

Survey on Some Ectoparasitosis in *Moolgarda seheli* from Suez Canal area, Egypt

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ABSTRACT

This survey study has been applied to a total number of 200 *Moolgarda seheli* that collected randomly and seasonally from different areas of the Suez Canal at Ismailia Governorate. Infected fish showed no obvious clinical abnormalities except in case of heavy infestation with the ectoparasites, where some infested fishes revealed respiratory manifestation and surface swimming. Other fishes showed hemorrhagic areas on the gill cover, abdomen, and fins. The results of this survey revealed 2 phyla of economically important fish parasites which were three copepods (*Lernanthropus* species, *Caligus lichiae*, and *Lepeophtheirus lichiae*) isolated from the gills and one monogenean (*Benedenia sekii*) isolated from the gill and the buccal cavity of all examined fish. The total prevalence of infestation was 31% where *Lernanthropus*, *Caligus* species and monogenea were 24.5%, 5% and 13%; respectively while the mixed infestation between crustaceans with monogenea was 7%. The seasonal prevalence of ectoparasitic infestation was the highest in winter (67.5%) followed by spring then autumn and the lowest was summer (10%). The highest infestation of *Lernanthropus* species was recorded in the winter (50%) and the lowest in summer (10%). On other hand, the highest infestation of *Caligus* was highest in the spring (33.33%) and disappeared in the other seasons. The seasonal prevalence of monogenean infestation was the highest in the spring (43.33%) and disappeared in the autumn and summer. Molecular identification of *Benedenia* species using PCR analysis of the 28SrRNA (mix of C1/D2 pairs) generated larger sequence fragments which were amplicons at approx. 800 bp. The partial sequencing and phylogenetics of the positive sample revealed that our sample was closer related to *Benedenia sekii* followed by *Benedenia sciaenae* from Australia which were 97.9% and 97.2%; respectively. The histopathological changes of infested fish with ectoparasite revealed severe atrophy of the gill lamellae along with mechanical destruction, other fish revealed focal infiltrations with leukocytes, in addition to congestion of the gill arch.

INTRODUCTION

The objectives of this research are to provide adequate knowledge about the most ectoparasitic diseases affecting *Moolgarda seheli* from Suez Canal area to detect

the clinical picture and post mortem lesions of these diseases on the infested fish. To study the total and seasonal prevalence's of these diseases. To benefit with PCR analysis by using 28 SrRNA (mix of C1/D2 pairs) as marker for identification of one fish parasite (*Benedenia* species) and phylogenesis with others in the same genera. To study histopathological alterations in infested fish with parasites.

Over the past few years in Egypt, marine sector of the aquaculture industry has been developed to cover the limitation of the freshwater resources usage. *Moolgarda seheli* belongs to family *Mugilidae* that consists around the world of more than 72 species from 17 fish genera. It is one of the commercially important fish species in Suez Bay and Egypt, although it has a lower growth rate, fetches a higher market price compared to the other mullet in Egypt because of its highly appreciated taste (Nelson, 2006). With the development of semi- intensive and intensive fish farming. The importance of parasites as disease-causing agents has become more evident, because of their ability to evolve rapidly the most serious limiting factors in aquaculture (Antonelli *et al.*, 2016). Ectoparasite infestation lead to great economic losses due to not only resulted from direct harm to fish, but also from disfigurement which rendered fish grown for food and ornamental fish unsuitable for sale, thus impose a big loss to fish industry (Piasecki *et al.*, 2004). Crustacean diseases cause massive economic losses to fisheries not only from killing, stunting, or damaging these fishes, but also cause mortalities or impair immature fishes or are unfit for sale (Ali *et al.*, 2015). Copepods comprise the largest group of crustacean parasites on fish causing economical loss (Jithendran *et al.*, 2008) such as caligus species as mentioned by Boxshall and El-Rashidy (2009). Also, the presence of more than 100 species of the gill parasite *Lernanthropus* can cause high mortality in small juvenile of the European sea bass (*Dicentrarchus labrax*). (Athanasopoulou *et al.*, 2001) and in *Mugil cephalus* and *Moolgarda seheli* (Hassanin, 2016). Monogeneans have been considered as a factor limiting aquaculture productivity as it frequently causes mixed infections with other parasites and secondary bacterial infections (Antonelli *et al.*, 2010) such as *Neobenedenia* which considered as harmful ectoparasite that can cause disease and mortality in aquaculture systems (Brazenor *et al.*, 2018). The external parasites have various patterns in spatial distribution, patterns that influence climate change. Climate change may be conducive to the production and distribution of parasites. This could have economic impacts on marine ecosystem function and structure (Morris & Costello, 2019). mostly monogenetic infestation in marine aquaculture systems increased in summer season and decreased in winter season (Bayoumy, 2003; Abdel-Mawla & Shalaby, 2014), others proved that spring season is the highest season as El-Lamie (2007) and Eissa *et al.* (2016, a). The crustaceans attachment sites were the body surface and gill cavities of the fish (Maran *et al.*, 2009) with higher infestation in spring season and lower in winter one (Faisal, 2008). Clinical sigs appeared in infested fishes associated with intensity of parasites as low intensity showed no clinical sigs, no harm on fish but when fish are crowded or stressed, and water quality deteriorates,

