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Helminth parasites on the Anatolian khramulya, *Capoeta tinca* (Heckel, 1843) from northwestern Türkiye, with new host and geographical records

Nurten AYDOGDU [1,*] and Hatice TORCU-KOC [2]

1. Balıkesir University, Graduate School of Natural and Applied Sciences, Balıkesir, Türkiye
2. Balıkesir University, Faculty of Science and Arts, Department of Biology, Balıkesir, Türkiye
* Corresponding author: N. Aydogdu, E-mail: aydogdunurten98@gmail.com

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Abstract. In this study, it was aimed to determine the helminth fauna of *Capoeta tinca*, a fish species endemic to Turkey, collected from Nilüfer Stream (Bursa) between the 2020 Spring (April) and Winter 2021 (February). 81 *Capoeta tinca* individuals were caught and examined for ichthyo-helminths. A total of 242 parasites of 4 species were detected in the host fish. *Dactylogyrus pulcher* (6.1%, 16:5 parasite/fish) and *Paradiplozoon homoion* (20%, 63:17 parasite/fish) were found on the gills of the host fish. *Allocreadium isoporum* (33%, 149: 27 parasite/fish) and *Rhabdochona fortunatowi* (9.8%, 14:8 parasite/fish) were recorded in the intestines of the host fish. Among these parasites, *A.isoporum* was the most common parasite species (33%). Infection values of the helminth parasite species found were evaluated based on season, sex, and host size, and the results were compared with other studies. *P. homoion*, *A.isoporum*, and *R. fortunatowi* are reported for the first time from this host fish. Additionally, Nilüfer Stream was given as a new locality record for *A. isoporum* and *R. fortunatowi*.

Keywords: *Capoeta tinca,* helminth parasites, new host and locality records, Nilüfer Stream.

Introduction

The species belonging to the genus Capoeta are generally known as scrapers (Geldiay & Balık 2007, Zareian et al. 2018). It has been reported that 86 species of the genus Capoeta are distributed worldwide (Frose & Pauly 2022). Fish species from this genus, part of the Cyprinidae family, are widely distributed across the Mediterranean, Middle East, Caucasus, and Southwest Asia (Kaya 2019). It has been determined that 18 of the 86 species of this genus distributed worldwide are distributed in the inland waters of Turkey (Kaya 2019). Twelve of these 18 species are endemic to Turkey (Çiçek et al. 2018). Despite the diverse range of specimens, there is limited information on the helminth parasites of fish species from the *Capoeta* genus, and this knowledge remains inadequate. Additionally, it is notable that there are limited or no studies in our country examining the endemic fish species of this genus in terms of ichthyo-helminthology.

Based on our most comprehensive literature review, only 7 of the endemic fish species belonging to this genus have been studied ichthyo-helminthologically (Öge & Sarımehmetoglu 1996, Aydogdu & Altunel 2002, Turgut 2005, Özgül 2008, Heckmann et al. 2010, Turgut et al. 2011, Aydoğdu et al. 2011a, b, Aydogdu et al. 2015, Smales et al. 2015, Nejat et al. 2023). Anatolian khramulya, *Capoeta tinca*, one of the endemic species of this genus, is distributed in the Susurluk and Sakarya Rivers and the Eber Lake Basin in our country (Kaya 2019). The presence of helminth parasites of *C. tinca* in Turkey has been investigated by some of the above–mentioned authors so far (Öge & Sarımehmetoglu 1996, Aydogdu & Altunel 2002, Turgut 2005, Özgül 2008, Heckmann et al. 2010, Turgut et al. 2011). They reported on the occurrence of helminth species, *Dactylogyrus crucifer*, *D. narzikulovi*, *D. crucifer*, *Gyrodactylus narzikulovi*, *G. varicorhini*, *Gyrodactylus* sp., *Clinostomum complanatum*, *Diplostomum* sp., *Molnaria intestinalis*, *Contracaecum* sp., *Pomphorhynchus spindletrancatus* in *Capoeta tinca*.

The aim of this study on helminth parasites of the Anatolian khramulya in a different locality in Turkey is to provide more data on helminth parasites of *Capoeta tinca*. Thus, to contribute to increasing the diversity of the helminth mentioned above parasite species recorded so far in *Capoeta tinca* and to assess their dependence on the season, host length, and sex.

