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## Analysis of the helminth community of *Notothenia coriiceps* (Actinopterygii: Nototheniidae) collected in the water area of the Argentine Islands, West Antarctica

**Abstract.** Helminth community of the Antarctic black rockcod, *Notothenia coriiceps*, was examined using the fish samples collected in 2014–2015 (106 specimens) and 2020–2021 (78 specimens) in the water area of the Argentine Islands, West Antarctica. In total, 30,951 helminth specimens were collected and identified. We analyse the helminth infra- and component communities and investigate possible changes in the main parameters of helminth communities of *N. coriiceps* during the six-year period. Thirty species of helminths from five taxonomic groups were recorded: one species of Monogenea, 5 of Nematoda, 4 of Cestoda, 9 of Trematoda, and 11 of Acanthocephala. *Notothenia coriiceps* was found to be the definitive host of 18 helminth species; 12 species parasitize it in the larval stage using *N. coriiceps* as the second intermediate or paratenic host. The proportion of larval helminths in the samples was lower in 2014–2015 (73.4%) than in 2020–2021 (81.4%). The number of dominant helminth species (infection prevalence >50%) increased from seven in 2014–2015 to nine in 2020–2021. In helminth infracommunities, the species richness was similar in two samples. On the other hand, we found significantly higher helminth abundance in the infracommunities from the sample collected in 2020–2021. In the helminth component community, the diversity indices (Shannon, Simpson, Pielou, Berger-Parker) evidenced higher evenness and lower domination in the sample collected in 2014–2015 compared to the sample collected in 2020–2021. Lower evenness in 2020–2021 was due to the larger relative abundance of larval *Pseudoterranova* sp. and *Corynosoma* spp. We suggest a deeper investigation of the role of separate helminth species in the component community changes, as well as further monitoring of component community parameters as prospective directions for future studies of helminth communities of *N. coriiceps* in West Antarctica.

**Keywords:** Antarctic black rockcod, component community, diversity indices, infracommunity, species richness

### 1 Introduction

Parasitic organisms are an important component of marine biodiversity throughout the world (Polyanski, 1961; Palm, 1999; Klimpel et al., 2001; 2017). Complex life cycles of separate groups of metazoan parasites include various invertebrate and vertebrate animals as their intermediate, definitive and paratenic hosts (Marcogliese, 2002). Because of the complexity of par-

asite systems in marine and oceanic ecosystems, all changes in the composition of parasite communities reflect the changes in the state of ecosystems more rapidly than they could be documented by the monitoring of geological or oceanographic parameters (Möller, 1987; Mouritsen & Poulin, 2002; Hudson et al., 2006; Poulin & Mouritsen, 2006; Kvach & Kuzmina, 2020). In the regions of the Arctic and Antarctic with high endemism of fauna, parasitological

study is of increasing importance, because parasites may serve as natural markers for the identification of fish stocks as well as reflect changes in the state of polar marine ecosystems (Williams et al., 1992; MacKenzie, 2002; Marcogliese & Jacobson, 2015; Klimpel et al., 2017; Kvach & Kuzmina, 2020; Kuzmina et al., 2022a).

The fish fauna in the Southern Ocean around Antarctica is dominated by the perciform suborder Notothenioidei, which comprise up to 90 % of the fish biomass and about 77 % of fish species diversity (Near, 2009; Near et al., 2012). Notothenioidei are included in the food chains in Antarctic ecosystems as a food source for various fishes, mammals, and birds (Klöser et al., 1992; Palm et al., 1998; Barrera-Oro, 2002; La Mesa et al., 2004; Alt et al., 2021) and are involved in the life cycles of different groups of parasites of the predatory fish, fish-eating birds, and marine mammals as their intermediate and/or paratenic hosts (Rocka, 2006). Therefore, the parasite fauna of this group of bony fish has high species diversity in all ecoregions of the Southern Ocean (Palm et al., 1998; 2007; Zdzitowiecki & Laskowski, 2004; Laskowski & Zdzitowiecki, 2005; Oguz et al., 2015; Kuzmina et al., 2020; 2021a; 2021b; 2022b).