parasites multiply rapidly and cause serious damage. Typically, heavily infected fish don't eat well and exhibit low growth rate, discoloration and mucus secretion. Weakened fish become more susceptible to opportunistic bacterial pathogens presented in the water and became pathogenic microorganisms that resulting in major stock losses (**Kayis et al., 2009**). The ability of scientists to describe and define biodiversity in parasitology has been transformed by molecular techniques (primarily DNA sequencing) (**Bickford et al., 2007; Detwiler et al., 2010; Padial et al., 2010; Sepúlveda & González, 2019**). DNA barcoding, one of the best of genetic measures, provides a means of identifying known species by comparing sequence similarities, and has shown strong resolution at the species level for different parasite groups such as monogenea (**Chaabane et al., 2016 ; Sepúlveda & González, 2019**).

2. MATERIALS AND METHODS

2.1.Fish:

A total number of 200 of *Moolgarda seheli* of different lengths and various body weights were collected randomly and seasonally from different areas of Suez Canal at Ismailia Province. The collected fish samples were identified according to Langdon and Jones (2002).

2.2.Clinical picture:

Clinical examination has been done on the live or freshly dead fish. Fish specimens were grossly examined for detection of any ectoparasites and any clinical abnormalities according to **Amlacker (1970)** and the postmortem examination according to the methods described by **Lucky (1977)**

2.3.Parasitological examination:

Fish specimens were examined macroscopically and microscopically then collected crustacean parasites were stained and fixed according to **Lucky (1977)** while monogenetic trematodes were stained and fixed according to **Pritchard and Kruse (1982)** .

2.4.Molecular detection of *Benedenia* species (Monogenetic trematodes):

The genomic DNA extraction and purification of the parasite was performed using the procedures provided by ABT DNA Mini Extraction Kit (spin Column) (Catalogue number: ABT001) of the collected parasites preserved in 70% ethanol in Eppendorf tube. Extracted DNA was stored in hydration solution at 4 °C. PCR amplification for the ribosomal 28S RNA 28S partial sequences from purified genomic DNA using specific primer combinations C1/D2 (approx.800 bp) where C1 (5'-ACCCGCTGAATTTAAGCAT- 3') as forward primer and D2 (5'-TGGTCCGTGTTTCAAGAC - 3') as reverse primer, as discussed by **Chisholm et al. (2001); Perkins et al. (2009); Moreira et al. (2019)** . PCR was carried out using of 50 µL of total reaction volume (2X Red master mix1X: Forward primer 20 picomole, Reverse primer20 picomole, DNA extract100 ng, Nuclease free water Up to 50µL). Standard cycle conditions for PCR were set as initial denaturation for 3 min at 95°C, followed by 35 cycles of 30 s at 95°C, 30 s at 50°C, 90 s at 72°C and final extension of 5 minutes at 72°C. To confirm the targeted PCR amplification, five µl of the PCR product was electrophoresed along with 100bp DNA molecular weight 1% agarose gel containing

ethidium bromide (at the rate of 0.5µg/ml) at constant 80V for 30 min in 1X TAE buffer. The amplified product was visualized as a single compact band of expected size under UV light and documented by Samsung Note 4 smart phone

Sequencing of the PCR products using the amplified PCR products were submitted to Solgent Co Ltd (South Korea) for gel purification and sequencing. PCR using Solgent EF-Taq, PCR Machine name: 9700(ABI).

2.5.DNA Alignment and Phylogenetic Analysis:

Nucleotide sequences were downloaded from GenBank and aligned with the identified sequences, using MAFFT alignment. Phylogenetic trees were constructed using the Neighbor joining method, employing the Kimura 2-parameter method. The trees were assessed using 1000 bootstrap replicates. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The optimal tree with the sum of branch length = 1.01 is shown. This analysis involved 48 nucleotide sequences. All ambiguous positions were removed for each sequence pair. Subsequently, the 28S rRNA alignment was trimmed to remove sequences that could not be aligned unambiguously and sequences from the genes concatenated to give a final alignment length 397 positions in the final dataset. Evolutionary analyses were conducted in MEGA. (Kumar *et al.*, 2018)

2.6.Histopathological examination- :

Specimens for histopathological techniques were freshly taken from affected gills of naturally infested fish. Specimens were trimmed and fixed in 10% phosphate buffered formalin, processed routinely and stained with H&E stain then examined (Roberts, 2001).

RESULTS

3.1.Clinical picture and postmortem finding:

The clinical examination of naturally infected *Moolgarda seheli* showed no noticeable clinical abnormalities except in case of heavy infestation with the copepod crustacean parasites. Some infested fish revealed respiratory manifestation, surface swimming and opened mouth. Other fish showed hemorrhagic area on gill cover, abdomen and fins. In some cases, the *Lernanthropus* species was seen by the naked eye (egg sac of copepods) in the form of black lines among the gill filaments (Figure 1.D). In case of family Capsalidae large number of visible, white colored parasites were found attached to the gill filaments and/or buccal cavity by its haptors. Infected gills were covered with mucous layer. Heavily infested gill showed excessive mucous secretions and paleness (Figure 1. A, B&C).