Material and methods

Eighty-one specimens of *Capoeta tinca* were sampled at three-month intervals between spring 2020 and winter 2021. The fish were caught from Nilüfer Stream (40°10'44.8"N 28°58'13.0" E) by electrofishing. Since the fish samples were obtained at the stream stations, the electrofishing (SAMUS 725MP) method was used to catch fish individuals. Fish sampling was done within the scope of the permission numbered "21264211-288.04-E.774109". The fish were put into containers of fresh water and immediately transported to the research laboratory. The fish were kept in aerated tanks in the laboratory and examined for helminth parasites in approximately 3–4 hours after collection. The fish were killed by severing the spinal cord behind the head, and then the total length of each fish was recorded. At necropsy, the sexes of each fish were determined macroscopically. Standard dissection and examination techniques were used to recover the helminths. Specimens were fixed using the protocols by Fernando et al. (1972), and the monogeneans were stained using the guidelines by Malmberg (1957) and Georgiev et al. (1986). All specimens were identified at the species level using the identification keys of Gussev (Gussev 1985, Gussev et al. 1987), Khotenovsky (1985), Moravec (1994), Hoffman (1999), Gibson et al. (2002), Khalil et al. (1994). Prevalence, intensity, and abundance of infections were calculated according to Bush et al. (1997). All parasitological data (seasons, host fish sex, and length difference) were analyzed using the SPSS v. 28 software package for Windows. The significance level of $p \leq 0.05$ was used.

For molecular analysis, the methodology previously described by Aydogdu et al. (2020a, b) was used to characterize the diplozoid, *Paradiplozoon homoion,* and its identity was confirmed through DNA analysis. Before DNA isolation, the samples were centrifuged at 3000 RPM in 1.5 ml microcentrifuge tubes, and the ethanol in the upper part was removed. DNA isolation was performed using the Qiagen DNA mini Kit (QIAamp DNA mini kit; Qiagen, Hilden, Germany)

following the manufacturer's instructions. The purity levels of the isolated DNA samples were measured first with the Maestrogen Nano (Maestrogen, Taiwan) spectrophotometer and then with the Qubit 4 fluorometer (Thermo Fisher Scientific, Waltham, MA, USA) systems. After isolation, DNA samples were amplified using Promega goTaq polymerase and buffers. In PCR studies, forward 5'-GGCTYRYGGNGTCGATGAAGAACGCAG-3', reverse 5'-GCCGGATCCGAATCCTGGTTAGTTTCTTTTCCT-3' primers targeting ITS2 rDNA regions that were synthesized by Sentebiolab were used. Reaction conditions and primers were optimized with reference to Matejusová et al. (2001). Post-PCR samples were validated at 805 base pairs using the Qiagen QIAxcel Advanced capillary electrophoresis system (Qiagen, Hilden, Germany). The purification and sequencing of PCR samples were performed by Sentebiolab using an ABI 3130 (Applied Biosystems Inc.) capillary electrophoresis device. The obtained sequencing results were analyzed to differentiate species using NCBI's BLAST system (Altschul et al. 1990). Sequence data were published in GenBank – Accession number OP558585 (data not shown).

For phylogenetic analyses, the sequence obtained in this study was aligned with the data in the literature using the ClustalW algorithm in the MEGA-X program (Kumar et al. 2018). As a result of the alignment, non-informative parts of the sequences were cut from the beginning and end. Then, jModeltest v. 2.1.5 (Darriba et al. 2012) program was used to determine the mutation model that best fits the data obtained. Among 56 mutation models, it was determined that the most appropriate mutation model for the data set was the GTR (general time reversible model) according to the Akaike information criterion (AIC). MrBayes 3.1.2 (Huelsenbeck et al. 2001) program was used to construct the phylogenetic tree. *Sindiplozoon* spp. sequences were used as outgroups. Markov Chain Monte Carlo analysis was carried out over four chains with two distinct runs for 10 million generations until the split frequency fell below 0.01. The saturation of the analysis (ESS values) was monitored using the Tracer v.1.7 program (Rambaut et al. 2018). 25% of the trees obtained by sampling every 1000 generations were removed by burn-in. The consensus tree obtained from the analysis was viewed and edited in the Figtree v1.4.2 (Rambaut 2014) program (Figure 7).

Results

Eighty-one individuals of *Capoeta tinca* were examined; 47.58% were determined to be infected by at least one helminth species on the gills or the intestinal tract, while 22% were infected with at least two species. A total of 234 helminths, two monogeneans, *Dactylogyrus pulcher* (Figure 1, 2) and *Paradiplozoon homoion* (Figure 3), one nematode, *Rhabdochona fortunatowi* (Figure 4, 5), and one trematode, *Allocreadium isoporum* (Figure 6), were found and reported for the first time. *Allocreadium isoporum* was the most prevalent and abundant species (Table 1).