The Antarctic black rockcod, *Notothenia coriiceps* Richardson, 1844 is the dominant inshore demersal fish in waters off the west Antarctic Peninsula, including the South Shetland Islands (Iken et al., 1997; Near, 2009; Near et al., 2012). *Notothenia coriiceps* is an euryphagous and opportunistic feeder that feeds mostly on macroalgae, amphipods, euphausiids, gammarideans, krill or salps; its diet reflects the food availability at feeding grounds (Barrera-Oro & Casaux, 1990; Coggan, 1997; Iken et al., 1997; Casaux & Barrera-Oro, 2013). Thus, this fish species is included in the life-cycle of all main taxonomic groups of Antarctic metazoan parasites. In the coastal water area of the Argentine Islands, *N. coriiceps* is the most abundant species of fish; its proportion in fish catches in the waters close to the Ukrainian Antarctic Akademik Vernadsky station (hereinafter — Vernadsky station) ranged from 51.2% up to 95.4% (Manilo, 2006; Trokhymets et al., 2010). Therefore, we can consider *N. coriiceps* as the most suitable fish species for

the examining of the circulation of various groups of parasites in the Argentine Islands region, West Antarctica as well as an indicator species of teleost fishes for long-term monitoring studies of the parasite fauna of the region.

Monitoring studies of the state of Antarctic biological systems have been carried out for more than half a century (Klimpel et al., 2017); for more than 25 years, such studies have been performed on the Vernadsky station. During the last decade, extensive fish parasitological study was initiated in the water area of the Argentine Islands, near the Vernadsky station (Kvach & Kuzmina, 2020; Kuzmina et al., 2020; 2021a; 2021b; 2022a). More than 30 helminth species were found in 6 teleost fish species of this area (Kuzmina et al., 2021a); all these helminths were found to be generalists which easily infect various fish hosts. The first analysis of the parasitological data collected from *N. coriiceps* revealed certain changes in the structure of the parasite community as well as the increase of the helminth species richness during the last decades (Kuzmina et al., 2020; 2022a).

In this study, we investigated the samples of helminths collected from *N. coriiceps* in 2014—2015 and 2020—2021. The available material allowed the analysis of helminth infra- and component communities and the comparison of community parameters in two samples and the investigation of possible changes in the main parameters of helminth communities of *N. coriiceps* during a six-year period.

## 2 Materials and methods

### *Host examination, helminth collection and identification*

Field studies and collection of helminths were carried out in 2014—2015 and 2020—2021 during the XIX and XXV Ukrainian Antarctic expeditions at the Vernadsky station on the Galindez Island, Argentine Islands, West Antarctica (65°15' S, 64°15' W). In total, 184 specimens of the Antarctic black rockcod (106 in April 2014 — January 2015, 78 in February 2020 — January 2021) were caught using a fishing rod off the island shore at depths from 10 to 30 m. All fish were immediately transported to the laboratory,

measured and examined using the standard parasitological techniques (see Zdzitowiecki & Laskowski, 2004; Weber & Govett, 2009). In the sample collected in 2014–2015, the total body length of fish specimens was of  $32.2 \pm 5.8$  cm (21.5–44.5 cm) (Kuzmina et al., 2020). Fish specimens collected in 2020–2021 were of  $31.4 \pm 6.8$  cm (18.5–47.7 cm) long. Differences in body length between the samples collected in 2014–2015 and 2020–2021 were statistically insignificant ( $t$ -test  $p = 0.38$ ).

Parasites were collected manually from the skin, body cavity, stomach, intestine, liver, and mesentery. All collected parasites were washed in saline and fixed in 70% ethanol. Acanthocephalans were kept in tap water for 30 min to 3 h for proboscis evagination prior to their fixation in ethanol. Identification of the parasites was performed in the laboratory of the I. I. Schmalhausen Institute of Zoology in Kyiv, Ukraine, under light microscopes using morphological criteria. Identification of acanthocephalans of the genus *Corynosoma* Lühe, 1904 from cysts was performed after their excystation. Due to complications of the excystation technique, all encysted stages of *Corynosoma* spp. collected in 2014–2015 were identified only to the genus level. Due to this, we combined all specimens of *Corynosoma* spp. into one taxon in the statistical analysis of helminth communities. In total, 30951 helminth specimens were collected and identified. All helminth specimens were deposited in the Parasitological Collections of the Department of Parasitology of the I. I. Schmalhausen Institute of Zoology in Kyiv, Ukraine (collection numbers Nc-1-2014 — Nc-106-2014; Nc-1-2020 — Nc-78-2020).

