities, in agreement with previous studies on Procellariiformes (Melo et al., 2012; Schramm et al., 2018).

CONCLUSIONS

This study demonstrates that Procellariiformes stranded on the coast of São Paulo harbor a different parasitic community. The occurrence of parasites was unevenly distributed among the host species, with *Seuratia shipleyi*, *Renicola sloanei*, and *Contracaecum pelagicum* representing the dominant taxa, and the gastrointestinal tract and mouthparts being the most frequently infected organs.

The high prevalence and research intensity observed in several host species indicates that parasitism is a relevant component of seabird health and can increase vulnerability to physiological stress during periods of high energy demand, such as migration. Associations between parasites and hosts have identified species of the genus *Puffinus* as important reservoirs of parasitic diversity in the scientific community.

After analyzing 1010 Procellariiformes necropsied over five years, this study provides robust evidence on the diversity and parasitic community of Procellariiformes on the Brazilian coast, thus serving as an innovative reference for future ecological, epidemiological, and conservation assessments.

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Conflict of interest statement.- The authors declare that they have no conflicts of interest.

Credit author statement.- Juliana Plácido Guimarães and Camila Brandão Seabra Castro – Conceptualization, Formal analysis, Writing – original draft. Raquel Beneton Ferioli[c], Gustavo Valença [c], Matheus Zochio[d], Andrea Maranho[d], Thais Marcondes[e], Júlia Bolsoni – Data curation, Validation, Writing – review. Claudia Carvalho do Nascimento and Carolina Pacheco Bertozzi – Writing – review & editing.

Data availability statement.- The data used in this study were extracted from the Aquatic Biota Monitoring Information System (SIMBA), an open-access system (https://simba.petrobras.com.br), of the Santos Basin Beach Monitoring Project (PMP-BS), developed to meet the requirements of the federal environmental licensing, conducted by IBAMA, for oil and natural gas exploration and production activities.