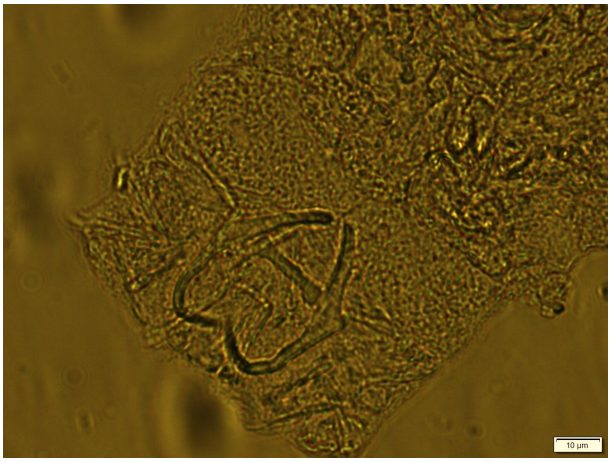

Figure 1. *Dactylogyrus pulcher* haptor.

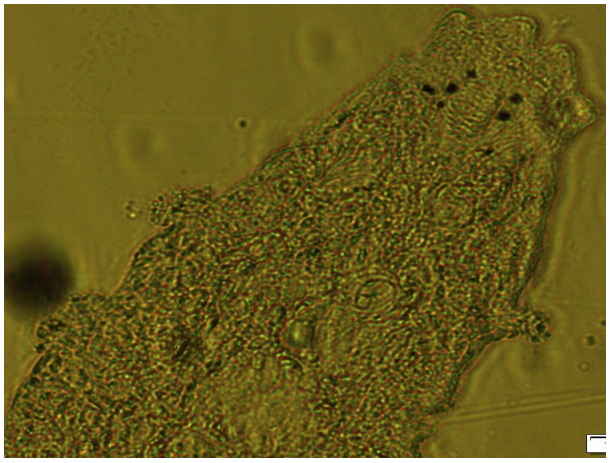

Figure 2. *Dactylogyrus pulcher* copulatory organ (Scale bar= 10 µm).

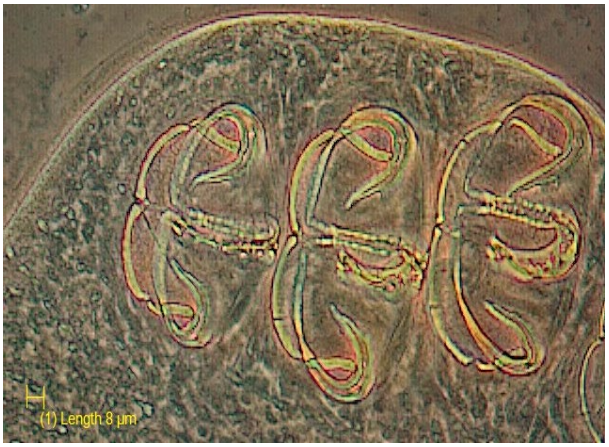

Figure 3. *Paradiplozoon homoion* clamps (Scale bar= 8 µm).

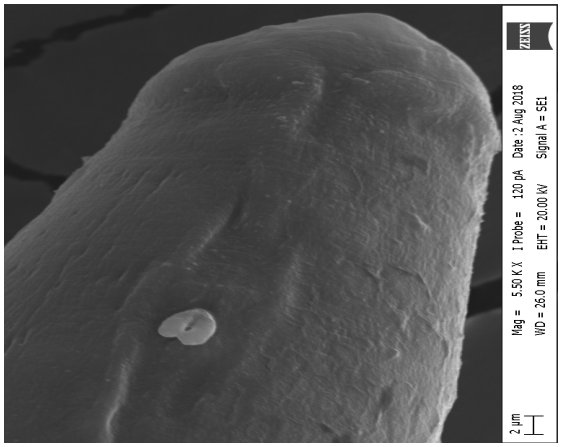

Figure 4. *R. fortunatowi* scanning electron micrographs, deirids.