#### Data analysis

For each helminth taxon, the prevalence and mean intensity of infection were calculated as suggested by Bush et al. (1997), separately for each sample. Additionally, the relative abundance of each taxon was estimated as the percentage of specimens in the whole sample of helminths. For the helminth infracommunities, the mean, median, minimum, and maximum numbers of species and specimens were calculated. Of 184 collected specimens of *N. coriiceps*, only 183

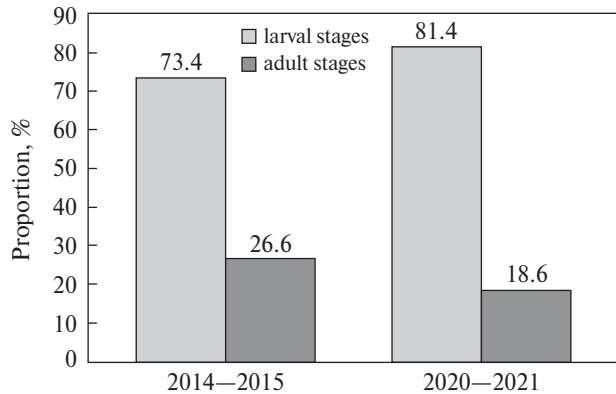
specimens were included in the helminth community analysis because the data were incomplete for one rockcod specimen collected in 2014–2015. The median values of both the species richness and the specimen abundance in two samples were compared using the Mann-Whitney  $U$ -test in PAST 3.0 software (Hammer et al., 2001). Additional comparison of the infracommunities' similarity in two samples was performed by ANOSIM and SIMPER methods using PRIMER 6.0 software (Clarke & Gorley, 2006). For this analysis of the helminth communities, we considered it possible to combine five species of *Corynosoma* into one unit, *Corynosoma* spp. The correlation between the host size and the helminth species richness and abundance in the infracommunities, the estimated species richness in the component community, and the diversity indices were calculated using PAST 3.0.

### 3 Results

#### 3.1 Helminth community composition and structure

All individuals of *N. coriiceps* examined in 2014–2015 and 2020–2021 were infected with at least one species of helminths. Thirty species of helminths from five taxonomic groups were found: 1 species of Monogenea, 5 species of Nematoda, 4 species of Cestoda, 9 species of Trematoda, and 11 species of Acanthocephala (Table 1). The acanthocephalans from the genus *Corynosoma* were collected as tissue cysts; in the statistical analysis, they are considered as a single taxon, *Corynosoma* spp.

Twenty-five helminth taxa were used in the present analysis. Ectoparasitic helminths from the class Monogenea, which were studied separately by specific techniques, were not included. In the analysis, trematodes composed the most diverse group (9 species), while acanthocephalans were the second largest group (6 species and *Corynosoma* spp.). The actual number of acanthocephalan species found in the studied samples of *N. coriiceps* was larger since we identified at least five species from the genus *Corynosoma*: *C. bullosum* (Linstow, 1892), *C. evae* Zdzitowiecki, 1984, *C. hamanni* (Linstow, 1892), *C. pseudohamanni* Zdzitowiecki, 1984, and *C. shackletoni* Zdzitowiecki, 1978.



**Figure.** Proportion (in %) of larval and adult helminths parasitizing *Notothenia coriiceps* in the Argentine Islands water area, West Antarctica, in different years

Therefore, acanthocephalans showed the highest diversity among the helminths of *N. coriiceps*, being represented by 11 species.

*Notothenia coriiceps* was found to be the definitive host of 18 helminth species from 4 taxonomic groups: the nematodes *A. nototheniae* and *D. fraseri*, all 9 species of trematodes, and 6 species of acanthocephalans from the genera *Metacanthocephalus*, *Aspersentis* and *Echinorhynchus* parasitize the Antarctic rockcod in the adult stage. All other species, including 3 nematode species, 4 cestodes and all acanthocephalans from the genus *Corynosoma* parasitize *N. coriiceps* as larval stages and use this fish species as the second intermediate or paratenic host. Over the period from 2014–2015 to 2020–2021 the proportion of helminth larval stages parasitizing *N. coriiceps* increased from 73.4% to 81.4% (Figure).