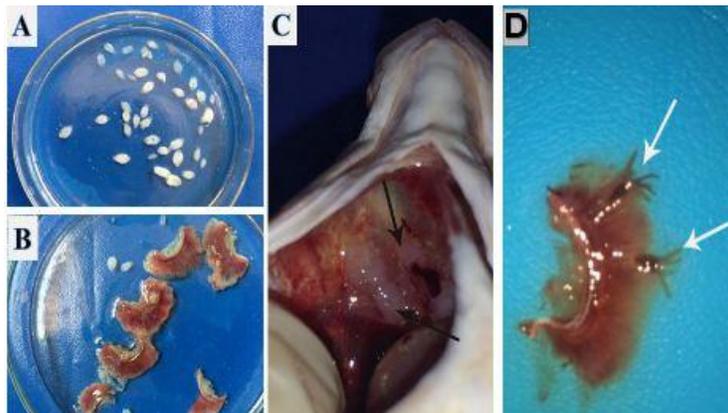


Figure 1: showing ectoparasitic infestation in the *Moolgarda seheli* as **A,B:** *Benedenia* species. in petri dish collected from different *M.seheli* **C:** buccal cavity and gills operculum showing *Benedenia* sp. (arrows). **D:** gill showing egg sacs of females *Lernanthropus* species.

Parasitological examination of all examined fish revealed 3 copepods parasites 1 species of family: Lernanthropidae (*Lernanthropus* species) isolated from the gills of *Moolgarda seheli* was the same as described by **Blainville (1822)**. Mandible was slender had 7 denticles. The first maxilla consists of 3 segments; the terminal is conical, and the basal segment has 2 distal broad spines. The second maxilla consists of segments; the terminal segment was provided with 2 rows of blunt teeth and blunt spines on the inner margins. The third segment had single distal spine. The exopod had 5 short distal spines, while the endopod had slender bristled seta. The 5th legs were absent. The female is somewhat cylindrical and measured 3.1 mm and 1 mm in width at the middle of the body. The head separated by a constriction from the rest of the body. The egg strings are elongated and uniseriate, strongly flattened eggs (Figure 2., a & b). Other 2 species of family: Caligidae (one of genus caligus: *Caligus lichiae* and other one genus Lepeophtheirus: *Lepeophtheirus lichiae*). *Caligus lichiae* is a crustacean parasite was isolated from the gills of infested fishes. These species can be distinguished by posterolateral corners of genital complex projecting laterally; female maxilliped with small myxal process. the corpus of the male maxilliped has three triangular processes along the myxal margin. The fourth process is minute and located proximally on the myxal margin the raised array of denticles on the ventral surface of the apron of leg 3 comprised 14–19 denticles (Figure 3. F). It was the same described by **Brian (1906)**. *Lepeophtheirus lichiae* was isolated from the gills of the infested fishes. Their morphological characters were as described by **Barnard (1948)**. Adult female characterized by caligiform body, comprising cephalothorax incorporating first to third pedigerous somites, free fourth pedigerous somite, genital complex and 1-segmented abdomen. Dorsal cephalothoracic shield subcircular, excluding marginal membranes, lateral margins evenly convex and ornamented with array of about 14 small dorsal sensilla plus 13 small compound sensilla beneath marginal membrane along each side, anteromedial part of frontal plate ornamented with numerous sensilla. The most obvious distinguishing character of *L. lichiae* is the extreme development of the spiniform fifth leg where it was conical, spinous process located behind lobate posterolateral corner of genital complex and extending posteriorly slightly beyond mid-length of caudal ramus. The length of spinous fifth leg was about 83% of length of genital complex (**Sakarya et al., 2019**) (Figure 3., G&H). Also one monogenetic trematodes of family: Capsalidae (*Benedenia sekii*) was isolated from the gill and oral cavity of *M. seheli* with range (2-7) per fish. *Benedenia sekii* was characterized by broad body where body margin extending to anterior edge of anterior attachment organs. Pharynx was larger than anterior attachment organs. Haptor was larger, circular and equipped with relatively small accessory sclerites lying just posterior to haptor center. Haptoral tendons were visible. It was identified based on **Yamaguti (1937)**; **Whittington et al. (2001)**, where can be distinguished from other species by a combination of the following characters: broad body; tiny anterior and posterior hamuli relative to accessory sclerites; all median sclerites located posteriorly on haptor; details of marginal valve; long thin penis; and close proximity of common genital pore and vaginal pore (Figure 4).

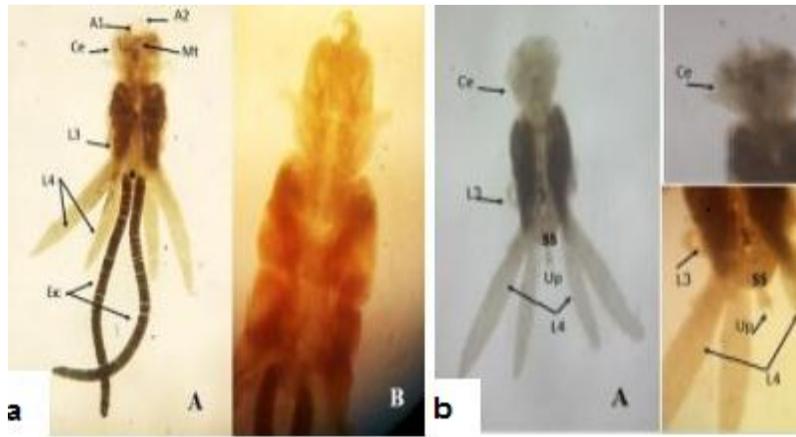


Figure 2: showing the Light photomicrograph of Genus: *Lernanthropus* a: female of *Lernanthropus* sp. b: male of *Lernanthropus* species.