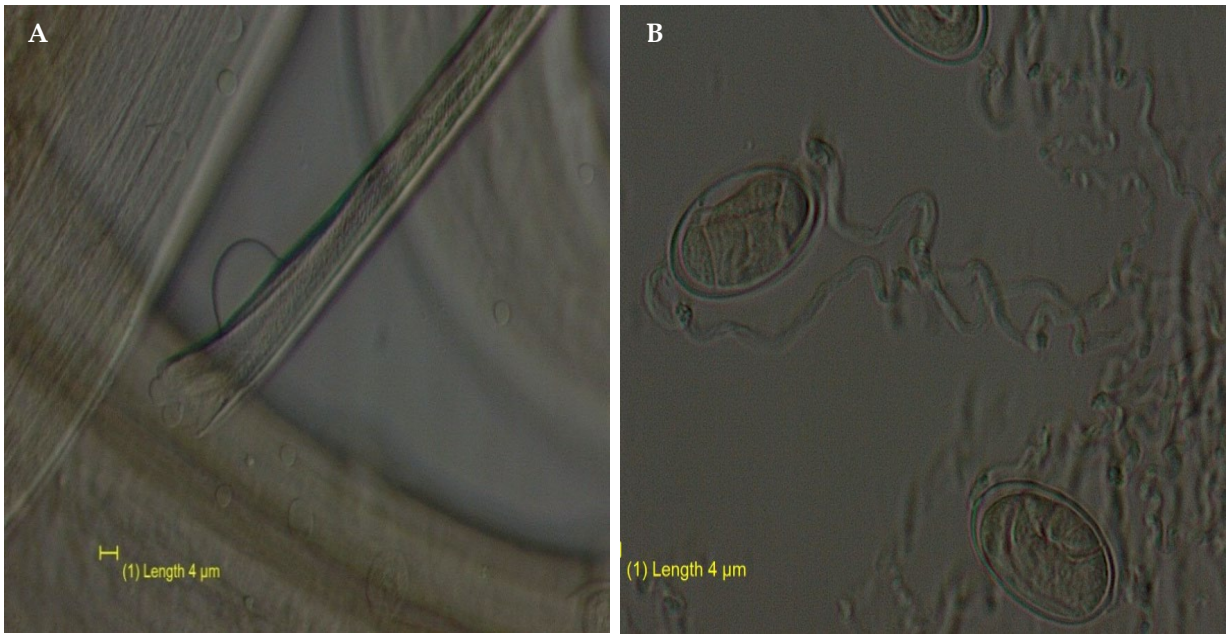

Figure 5. *Rhabdochona fortunatowi*: [A] posterior end of male; [B] fully–developed eggs (Scale bar= 4 µm).

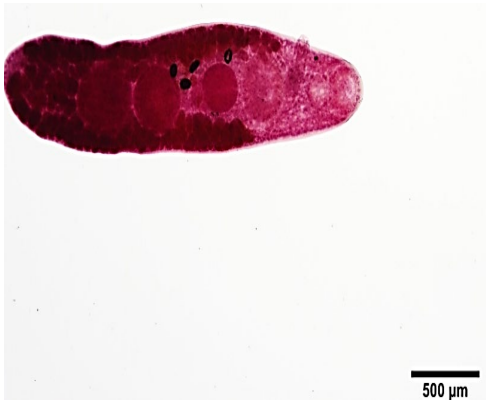

Figure 6. *Allocreadium isoporum* totalview.

Table 1. Distribution of infection value of helminth parasites in *Capoeta tinca* from Nilüfer Stream, Bursa Province.

Parasite species	Number of infected fish	Number of collected parasites	Prevalence (%)	Mean intensity	Abundance
D. pulcher	5	16	6.1	3.2	0.2
P. homoion	17	63	20	3.7	0.7
A. isoporum	27	141	33.3	5.2	1.7
R. fortunatowi	8	14	9.8	1.7	0.1

However, this is also the first molecular characterization of *P. homoion* from *C. tinca* from Turkey. The ITS2 gene was amplified for definitive diagnosis. The length of the PCR product was approximately 805 bp. Based on the BLAST analysis, the sequence result showed a 98- 100% match with *P. homoion*. All nucleotide sequences were submitted in GenBank (accession number OQ435904, http://www.ncbi.nlm.nih.gov, data not shown). As a result of the BLAST analysis, the sequences of *P. homoion* are 100% similar to accession number MT417728 sequences presented by Benovics et al. (2020), confirming the identification of the species.

In the constructed BI phylogenetic tree, the genus *Sindiplozoon* and the genus *Paradiplozoon* are separated (PP=1.0). Although the support values of the nodes vary between 0.54-1.0, the values are generally high. The sample obtained in this study was clustered with *P. homion* species within the branch containing the *Paradiplozoon genus* (PP=1.0). In light of these findings, as a result of molecular analysis, it was determined that the sample obtained from the study was *P. homion*. This coincides with the results obtained from morphological analyses (Figure 7).

The comparison of *P. homoion* in the current study was made with the twenty-five *P. homoion* samples from Turkey and other studies from different countries. During this study, *A. isoporum* was found throughout the year, with the highest prevalence values in the spring. Its highest mean intensity and abundance were also found in spring (9.1 and 5.5, respectively) (Table 2). *D. pulcher* was the most prevalent in the summer, while *P. homoion* and *R. fortunatowi* had the most prevalence in the autumn (Table 2). Differences in occurrence and infection levels of the four species during the seasons were statistically significant (*D. pulcher* (p=0.026), *P. homoion* (p=0.023), *A. isoporum* (p=0.003), *R. fortunatowi* (p=0.036)).