In the helminth sample collected in 2014–2015, 7 taxa had an infection prevalence higher than 50%: the nematode larvae *Pseudoterranova* sp., diphyllobothriid metacestodes, the trematodes *M. pennelli* and *G. bowersi*, and the acanthocephalans *M. johnstoni*, *M. rennicki* and *Corynosoma* spp. (Table 1). In 2020–2021, the core of *N. coriiceps* helminth community was expanded by bilocular metacestodes ( $P = 62.8\%$ ) and the nematode *Contracaecum* sp. ( $P = 59.0\%$ ) and thus comprised 9 taxa.

In 2014–2015, the helminth sample contained 8 species found in less than 10% of hosts; they were as-

signed to a group of rare species. Among them, the trematodes *L. macrocotyle*, *M. microtestis*, and *C. kerguelensis* were found each in a single host. Nematode larvae *Anisakis* sp. were harboured by only two *N. coriiceps*. The group of rare species in 2014–2015 also included the nematode *D. fraseri* and the trematodes *L. garrardi*, *N. antarctica*, and *D. johnstoni*. In the sample collected in 2020–2021, the group of rare species comprised 9 helminth species. In addition to the previously mentioned *Anisakis* sp., *L. macrocotyle*, *L. garrardi*, *N. antarctica*, *D. fraseri*, and *D. johnstoni* it included the nematode *A. nototheniae*, monolocular metacestodes, and the acanthocephalan *E. petrotschenkoi*.

In both samples, acanthocephalan larvae of the genus *Corynosoma* composed the majority of helminth specimens: 48.5% in 2014–2015 and 55.3% in 2020–2021. In 2014–2015, 4 more species had a relative abundance higher than 5%: the nematode *Pseudoterranova* sp., the trematode *M. pennelli*, and the acanthocephalans *M. johnstoni* and *M. rennicki* (Table 1). In 2020–2021, this group of predominating species lacked both acanthocephalans, while diphyllobothriid metacestodes entered the group with a relative abundance of 7.5%.

### 3.2 Parameters of helminth infracommunities and component community in 2014–2015 and 2020–2021

Of the 25 helminth taxa used in the combined sample, 24 were found in the sample collected in 2014–2015, and 23 were in the sample collected in 2020–2021. Estimated species richness in the component helminth community varied depending on the estimator used (Table 2). It reached a maximum of 29 species in 2014–2015 and 30 species in 2020–2021 according to jackknife2. Interestingly, most estimators except Chao1 and bootstrap suggested higher species richness in the sample collected in 2020–2021.

In helminth infracommunities, the species richness was similar in the two samples. Mean and median values were slightly higher in 2020–2021 (Table 2). However, the Mann-Whitney *U*-test showed no significant differences between the median values in

**Table 1.** Composition of helminth community of *Notothenia coriiceps*; infection prevalence (P, %), relative abundance (RA, %), and mean intensity of infection (MI) are shown for each taxon