A: whole body copepod. **B:** lateral view in the photo of female and anterior part in the photo of male **C:** posterior end. **A1:** first antenna; **A2:** second antenna; **Mt:** mouth tube; **M:** maxilliped; **M2:** second maxilla; **Ce:** cephalothorax; **L1:** 1st thoracic leg; **L2:** 2nd leg; **L3:** 3rd leg; **L4:** 4th leg; **a:** abdomen; **SS:** spermatophore sac; **Up:** Uropods; **Ec:** egg sac

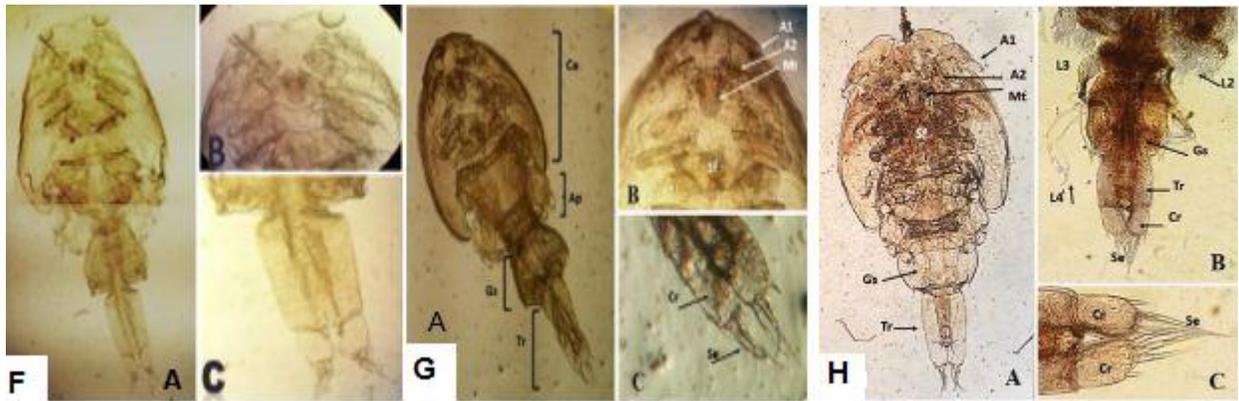


Figure 3: showing the Light photomicrograph of Family: Caligidae F: female of *Caligus lichiae* G : female of *Lepeophtheirus lichiae* H: male of *Lepeophtheirus lichiae* A: whole body of copepod, **B:** anterior part of Cephalothorax. **C:** posterior end. Lun: lunule; Fp: Frontal plate; **A1:** first antenna; **A2:** second antenna; **Mt:** mouth tube; **M:** maxilliped; **M2:** second maxilla; **Sf:** Sternal furca; **L1:** 1st thoracic leg; **L2:** 2nd leg; **L3:** 3rd leg; **L4:** 4th leg; **Es:** egg sac; **Ce:** cephalothorax; **Ap:** Apron; **GS:** genital segment; **abd:** abdomen; **Cr:** Caudal rami; **S:** spine.

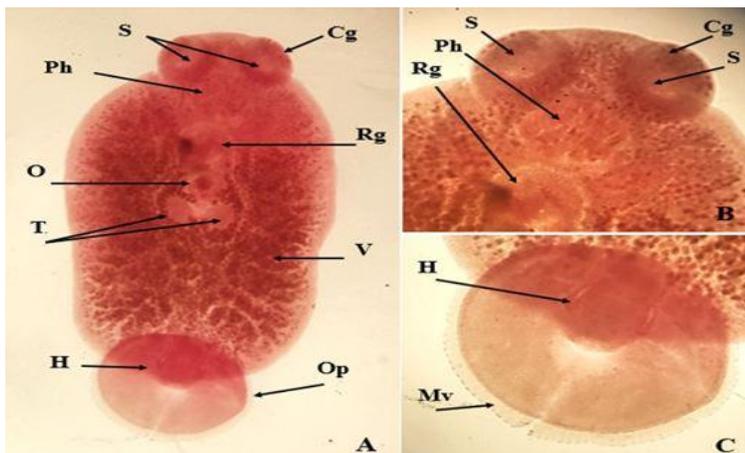


Figure 4: Monogenean parasite isolated from *Moolgarda seheli* A: whole fluke of *Benedenia sekii* stained with alum carmine **B:** Anterior end. **C:** opisthaptor of *benedenia*. **Cg:** Cephalic gland, **S:** Sucker, **Ph:** Pharynx, **Rg:** Region of genitalia, **O:** Ovary, **T:** Testes, **V:** Vetelline glands, **Op:** opisthaptor, **Mv:** Marginal valve, **H:** Hooks.