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Figures

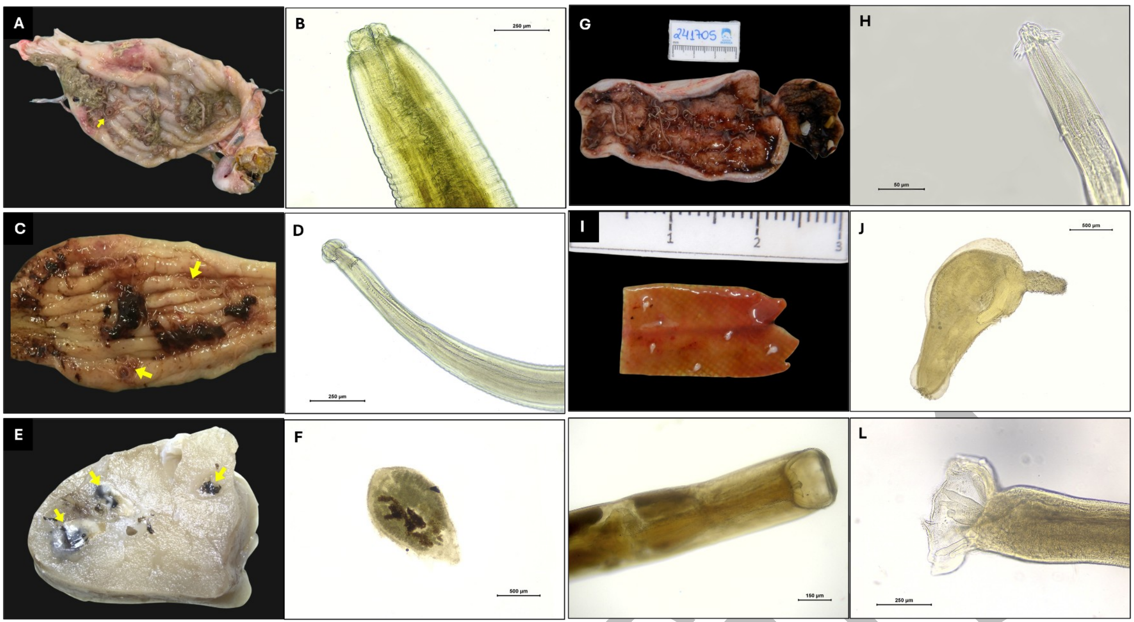

Fig.1. A: Proventriculus of Calonectris diomedea borealis infected with Contracaecum pelagicum (GREMAR); B: Anterior end of C. pelagicum under light microscopy (Biopesca); C: Seuratia shipleyi in the stomach of Puffinus puffinus (GREMAR); D: Anterior end of S. shipleyi (Biopesca); E: Renicola sloanei in the kidney of Puffinus puffinus (GREMAR); F: General view of R. sloanei recovered from the renal parenchyma (Biopesca); G: Proventriculus of Puffinus gravis showing the presence of nematodes, Stegophorus diomedeae and Contracaecum pelagicum (Biopesca); H: Anterior end of Stegophorus diomedeae recovered from the stomach (Biopesca); I: Corynosoma australe in the intestine of Puffinus griseus (Biopesca); J: General view of C. australe recovered from the intestine (Biopesca); K: Anterior end of Cyathostoma phenisci under light microscopy (Biopesca); L: Posterior end of a male specimen of C. phenisci, showing spicules and dorsal ray (Biopesca).

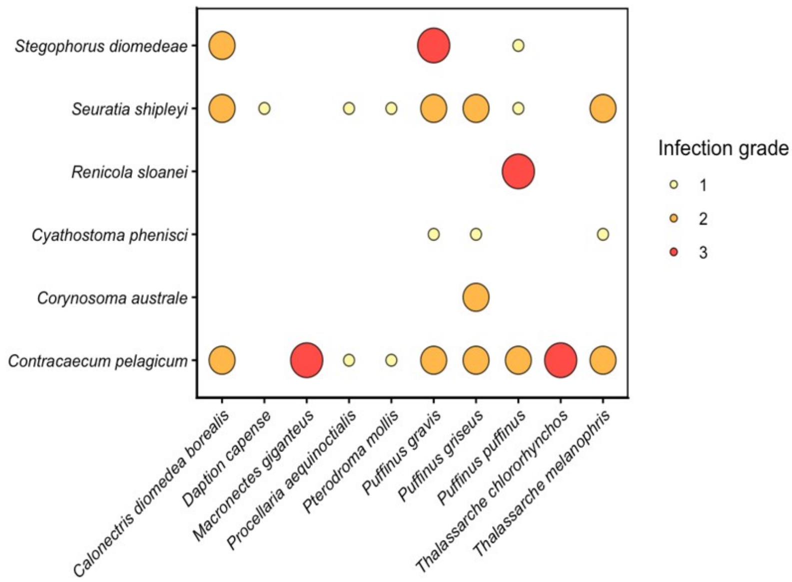

Fig.2. Heatmap showing infection intensity (0–3) of parasites in different species of stranded Procellariiformes along the coast of São Paulo State. The horizontal dendrogram groups host species according to the similarity of their parasitic profiles.

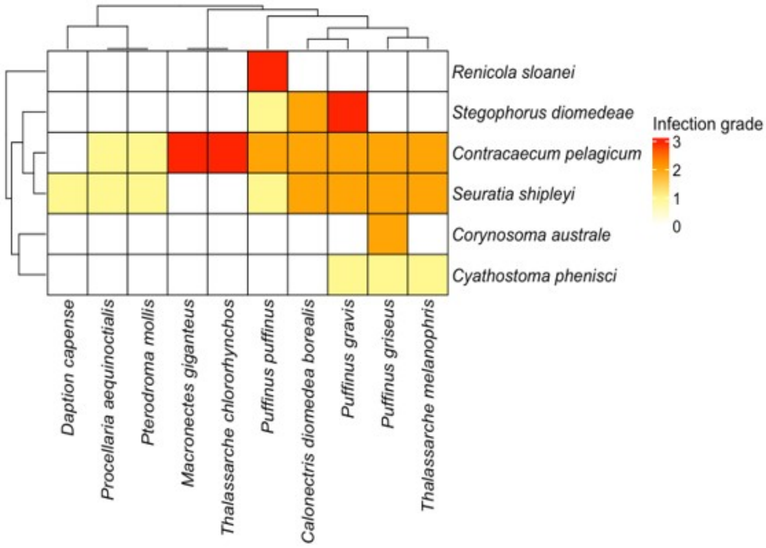

Fig.3. Bubble plot representing host–parasite associations. Each bubble denotes a host–parasite relationship, with size proportional to infection intensity (1 = low, 2 = moderate, 3 = high) and color indicating infection level.