Species	P, %		RA, %		MI		
	2014—2015*	2020—2021	2014—2015*	2020—2021	2014—2015*	2020—2021	
<b>PLATYHELMINTHES: MONOGENEA</b>							
1	<i>Pseudobenedenia nototheniae</i> Johnston, 1931	31.40	43.59	1.81	2.15	5.65	4.94
<b>NEMATODA: CHROMADOREA</b>							
2	<i>Pseudoterranova</i> sp.	95.24	97.44	8.01	11.51	12.66	22.95
3	<i>Contraecaecum</i> sp.	31.43	58.97	0.59	1.02	2.85	3.37
4	<i>Anisakis</i> sp.	1.90	6.41	0.03	0.06	2.00	1.80
5	<i>Ascarophis nototheniae</i> Johnston et Mawson, 1945	10.48	1.28	0.88	0.01	12.64	1.00
6	<i>Dichelyne fraseri</i> (Baylis, 1929)	4.76	5.13	0.04	0.03	1.40	1.25
<b>PLATYHELMINTHES: CESTODA</b>							
7	<i>Diphyllobothrium</i> sp.	76.19	83.33	4.76	7.45	9.40	17.35
8	Monolocular metacestode	13.33	1.28	0.13	0.01	1.50	1.00
9	Bilocular metacestode	39.05	62.82	0.58	1.42	2.24	4.39
10	Trilocular metacestode	15.24	21.79	0.15	0.17	1.44	1.53
<b>PLATYHELMINTHES: TREMATODA</b>							
11	<i>Macvicaria pennelli</i> (Leiper & Atkinson, 1914)	88.57	94.87	15.74	10.08	26.74	20.64
12	<i>Genolinea bowersi</i> (Leiper et Atkinson, 1914)	70.48	78.21	4.38	4.34	9.36	10.79
13	<i>Elytrophalloides oatesi</i> (Leiper et Atkinson, 1914)	41.9	46.15	0.96	1.02	3.45	4.31
14	<i>Lepidapedon garrardi</i> (Leiper et Atkinson, 1914)	8.57	6.41	0.08	0.11	1.44	3.20
15	<i>Neolebouria antarctica</i> (Szidat & Graefe, 1967)	5.71	6.41	0.11	0.05	2.83	1.40
16	<i>Derogenes johnstoni</i> Prudhoe et Bray, 1973	3.81	2.56	0.03	0.02	1.00	1.50
17	<i>Caudotestis kerguelensis</i> (Prudhoe & Bray, 1973)	0.95	0	0.01	0	1.00	0
18	<i>Macvicaria microtestis</i> Zdzitowiecki et Cie-lecka, 1997	0.95	0	0.01	0	1.00	0
19	<i>Lecithaster macrocotyle</i> Szidat et Graefe, 1967	0.95	1.28	0.01	0.01	1.00	2.00
<b>ACANTHOCEPHALA: PALAEACANTHOCEPHALA</b>							
20	<i>Metacanthocephalus rennicki</i> (Leiper & Atkinson, 1914)	87.62	71.79	5.79	2.21	9.95	5.98
21	<i>M. johnstoni</i> Zdzitowiecki, 1983	89.52	84.62	6.66	3.50	11.20	8.03
22	<i>M. campbelli</i> (Leiper & Atkinson, 1914)	31.43	35.90	0.77	0.85	3.70	4.61
23	<i>M. dalmori</i> Zdzitowiecki, 1983	45.71	29.49	1.44	0.63	4.75	4.13
24	<i>Aspersentis megarhynchus</i> (von Linstow, 1892)	13.33	16.67	0.35	0.18	4.00	2.15
25	<i>Echinorhynchus petrotschenkoi</i> (Rodjuk, 1984)	0	1.28	0	0.01	-	1.00
26	<i>Corynosoma</i> spp.**	93.33	97.44	48.49	55.30	78.20	110.21

Note: \* — Kuzmina et al. (2020) with modifications; \*\* — *Corynosoma* spp. includes 5 species: *C. bullosum* (Linstow, 1892), *C. evae* Zdzitowiecki, 1984, *C. hamanni* (Linstow, 1892), *C. pseudohamanni* Zdzitowiecki, 1984, and *C. shackletoni* Zdzitowiecki, 1978



the two samples ( $p = 0.12$ ). In both samples, the helminth species richness in the infracommunities positively correlated with the host size (total body length), Spearman’s correlation coefficient equaled 0.29 in the sample collected in 2014–2015 and 0.46 in the sample collected in 2020–2021 ( $p < 0.01$  in both samples). On the other hand, the helminth abundance in the infracommunities was higher in the sample collected in 2020–2021 compared to that collected in 2014–2015. The mean number of helminths per fish was 150 (median 135) in 2014–2015 vs. 194 (median 166) in 2020–2021. These differences were confirmed as significant by the Mann-Whitney  $U$ -test ( $p = 0.02$ ). In both samples, the helminth abundance in the infracommunities positively correlated with host size; Spearman’s correlation coefficient was 0.43 in the sample collected in 2014–2015 and 0.49 in the sample collected in 2020–2021 ( $p < 0.01$  in both samples). The higher abundance of helminth

infection in 2020–2021 was mostly due to higher infection intensity of larval nematodes (*Pseudoterranova* sp., *Contracaecum* sp.), diphyllbothriid metacestodes, and the acanthocephalans *Corynosoma* spp. (see Table 1).

The general similarity between the helminth infracommunities in both samples was confirmed by the ANOSIM routine. The ANOSIM  $R$  equaled 0.045 ( $p = 0.4\%$ ), which means that the differences were almost absent. SIMPER analysis showed the same values of the similarities among the infracommunities in each sample: 49.5% in the sample collected in 2014–2015 and 51.6% in the sample collected in 2020–2021. Average dissimilarity between the two samples of infracommunities was 50.6%. The analysis named 3 helminth taxa with high contribution to the dissimilarity: *Corynosoma* spp. (contribution 41.7%), *M. pennelli* (contribution 14.0%), and *Pseudoterranova* sp. (contribution 9.0%).