3.3. Molecular detection of *Benedenia* species (Monogenetic trematodes):

Recognition of *Benedenia* species (family: Capsalidae, monogeneans) used 28S rRNA gene selected the target sequence of C1/D2 primer combinations. The results obtained upon gel electrophoresis analysis of clearly visible bands were detected around 800bp sequence.

3.4. DNA sequence characteristics:

Primer C1/D2 pairs for 28SrRNA generated larger sequence fragments (approx. 800 bp) but because alignment was ambiguous, were excluded from analyses reducing the final number of characters to only approximately 397 bp after removing the gaps which used in analyses for 48 sequence in family Capsalidae. These sequences were selected from GenBank blast result of the *Benedenia* query sample.

3.5. Phylogenetic analyses:

The phylogenetic tree of family capsalidae split into three major clades (Figure 5) .The Sequences of C1 28S rRNA of benedenia species taken from Egypt (Ismailia) (sequenced in this study) and recorded in this study showed a close relationship between species that was recorded from NCBI (National Center for Biotechnology Information). The best similarity of benedenia species (query sample) was recorded with *Benedenia sekii* from Australia (FJ971971.1) which was 97.9% followed by 98 bootstrap value and *Benedenia sciaenae* from Australia (FJ971970.1) which was 97.2% followed by 94 bootstrap value were these species in the same genus *Benedeniinae*. The least similarity was recorded with *Entobdella stenolepis* from Canada (FJ971991.1) which was 86.3% and *Capsala martinieri* from South Africa (FJ971980.1) which was 87.6% were these species in different genera (*Entobdella* and *Capsala*) other than *Benedeniinae* (Table 1) .

3.6. Prevalence and seasonal variations:

As shown in Table 2 ,the total prevalence of infestation was (31%) where the total prevalence of *Lernanthropus* was (24.5%), *Caligus* Species was (5%) and monogenea was (13%). The total prevalence of mixed infestation between crustaceans with monogenea was (7%). The seasonal prevalence of parasitic infestation was mostly highest in winter season and the lowest was summer season as in *Lernanthropus* species Infestation. On other hand, highest infestation of caligus was recorded the highest in the spring season and disappeared in the other seasons and monogenean infestation was highest in the spring season and disappeared in the autumn and summer seasons .

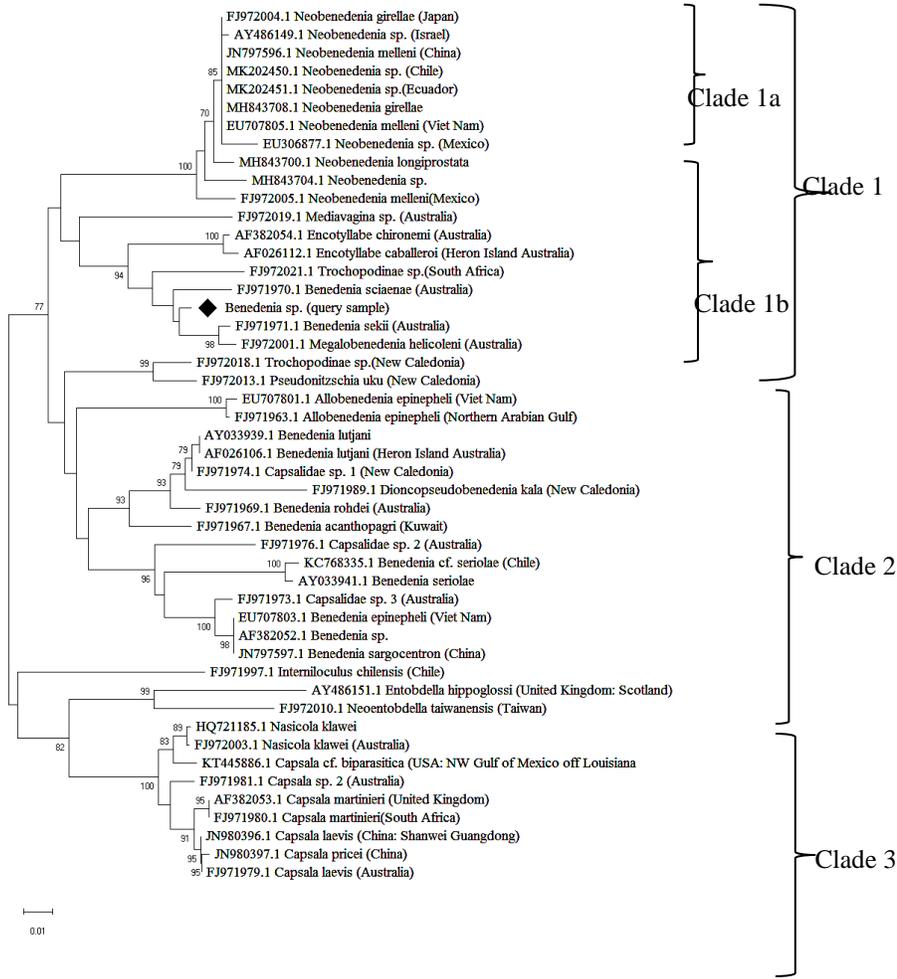


Figure 5: phylogenetic tree based on 28S rRNA of *Benedenia* spp. from Egypt (Ismailia) and other Sequences from GenBank, inferred using the Neighbor-Joining method, Kimura 2-parameter model, supporting with 1000 bootstrap which shown next to the branches. ◆ Sequences of C1 primer of benedenia spp. taken from Egypt (Ismailia).