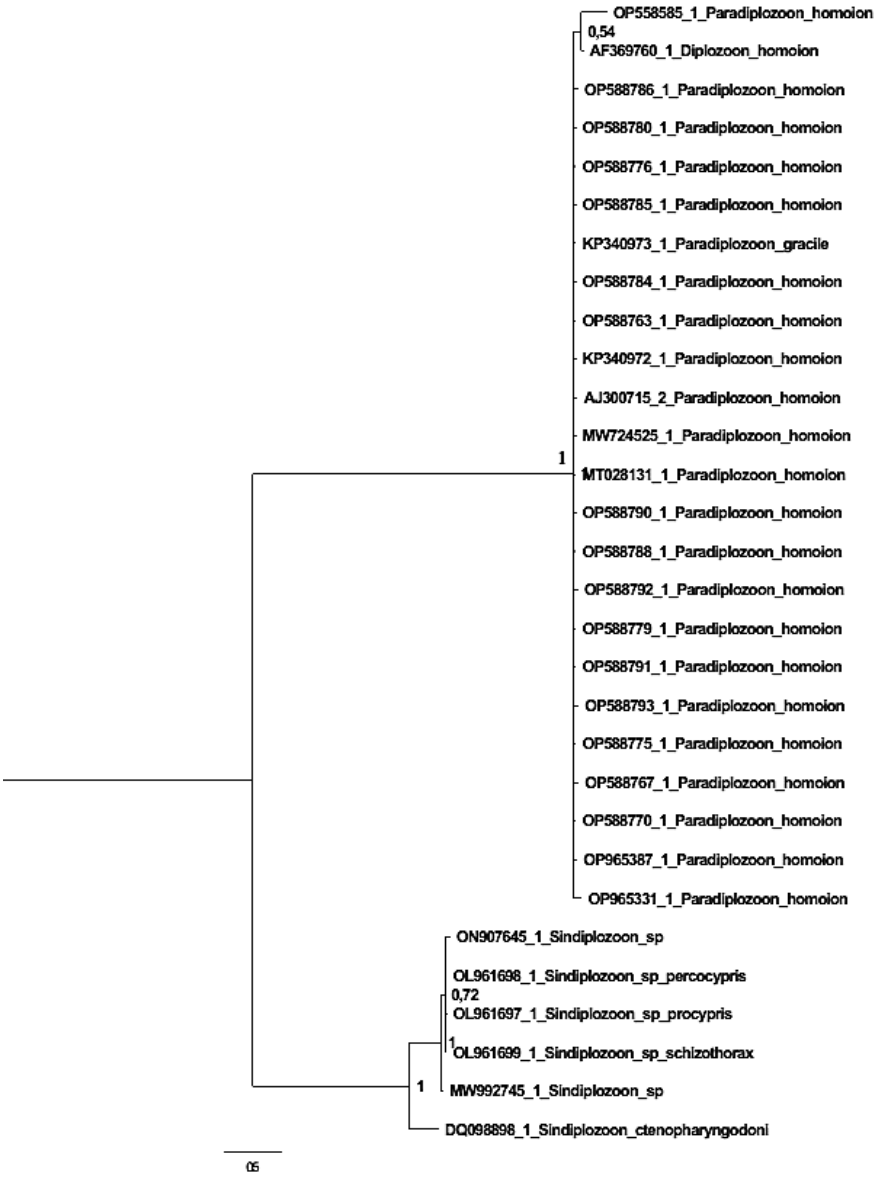

Figure 7. Phylogenetic tree of *Paradiplozoon homoion* constructed by Bayesian Inference (BI)

Helminth infection parameters also varied with total fish length. All fish size classes were infected by *P. homoion* and *A. isoporum* with prevalences of 18.7–22.2 % and 20–50%, respectively (Table 3). Infection prevalence levels for *P. homoion* were highest in fish length classes 8.5-13.5 cm long (II. group) while the mean intensity was also the highest in fish the same classes (II. group) (Table 3). *D. pulcher* and *R. fortunatowi* were not detected in length class I, otherwise, *R. fortunatowi* was the most prevalent in length class III. The highest prevalence levels of *D. pulcher* were observed in the fish lengths 13.6 < cm long, while changes in abundance levels of its infection were equal in fish length II- III groups (Table 3). Prevalences, mean intensity, and abundance were the highest in *A. isoporum* for length class I. (Table 3). The relationship between the number of *A. isoporum* and fish length was significant (p=0.041). However, no statistically significant correlation was found between the numbers of the other three parasite species (*D. pulcher*, *P. homoion,* and *R. fortunatowi*) and the host fish length (p=0.485, p=0.813, p=0.165, respectively).

The most prevalent species was *A. isoporum,* with the highest intensity and abundance in males and females (Table

4). Overall, only the total number of parasites collected from the males of *D. pulcher*, 12, was greater than that collected from the females, 4 (Table 4). However, more males than females were sampled, and no statistically significant differences were found (p=0.776). The prevalence, mean intensity, and abundance of infection of *P. homoion* were the highest in females (Table 4). Nevertheless, no statistically significant differences were found between three helminth parasites (*P. homoion*, *A. isoporum,* and *R. fortunatowi*) about the host fish sex (p=0.894, p=0.874, p=0.085, respectively).