In the helminth component community, all the diversity indices calculated for the two samples showed higher evenness and lower domination in the sample collected in 2014–2015 compared to the sample collected in 2020–2021 (Table 3). Nevertheless, the level of dominance estimated by the Berger-Parker index was rather moderate (around 50%) in both samples and identified by the relative abundance of the same taxon, namely the larval stages of acanthocephalans *Corynosoma* spp.

#### 4 Discussion

This work presents the first comparative analysis of the main parameters of helminth infracommunities and component communities of *N. coriiceps* from the area of the Vernadsky station, Argentine Islands over a 6-year period. Representative helminth samples compared in the present study were collected during almost the same seasons (April 2014 – January 2015, February 2020 – January 2021). First parasitological examinations of teleost fish in the water area of Galindez Island near the Vernadsky station were performed in 2002 (Zdzitowiecki & Laskowski, 2004; Laskowski & Zdzitowiecki, 2005); 21 helminth species of five taxonomic groups were found in *N. coriiceps*. The

**Table 2.** Species richness parameters in helminth communities of *Notothenia coriiceps*

Parameters	Samples	
	2014–2015	2020–2021
Observed species richness (S)	24.0	23.0
Estimated S (Chao1)	27.0	24.5
Estimated S (Chao2)	25.5	26.0
Estimated S (jackknife1)	27.0	27.0
Estimated S (jackknife2)	29.0	30.0
Estimated S (bootstrap)	25.3	24.6
Species richness in infracommunities, mean [median] (min–max)	8.7 [9.0] (3–14)	9.1 [9.5] (3–14)
Margalef’s index of species richness	2.4	2.3

**Table 3.** Diversity indices in the helminth component community of *Notothenia coriiceps* in 2014–2015 and 2020–2021

Sample	Shannon index	Simpson index	Pielou evenness	Berger-Parker dominance
2014–2015	1.78	0.72	0.56	0.48
2020–2021	1.61	0.66	0.51	0.55

results of the parasitological examination of Antarctic rockcod in 2014–2015 expanded the list of its recorded helminths to 28 species (Kuzmina et al., 2020) due to the finding of 7 new helminth species, namely the trematode *C. johnstoni*, monolocular metacestodes, the nematodes *Anisakis* sp. and *D. fraseri*, and the acanthocephalans *M. rennicki*, *M. campbelli*, and *C. evae*. Also, a preliminary comparison of helminthological data obtained in this location in 2002 and 2014–2015 revealed statistically significant dissimilarity between helminth infracommunities of *N. coriiceps*, namely the helminth species richness was significantly higher in the sample collected in 2014–2015 (Kuzmina et al., 2022a). Statistical analysis of the dissimilarity named 3 helminth species, the metacestodes of *Diphyllobothrium* sp., the acanthocephalan *M. rennicki*, and the trematode *N. antarctica*, which were found to make the most significant contribution to the dissimilarity. Using those data, it was impossible to analyze the parameters of *N. coriiceps* helminth infracommunities and component communities. Nevertheless, a trend of the changes in the composition and structure of the helminth community in *N. coriiceps* over a decade and a half was revealed.

Parasitological studies performed in 2020–2021 enabled the finding of two rare acanthocephalan species, *E. petrotschenkoi*, which was not previously recorded in *N. coriiceps* in this region, and *C. shackletoni*. Thus, the helminth fauna of *N. coriiceps* was expanded to 30 species. This is the largest number of helminth species found in *N. coriiceps* from a single locality of West Antarctica compared to 12 species recorded from King George Island by Muñoz and Rebolledo (2019), or 18 species found by Palm et al. (1998) and 21 species previously found by Zdzitowiecki & Laskowski (2004) in the water area of Galindez Island. In the present study, separate estimators suggested the existence of 1–7 more helminth species parasitizing *N. coriiceps* (Table 2). In our opinion, such species might be extremely rare or just occasional parasites of this host.