Table 1: showing Sequence Identity Matrix of the *Benedenia* sp (query sample) (sequenced in this study) with the other sequence from GenBank.

Seq->	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1 <i>Benedenia</i> sp.(Query sample)	100	94.4%	97.9%	97.2%	94.4%	89.4%	91.6%	90.4%	90.9%	91.1%	90.4%	90.1%	89.9%	87.1%	88.9%	87.6%	86.3%
2 AF026112.1 <i>Encotyllabe caballeroi</i> (Heron Island, Australia)	94.4%	100	93.1%	93.9%	91.1%	88.1%	89.1%	88.6%	88.4%	89.6%	88.6%	87.4%	88.1%	85.3%	86.9%	85.6%	83.6%
3 FJ971971.1 <i>Benedenia sekii</i> (Australia)	97.9%	93.1%	100	96.4%	95.9%	89.4%	90.1%	88.9%	91.1%	90.4%	88.9%	89.9%	88.4%	86.1%	87.4%	85.8%	84.6%
4 FJ971970.1 <i>Benedenia sciaenae</i> (Australia)	97.2%	93.9%	96.4%	100	94.2%	89.6%	90.6%	88.9%	90.6%	89.4%	88.9%	90.1%	88.4%	87.1%	87.9%	86.3%	84.6%
5 FJ972021.1 <i>Trochopodinae</i> sp.(South Africa)	94.4%	91.1%	95.9%	94.2%	100	87.1%	87.4%	89.6%	88.1%	88.4%	89.6%	87.9%	88.6%	85.8%	87.4%	85.6%	83.8%
6 EU070803.1 <i>Benedenia epinepheli</i> (Viet Nam)	89.4%	88.1%	89.4%	89.6%	87.1%	100	90.6%	87.9%	93.6%	92.1%	87.9%	92.4%	87.4%	93.4%	86.3%	85.6%	85.3%
7 FJ971963.1 <i>Allobenedenia epinepheli</i> (Northern Arabian Gulf)	91.6%	89.1%	90.1%	90.6%	87.4%	90.6%	100	88.6%	90.1%	90.6%	88.6%	90.1%	87.9%	89.1%	87.1%	86.6%	87.1%
8 EU070805.1 <i>Neobenedenia melleni</i> (Viet Nam)	90.4%	88.6%	88.9%	88.9%	89.6%	87.9%	88.6%	89.1%	100	89.9%	89.9%	86.1%	87.4%	87.4%	83.8%		
9 AF026106.1 <i>Benedenia lutjani</i> (Heron Island, Australia)	90.9%	88.4%	91.1%	90.6%	88.1%	93.6%	90.1%	89.1%	89.2%	95.7%	100	89.1%	89.1%	90.4%	86.1%	85.6%	84.6%
10 FJ971967.1 <i>Benedenia acanthopagri</i> (Kuwait)	91.1%	89.6%	90.4%	89.4%	88.4%	92.1%	90.6%	89.4%	95.7%	89.4%	89.4%	100	94.9%	89.9%	89.9%	86.1%	83.8%
11 FJ972004.1 <i>Neobenedenia girellae</i> (Japan)	90.4%	88.6%	88.9%	88.9%	89.6%	87.9%	88.6%	100	89.1%	89.4%	89.9%	89.9%	100	89.9%	89.9%	86.1%	83.8%
12 FJ971969.1 <i>Benedenia rohdei</i> (Australia)	90.1%	87.4%	89.9%	90.1%	87.9%	92.4%	90.1%	89.9%	98.2%	94.9%	89.9%	89.9%	89.9%	100	89.9%	86.1%	83.8%
13 MH843700.1 <i>Neobenedenia longiprostata</i>	89.9%	88.1%	88.4%	88.4%	88.6%	87.4%	87.9%	98.9%	89.1%	89.4%	98.9%	89.9%	89.9%	89.9%	100	85.6%	83.1%
14 KC768335.1 <i>Benedenia cf. seriolae</i> (Chile)	87.1%	85.3%	86.1%	87.1%	85.8%	93.4%	89.1%	86.1%	90.4%	90.4%	86.1%	89.8%	85.6%	85.6%	85.6%	100	83.6%
15 FJ972003.1 <i>Nasicola klawei</i> (Australia)	88.9%	86.9%	87.4%	87.9%	87.4%	86.3%	87.1%	87.4%	86.1%	87.3%	87.4%	86.1%	86.9%	85.6%	87.4%	87.4%	100
16 FJ971980.1 <i>Capsala martinieri</i> (South Africa)	87.6%	85.6%	85.8%	86.3%	85.6%	85.6%	86.6%	87.4%	85.6%	86.8%	87.4%	85.1%	86.9%	85.3%	87.4%	89.1%	89.1%
17 FJ971991.1 <i>Entobdella stenolepis</i> (Canada)	86.3%	83.6%	84.6%	84.6%	83.8%	85.3%	87.1%	83.8%	84.6%	84.8%	83.8%	83.8%	83.1%	83.6%	88.6%	89.1%	89.1%