Table 2. Distribution of infection value of helminth parasites in C.tinca from Nilüfer Stream, Bursa Province, according to seasons

Name of parasites	Infection parameters	Seasons			
		Spring 2020 (n: 20)	Summer 2020 (n: 20)	Autumn 2020 (n: 20)	Winter 2021 (n: 21)
D. pulcher	Infected Fish	–	4	1	–
	Prevalence (%)	–	20	5	–
	Mean intensity	–	3.5	2	–
	Abundance	–	0.7	0.1	–
	Total parasite no	–	14	2	–
P. homoion	Infected Fish	4	–	8	5
	Prevalence (%)	20	–	40	23.8
	Mean İntensity	2	–	4	4.6
	Abundance	0.4	–	1.6	1
	Total parasite no	8	–	32	23
A. isoporum	Infected Fish	12	5	4	6
	Prevalence (%)	60	25	20	28.5
	Mean intensity	9.1	1.2	3.7	1.6
	Abundance	5.5	0.3	0.7	0.4
	Total parasite no	110	6	15	10
R. fortunatowi	Infected Fish	–	–	4	4
	Prevalence (%)	–	–	20	19
	Mean intensity	–	–	1.7	1.7
	Abundance	–	–	0.3	0.3
	Total parasite no	–	–	7	7

Table 3. Distribution of infection value of helminth parasites in C.tinca from Nilüfer Stream, Bursa Province, according to the host length

Fish length groups (cm)	Parasite species	Infected fish	Prevalence (%)	Mean intensity	Abundance	Total parasites
3.4-8.4 (n=16) (I. Group)	*D. pulcher*	–	–	–	–	–
	P. homoion	3	18.7	3	0.3	6
	A.isoporum	8	50	11.7	5.8	94
	R.fortunatowi	–	–	–	–	–
8.5-13.5 (n=44) (II. Group)	*D. pulcher*	3	4,5	4	0.2	12
	P. homoion	10	22.2	4.8	1	48
	A.isoporum	15	33	2.4	0.8	36
	R.fortunatowi	4	9	2	0.1	8
13,6< (n=20) (III. Group)	*D. pulcher*	2	10	2	0.2	4
	P. homoion	4	20	2.2	0.4	9
	A.isoporum	4	20	2.7	5.5	11
	R.fortunatowi	4	20	1.5	0.3	6

Table 4. Distribution of infection value of helminth parasites in C.tinca from Nilüfer Stream, Bursa Province, according to the host sex.

Fish sex groups	Parasite species	Infected fish	Prevalence (%)	Mean intensity	Abundance	Total parasites
Females (n=34)	*D.pulcher*	2	5.8	2	0.1	4
	P. homoion	8	23.5	4	0.9	32
	A.isoporum	11	32.3	7.5	2.4	83
	R.fortunatowi	6	17.6	1.6	0.2	10
Males (n=47)	*D. pulcher*	3	6.3	4	0.2	12
	P. homoion	9	19.1	3.4	0.6	31
	A.isoporum	16	34	3.6	1.2	58
	R.fortunatowi	2	4.2	2	0.08	4

Discussion

This study investigated the parasitic helminth fauna from *Capoeta tinca* in the Nilüfer stream, Bursa Province, North-Western Turkey. *Allocreadium isoporum* was the dominant parasite species in host fishes in this study. To our knowledge, four parasitic helminth species detected in this study are reported for the first time parasitizing this host fish, *C. tinca*.

Dactylogyrus pulcher is very common in fish belonging to the genera *Capoeta* (Gussev 1985). This species has been recorded only in two fish species, *Capoeta capoeta* (Turgut et al. 2011) and *Capoeta trutta* (Turgut et al. 2011, Koyun et al. 2019) in Turkey so far. Additionally, it has been previously reported from freshwater fish species, namely *Capoeta capoeta gracilis*, *Capoeta damascina* and, *Capoeta barrosipersica*, *Capoeta trutta,* and *Capoeta umbla,* living in different habitats of Iran and Iraq (Molnar & Jalali 1992, Roheiaminjan & Malek 2004, Pazooki et al. 2006, Jalali & Miar 2011, Raissy & Ansari 2012, Abdullah & Abdullah 2015, Manshadi & Mohammadi 2017). This is the first record of *D. pulcher* in *C. tinca,* and Nilüfer Stream is also the first sampling locality in Turkey. In Turkey, Koyun et al. (2019) found the infection prevalence values of this species between 3.5 and 50%, while Turgut et al. (2011) noted the mixed prevalence levels of *Dactylogyrus pulcher* and *Dactylogyrus turkestanicus* in *C. capoeta* and stated that it is not possible to determine the infection values of these *Dactylogyrus* species separately.