Detailed studies of fish helminths in the area of the Vernadsky station enable us to clarify the taxonomic position of some helminth species. Comprehensive morphological and molecular examination of dige-

nean trematodes from the Argentine Islands region allow us to prove that the trematode species identified as *Macvicaria georgiana* (Kovaleva & Gaevskaya, 1974) is in fact *Macvicaria pennelli* (Leiper & Atkinson, 1914) (Faltýnková et al., 2022). A detailed re-examination of the samples collected in 2014–2015 revealed one more trematode species, *Caudotestis kerguelensis* (Prudhoe & Bray, 1973), which was not mentioned in previous publications (Kuzmina et al., 2020; 2021a; 2022a). Particular examination of the acanthocephalan *A. megarhynchus* (von Linstow, 1892) performed on the fresh material collected in 2014 (Amin et al., 2021) allowed to re-establish the validity of this species which was erroneously synonymized with *Aspersentis austrinus* Van Cleave, 1929 (see Amin, 2013).

In the statistical analysis of the helminth communities, we considered it possible to combine 5 species of *Corynosoma* into one unit, *Corynosoma* spp. Despite the recommendation to achieve the highest possible taxonomic resolution in ecological studies of parasites (Poulin, 2019), we found two reasons for such a combination: (i) not all the cysts containing *Corynosoma* spp. were successfully excysted and identified in the sample collected in 2014–2015. Therefore, we did not have exact information on the abundance and occurrence of separate species. All species of the genus *Corynosoma* infecting *N. coriiceps* are biologically similar and may be considered as a single ecological unit.

In contrast to the previous comparative study (Kuzmina et al., 2022a), we did not find a significant increase in species richness in helminth infracommunities of *N. coriiceps*. However, the average number of helminth species per host was slightly larger in the sample collected in 2020–2021 (Table 2). Instead, we observed a significant increase of helminth abundance in the infracommunities. It is evident from the infection parameters of separate species (see Table 1) that such an increase was mainly due to increasing infection intensity of the larval nematodes *Pseudoterranova* sp., the acanthocephalans of the genus *Corynosoma*, and bilocular metacestodes. The former two taxa in their adult stage are parasitic on pinnipeds and fish-eating birds. Their increasing abundance in the paratenic host might be a result of an increasing number of definitive hosts in the region of investigation; this

correlation has been already supposed in previous observations (Kuzmina et al., 2021a; 2022b). Apparently, the increasing abundance of larval helminths was the main reason for the rather high and significant correlation between the helminth abundance in the infracommunities and the host size observed in the present study. Encysted larval stages accumulate in each individual fish host during its life; therefore, the larger (and older) the fish, the larger number of helminth larvae it harbours. Such a cumulative infection process was reported in other fish hosts (e. g. Drago, 2012; George-Nascimento & Oliva, 2015).

Most diversity indices, except for the Berger-Parker domination index, calculated for two samples appeared to be lower in the sample collected in 2020–2021 compared to that collected in 2014–2015. Since the observed species richness in the two samples did not differ dramatically (24 species in the first sample and 23 species in the second one), the decrease of Shannon, Simpson and Pielou indices was obviously caused by the decrease of the evenness in the helminth component community. Higher dominance in the helminth component community in 2020–2021 is related to the higher relative abundance of two taxa: the nematode *Pseudoterranova* sp. and the acanthocephalans of the genus *Corynosoma* (Table 1). In general, the increase of dominance in the parasite community of fish is connected to less favourable environmental conditions (Chapman et al., 2015).

We presume at least that the observed decrease of evenness in the helminth community of *N. coriiceps* is related to significant changes in the structure of the marine ecosystem near Galindez Island. Changes in the state of Antarctic marine ecosystems influence the diet of teleost fish and their parasite fauna (Moser & Cowen, 1991; Palm et al., 1998; Münster et al., 2017; Muñoz & Rebolledo, 2019). As *N. coriiceps* is an euryphagous and opportunistic feeder (Barrera-Oro & Casaux, 1990; Iken et al., 1997; Coggan, 1997; Casaux & Barrera-Oro, 2013), its parasite fauna is particularly affected by any alterations in marine ecosystems. The key role of notothenioid fish in the foodwebs of West Antarctica, as both predators and as prey to the majority of the higher-level predators (Palm et al., 1998; McCormack et al., 2021), provides an op-

portunity to use these fish species to assess changes in the state of the marine ecosystems. Our data, collected over 6 years, revealed small but significant changes in some parameters of the parasite community that would be estimated over a longer time span. Furthermore, we have to emphasize the importance of systematic and regular sampling at the same site to identify and evaluate the impact of individual environmental factors on the parasite community. Deeper investigations of the role of separate helminth species in the component community changes and further monitoring of component community parameters may be prospective directions for future studies of helminth communities of *N. coriiceps* in West Antarctica.