Table 2:Total and Seasonal prevalence of ectoparasites infestation in examined *Moolgarda seheli*

Season	<i>Lernanthropus</i> species		<i>Caligus</i> species		Monogenea (<i>Benedenia</i> species)		Total parasitic infection	
	Prevalence	Number of infested fishes	Prevalence	Number of infested fishes	Prevalence	Number of infested	Prevalence	Number of infested
Summer (n=30)	10%	3	0%	0	0%	0	10%	3
Autumn (n=100)	12%	12	0%	0	0%	0	12%	12
Winter (n=40)	50%	20	0%	0	32.5%	13	67.5%	27
Spring (n=30)	46.67%	14	33.33%	10	43.33%	13	66.67%	20
Total (n=200)	24.5%	49	5%	10	13%	26	31%	62

n examined fish per season

3.7. Histopathological findings:

As shown in Figure) microscopical examination of the gills of naturally infested *Moolgarda seheli* with *Lernanthropus* species showed section of parasite (arrows) that causing severe destruction and massive inflammatory reaction (stars). Higher magnification of gills showed cross section of the parasite and severe hyperplasia and leukocytic infiltration of gill lamellae, along with congestion. While gills infested with *Caligus* species showed sever destruction and complete loss of gill lamellae. Gills infested with monogenea species showed severe congestion and hemorrhages at the base of the gill arch as well as the primary lamellae along with destruction of gill lamellae.

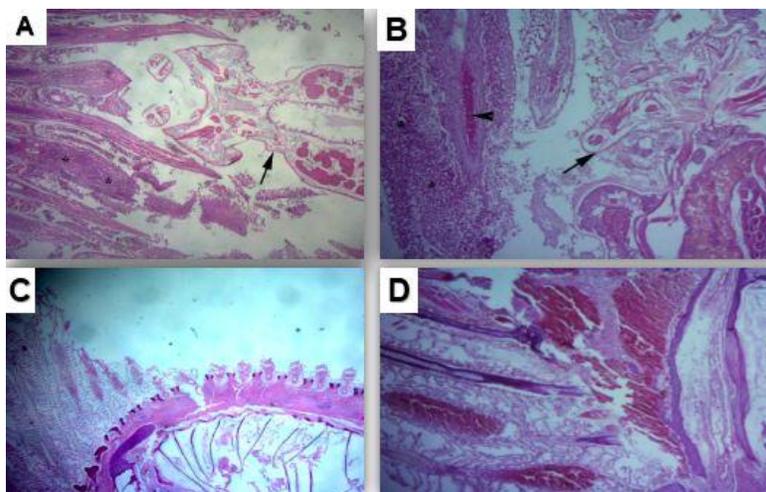


Figure 6:The histopathology of gills of *Moolgarda seheli* **A:** Gills infested with *Lernanthropus* species. showing section of parasite (arrows) that causing severe destruction and massive inflammatory reaction (stars). **B:** Higher magnification of gills infested with *Lernanthropus* species. showing cross section of the parasite and severe hyperplasia and leukocytic infiltration of gill lamellae (arrow heads, along with congestion (arrowhead). **C:** Gills infested with *Caligus* species. showing severe destruction and complete loss of gill lamellae. **D:** Gills infested with monogenea sp. showing severe congestion and hemorrhages at the base of the gill arch as well as the primary lamellae along with destruction of gill lamellae, H&E. A&C, X 40. B&D, X 100.

DISCUSSION

The main clinical sign of naturally infested *Moolgarda seheli* showed no obvious clinical abnormalities except in case of heavy infestation with the copepod crustacean parasites. The pervious results agreed with **El-Deen *et al.* (2013)**, **Abdel-Mowla *et al.* (2015)** and **Eissa *et al.* (2016)** . Regarding the postmortem examination of gills, it revealed marbling appearance with excessive mucus secretion and sticking of gill tips and grayish