Pazooki et al. (2006) and Koyun et al. (2019) investigated the influence of season on infection levels of this parasite. The highest prevalence of infection (20%) of *D. pulcher* in the summer samples was similar to that for the Zanjan Province by Pazooki et al. (2006). In contrast, Koyun et al. (2019) noted that this parasite species' prevalence and mean intensity levels were high, with 50% in *C. trutta* in autumn.

The variation in infection rates between *D. pulcher* and the fish length has not been studied. This study is also the first to investigate the variation in infection values of *D. pulcher* according to host fish size in Turkey. On the other hand, the variations of infection rates of *Dactylogyrus* spp. and host fish length have been investigated by Aydogdu et al. 2003, Koyun & Altunel 2007, Tekin-Ozan et al. 2008, Öztürk 2014, Aydogdu et al. 2015 and they found a positive relationship between the infection levels of *Dactylogyrus* and the length of the host fish. These study results are in agreement with the relevant studies. Contrary to this, Açıkel & Öztürk (2012) and Aydogdu & Kubilay (2017) found infection prevalence and mean intensity values of *D. vistulae* the highest in young fish. Turgut et al. (2012) and Selver et al. (2009) have demonstrated no relationship between Dactylogyrus and the host fish length and infection values.

The relationship between the level of *Dactylogyrus* species infection and the sex of the fish has been studied by Açıkel & Öztürk (2012), Öztürk (2014), Aydogdu et al. (2015), Elbay & Öztürk (2021), Aydogdu & Kubilay (2017), Açıkel & Öztürk (2012), and Aydogdu & Kubilay (2017) have found higher *Dactylogyrus infection* in male fish while Öztürk (2014) and Aydogdu et al. (2015) reported higher infection in female fish. These studies are in harmony with monogenean infection correlation with the sex of fish hosts (Blahoua et al. 2009, İbrahim 2012). In this study, based on morphological analysis, only one diplozoid species, identified as *Paradiplozoon homoion*, was found on the gills. We also confirmed the identification of the species as *P. homoion* using molecular data. In this context, in our study, 805 bp. of the ITS2 gene region was sequenced and compared with the data in the GenBank. The molecular identification and DNA sequences using the ITS2 gene marker here determined the true identity of the diplozoids from *C. tinca* as *Paradiplozoon homoion* (Figure 7). The BLAST analysis of these sequences revealed high homology (100%) with *P. homoion* sequences deposited by Benovics et al. (2020) (Submitted 26-April -2020, http://www.ncbi.nlm.nih.gov, unpublished). This is also the first molecular characterization of *P. homoion* from *C. tinca* from Turkey, based on the ITS2 sequence data. In this aspect, the present study raises the number of reports on the molecular characterization of *P. homoion* specimens collected from Turkey. *P. homoion* is the most recorded species of *Paradiplozoon* in Turkey (Aydogdu et al. 2009, Öztürk 2011, Tunç & Koyun 2018, Aydogdu et al. 2020 a, b etc.). The prevalence value calculated in this study was similar to that reported in *Alburnus albunus* by Tunç & Koyun (2018).

The seasonal variations in infection rates of this parasite in different fishes in Turkey have been studied by various authors many times. For example, Soylu (2007) and Aydogdu et al. (2020a, b) recorded the highest infection prevalences of this species in winter samples, while Koyun (2001) and Öztürk (2005) could not detect this parasite species in winter. Unlike these findings, Tunç & Koyun (2018) noted the highest prevalence of *P. homoion* infection in the summer and autumn, similar to our findings.

There are only four ichthyoparasitological studies to determine the relationships between infection levels of *P. homoion* and host fish length in Turkey (Koyun 2001, Soylu 2007, Öztürk 2011, Aydogdu et al. 2020a). Aydogdu et al. (2020a) only observed the highest infection prevalence levels in large fish. The findings in this context in our study are similar to the studies of these authors.

Concerning sex, prevalence levels of *P. homoion* were higher in female host fish than males, opposite to the highest mean intensity of infection in male fish Aydogdu et al. (2021). On the other hand, Tunç & Koyun (2018) recorded the highest infection rate of this species in male host fish individuals.

A. isoporum was the most prevalent and abundant species (Table 1). According to Özer (2021), Aydogdu et al. (2018), Mnisi (2017), and Emre & Kubilay (2019), *A. isoporum* has been previously reported in various species namely *Capoeta antalyensis*, *Capoeta angorae*, *Capoeta caelestis*, *Capoeta pestai*, and *Capoeta baliki*, all of which inhabit different regions in Turkey. They reported that the prevalence values of infection of this parasite species in the same fishes ranged from 4.4% in *C. angorae* to 38% in *C. pestai*. Comparing the above–mentioned values, the prevalence agrees with that reported by Emre & Kubilay (2019).