## Conclusions

1. Thirty species of helminths from five taxonomic groups were found to parasitize *N. coriiceps* in the water area of the Argentine Islands, West Antarctica, in 2014–2015 and 2020–2021: 1 species of Monogenea, 5 species of Nematoda, 4 species of Cestoda, 9 species of Trematoda, and 11 species of Acanthocephala.

2. *Notothenia coriiceps* was found to be the definitive host of 18 helminth species; 12 species use *N. coriiceps* as the second intermediate or paratenic host. The proportion of larval helminths in the samples was slightly lower in 2014–2015 (73.4%) than in 2020–2021 (81.4%).

3. The species richness in the helminth infracommunities and in the component community was similar in 2014–2015 and 2020–2021; the helminth abundance in the infracommunities was significantly higher in 2020–2021.

4. The number of dominant helminth species (infection prevalence >50%) in *N. coriiceps* increased from 7 in 2014–2015 to 9 in 2020–2021. In the helminth component community, the diversity and evenness were higher in 2014–2015 compared to 2020–2021. The component community apparently had lower evenness in 2020–2021 due to the higher relative abundance of larval helminths (*Pseudoterranova* sp. and *Corynosoma* spp.)

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tification of samples; TK, YK — writing the first draft of the manuscript, TK — project administration. All the authors contributed to the data analysis and discussion of the manuscript.

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**Аналіз угруповань гельмінтів *Notothenia coriiceps* (Actinopterygii: Nototheniidae), зібраних в акваторії Аргентинських островів, Західна Антарктика**

**Реферат.** Проведено дослідження угруповань гельмінтів гололобої нототенії (*Notothenia coriiceps*) на основі вибірок, що були зібрані у 2014–2015 рр. (106 екз.) та 2020–2021 рр. (78 екз.) в акваторії Аргентинських островів, Західна Антарктика. Загалом було зібрано та визначено 30,951 екземпляр гельмінтів. Проаналізовано структуру інфрагруповань та компонентних угруповань гельмінтів *N. coriiceps* і досліджено ймовірні зміни основних параметрів гельмінтних угруповань за шестирічний період. Виявлено 30 видів гельмінтів з п'яти таксономічних груп: Monogenea (1), Nematoda (5), Cestoda (4), Trematoda (9), Acanthocephala (11). Встановлено, що *N. coriiceps* є дефінітивним хазяїном для 18 видів гельмінтів; 12 видів паразитують на стадії личинки, використовуючи *N. coriiceps* як другого проміжного або паразитичного хазяїна. Частка личинок гельмінтів у пробах у 2014–2015 рр. була нижчою (73,4%), ніж у 2020–2021 рр. (81,4%). Кількість домінуючих видів гельмінтів (екстенсивність інвазії >50%) зростає з 7 у 2014–2015 рр. до 9 у 2020–2021 рр. В інфрагрупованнях гельмінтів видове багатство було подібним у двох вибірках. З іншого боку, ми виявили достовірно більшу чисельність гельмінтів у інфрагрупованнях із вибірки, зібраної у 2020–2021 рр. У компонентних угрупованнях гельмінтів індекси різноманітності (Шеннона, Сімпсона, П'єлоу, Бергера-Паркера) свідчили про вищу рівномірність та нижче домінування у вибірці, зібраній у 2014–2015 рр., порівняно з вибіркою, зібраною у 2020–2021 рр. Нижча рівномірність у 2020–2021 рр. була зумовлена більшою відносною чисельністю личинок *Pseudoterranova* sp. та *Corynosoma* spp. Ми пропонуємо більш глибоке дослідження ролі окремих видів гельмінтів у змінах в компонентних угрупованнях, а також моніторинг параметрів угруповань як перспективні напрямки подальших досліджень угруповань гельмінтів *N. coriiceps* у Західній Антарктиці.

**Ключові слова:** видове багатство, гололоба нототенія, індекси різноманітності, інфрагруповання, компонентне угруповання