Tables

Table 1. Number of parasitized hosts (NPH), total number of parasites recovered (NPR), prevalence (P%), mean infection intensity (MII), mean abundance (MA), and infection site* of parasites in Procellariiformes stranded along the coast of São Paulo State, Brazil

Host	Parasite Species	NPH	NPR	P%	MII	MA	Infection Site
Calonectris diomedea borealis (n=139)	*Contracaecum pelagicum*	7	73	5,0	10,4	0,5	CAV; ESO; STO; INT
	Seuratia shipleyi	31	368	22,3	11,9	2,6	ESO; STO; INT
	Stegophorus diomedeae	1	9	0,7	9,0	0,1	STO
Daption capense (n=3)	*Seuratia shipleyi*	1	5	33,3	5,0	1,7	STO
Macronectes giganteus (n=34)	*Contracaecum pelagicum*	2	45	5,9	22,5	1,3	ESO; STO
Procellaria aequinoctialis (n=118)	*Contracaecum pelagicum*	4	18	3,4	4,5	0,2	STO
	Seuratia shipleyi	17	103	14,4	6,1	0,9	ESO; STO
Pterodroma mollis (n=36)	*Contracaecum pelagicum*	1	4	2,8	4,0	0,1	ESO; STO
	Seuratia shipleyi	2	2	5,6	1,0	0,1	ESO; STO
Puffinus gravis (n=68)	*Contracaecum pelagicum*	11	207	16,0	18,8	3,0	CAV; ESO; STO
	Cyathostoma phenisci	1	2	1,5	2,0	0,0	AS
	Seuratia shipleyi	3	35	4,4	11,7	0,5	STO; INT
	Stegophorus diomedeae	2	48	2,9	24,0	0,7	STO
Puffinus griseus (n=19)	*Contracaecum pelagicum*	1	15	5,3	15,0	0,79	ESO; STO
	Corynosoma australe	1	7	5,3	7,0	0,37	INT
	Cyathostoma phenisci	1	1	5,3	1,0	0,05	AS
	Seuratia shipleyi	2	12	10,5	6,0	0,63	STO
Puffinus puffinus (n=349)	*Contracaecum pelagicum*	11	164	3,2	14,9	0,47	ESO; STO; INT
	Renicola sloanei	69	1314	19,8	19,0	3,77	REN
	Seuratia shipleyi	47	277	13,5	5,9	0,79	ESO; STO; INT
	Stegophorus diomedeae	1	2	0,3	2,0	0,01	STO
Thalassarche chlororhynchos (n=61)	*Contracaecum pelagicum*	3	90	4,9	30	1,5	ESO; STO; INT
Thalassarche melanophris (n=49)	*Contracaecum pelagicum*	4	86	8,2	21,5	1,8	CAV; ESO; STO
	Seuratia shipleyi	2	33	4,1	16,5	0,7	ESO; STO

*CAV: oral cavity; ESO: esophagus; STO: stomach; INT: intestines; AS: air sac; REN: kidney.

Table 2. Comparison of parasitological parameters between Northern and Southern Hemisphere migratory birds*

Group	P%	MII	MA	NPR	MPD
Northern Hemisphere migrants	36.4%	12.2	1.5	1–1,314	3.5 species
Southern Hemisphere migrants	14.2%	13.2	1.8	1–207	2.3 species

*Prevalence (P%), mean infection intensity (MII), mean abundance (MA), range of total number of parasites recovered (NPR), and mean parasite diversity (MPD).