Regarding the seasonal variation in *Allocreadium isoporum* infection, Aydogdu et al. (2018), Mnisi (2017), and Emre & Kubilay (2019) have reported on this variation. Our findings were similar to those of Aydogdu et al. (2018), who observed the highest prevalence and intensity for *A. isoporum* in *C. antalyensis* in summer. Similar findings have also been reported in *C. pestai* in Çayköy Stream by Emre & Kubilay (2019).

The variation of infection rates of *A. isoporum* parasitizing

in *Capoeta* species and host fish length has also been studied by the researchers listed above. These authors found the highest prevalence and mean intensity levels in medium and large length sizes in contrast to our findings.

This parasite species has also been previously reported from six different fish species belonging to other genera living in different habitats from Turkey except for the genus *Capoeta*. Koyun et al. (2015, 2016) and Aydogdu & Kubilay (2017) have studied the variation of infection rates of *A. isoporum* and host fish length. Surprisingly, our finding related to *A. isoporum* was similar to that of Koyun et al. (2016), who stated the prevalence was higher in small *Oxynoemacheilus tigris*.

As to sex, Aydogdu et al. (2018) recorded the highest infection prevalence values of this parasite in males of *C. antalyensis* (20.2%) among three *Capoeta* species, while this value was almost equal for the other two species. Similarly, Mnisi (2017) reported that this species' most prevalent and abundant values were in male individuals of *C. baliki*. In contrast to these findings, Emre & Kubilay (2019) recorded the highest infection prevalence and mean intensity values of this parasite species in female individuals of *C. pestai*. The data in our study are similar to those of Aydogdu et al. (2018) and Mnisi (2017).

Rhabdochona fortunatowi has been reported in only one study in Turkey up to now (Aydogdu et al. 2021). They reported this parasite species in two *Capoeta* spp. in Turkey. The prevalence of *R. fortunatowi* varied from 19% in *C. caelestis* from Göksu River to 8.4 % in *C. angorae* from Fırnız. In the present study, the prevalence value of 9.8% was similar to that reported in *C. angorae*. Interestingly, the mean intensity value (1.7) of *R. fortunatowi* in this study was similar to the mean intensity value (2.6) of *R. fortunatowi* in *C. angorae*. In addition, the present study raises the number of studies recorded on this species to two and the number of host fishes to three.

Regarding seasonality, *R. fortunatowi* specimens were only recorded in autumn and winter. The prevalence was the highest in autumn (20 %). The mean intensity and abundance were surprisingly equal in autumn and winter (Table 2). This observation was similar to that of Aydogdu et al. (2021), who reported the prevalence value for *R. fortunatowi* in *C. caelestis* in autumn as 20.0%.

The prevalence and mean intensity of *R. fortunatowi* about host length were reported in length classes by Aydogdu et al. (2021). They have revealed the relationship between this parasite infection and the sex of two *Capoeta* species. They reported that the prevalence of *R. fortunatowi* was high in female individuals of *C. caelestis*, similar to those of the findings of our study. At the same time, they recorded its highest prevalence in male individuals of *C. angorae*. As for their mean intensity results, Aydogdu et al. (2021) recorded for this species according to the host fish sex in Turkey, 5.1 and 1 in females and 5.8 and 3.2 in males individuals of *C. caelestis* and *C. angorae*, respectively. As can be seen from these values, the highest mean intensity value of *R. fortunatowi* was recorded in males in both host fishes. The higher mean intensity of *R. fortunatowi* in male hosts in this study is consistent with Aydogdu et al. (2021).

As a result of the conducted study of 81 individuals of *Capoeta tinca*, the endemic fish species to Turkey from the Nilüfer Stream from the Northwest region of Turkey, four parasite species were identified as the monogeneans *Dactylogyrus pulcher* and *Paradiplozoon homoion*, a digenean, *Allocreadium isoporum* and one nematode, *Rhabdochona fortunatowi*. Among these parasites, the prevalence and mean intensity of *A. isoporum* was 33% 5.5, respectively, and it was found to be the most prevalent and abundant parasite species *P. homoion*, *A. isoporum*, and *R. fortunatowi* are also the first records from this host fish. Additionally, Nilüfer Stream was determined as a new locality record for *A. isoporum* and *R. fortunatowi*. Thus, new knowledge has been contributed to these helminth species' geographical distribution and host range. Moreover, the present study evaluated the prevalence, mean intensity, and abundance of helminth parasites by season, host fish length classes, and sex.

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