discoloration this result agreed with that described by **Osman (2005)**. The previous result could be likened to the severe irritation caused by the parasite's movement and feeding activities. Excessive mucus secretion may also act as defense mechanism by which the host tries desperately to get rid of the irritating parasites. Gill marbling results from blood circulation obstruction in the branch filaments resulting in their destruction as a result of parasite feeding and hypertrophy pressure. This result agreed with **Abdel-Mowla & El-Ekiaby (2012)**; **El-Deen et al. (2013)**; **Eissa et al. (2017 b)** and **Qorany (2020)**. *Lernanthropus* species was isolated from the gills of *M. seheli* this agreed with the result obtained by **El-Deen et al. (2013)** and **Hassanin (2016)** who isolated the same parasite from *Mugil cephalus* and *Moolgarda seheli*. *Caligus lichiae* was isolated from the gills of *M. seheli*. The morphological feature was confirmed by **Brian (1906)**. This results was in agreement with that obtained by **Özak et al. (2019)** who collected from *Lichia amia* (Linnaeus) and from a second Carangid, *Seriola dumerili* (Risso), where both caught in the Gulf of Iskenderun, Turkey they mentioned that the *C. lichiae* is either extremely rare or has been confused with another species so they declare the write description of this species. *Lepeophtheirus lichiae* was isolated from the gills of *Moolgarda seheli*. The morphological feature was confirmed by **Barnard (1948)** and agreed with the result obtained by **Sakarya et al. (2019)** who collected from the dorsal body surface of the leerfish, *Lichia amia* (Linnaeus) caught in North-Eastern Mediterranean waters off the Turkish coast. *Benedenia sekii* (Family: Capsalidae) was isolated from gills and oral cavity of the *M. seheli* range from 2-7 parasites per fish. Its morphological character was agreed with **Sharples & Evans (1995)** and **Maran et al. (2014)** who obtained the same parasite from the body surface of *snapper Pagrus auratus*. Regarding the identification of *Benedenia species* (Family: Capsalidae monogeneans) parasite using PCR, where based on traditional morphological characters (different mainly by possession of an aseptate) Benedeniinae was large subfamilies consist of 13 genera and approximately 51 species, which represent about >25% of Capsalidae diversity (**Whittington, 2004**). The polyphyly of the Benedeniinae indicate extensively that relationships were widely misunderstood in this subfamily in addition to neobenedenia could be placed in a separate subfamily. The confusion of composition of the Benedeniinae, not realistic for a new subfamily to be built without first reexamining what the subfamily to which Neobenedenia presently belongs (Perkins et al., 2009). Therefore, the molecular methods set out here offer useful instruments for future studies of specimens of various fish species and geographical origins. In this study, molecular identification of *Benedenia* species using PCR analysis of the 28SrRNA (mix of C1/D2 pairs) generated larger sequence fragments which were a common molecular identification. The 28SrRNA (C1/D2 pairs) amplicons at approx. 800 bp were agreed with Chisholm et al. (2001) and Perkins et al. (2009). In some of the parasite taxas, many genetic studies have found cryptic complexes. (Bray, 2005). In these cases, morphological analyses showed a one parasite species infecting several hosts; however, the genetic information revealed several parasite species showing high host specificity (**Poulin & Keeney, 2008**). Therefore, partial sequencing and phylogenetics of 28S rRNA gene of C1/D2 pairs isolated from the positive sample with various nucleotide sequences were downloaded from GenBank (NCBI) and aligned with the identified sequences were analyzed. The results revealed that our sample were more closer related to *Benedenia sekii* from Australia (FJ971971.1) which was 97.9% followed by *Benedenia sciaenae* from Australia (FJ971970.1) which was 97.2% were these species in the same

genus *Benedeniinae*, while was far from *Entobdella stenolepis* from Canada (FJ971991.1) and *Capsala martinieri* from South Africa (FJ971980.1) were these species in different genera (*Entobdella* and *Capsala*) other than *Benedeniinae* and this result was agreed with **Perkins et al. (2009)**. Concerning the total prevalence of *Lernanthropus* species infestation of the examined *M. seheli* for was 24.5%. This result was nearly agreed with the result obtained by **El-Deen et al. (2013)** who recorded about 20% and **Abouzaid et al. (2018)** was 18% of the examined sea bass. While this result was higher than that obtained by **Hassanin (2016)** which recorded as 5.14% of *Lernanthropus* species from *M.seheli*. Concerning the total prevalence of *Caligus* Species infestation of the examined *M. seheli* was 5% (*Lepeophtheirus* was 4% *Caligus* was 1%). This result was closer to that obtained by **Jiann Hsiung et al. (2001)** which was 5.3% who detected *Caligus* species among the grey mullet, **Abdel-Mowla et al. (2015)** which was 5% in the *Scoberomorus commerson* and **Qorany (2020)** which was 2.15% in *Sparus aurata*. This result was lower than that obtained by **Hassanin (2016)** which recorded as 33.14% of caligus species from *Moolgarda seheli* from different location. This different is due to *Caligus* obtained in this study from one location which was the gills while in the other study collected from gills and skin. Concerning the total monogenetic trematodes (*Benedenia* species) infestation in the examined *M. seheli* was 13%. This result is closer to that obtained by **Eissa et al. (2017 a)** which was 22% in the other species. The parasite load (2-7) per fish was observed in wild fishes. This result was closer to that obtained by **Sikkel et al. (2009)** which wasn't more than 12% in ocean surgeonfish (*Acanthurus bahianus*). This result was less than obtained by **Jithendran et al. (2005)** which was (27%). This different in the results due to this study was performed in the cultured fish where the high intensity affect the immunity and increase the rate of infestation where, the benedenia species lived naturally on a local teleost species 'switched' to the larger biomass of cultured fish when sea temperatures dropped and perhaps depressed the immunological defenses (**Deveney et al., 2001**). Concerning the total prevalence of the mixed infestation between crustacean and monogenea in the examined fish was 7%. This result was closer to the result of mixed infection recorded by **Abd Al-Galill (2016)** which was 4%, while it was lower than obtained by **Qorany (2020)** which was 23.42% in other fish species. This difference is due to variation of the location where the fish collected, the climate temperature, crowding and fish species with different habitat. Regarding to the seasonal prevalence of *Lernanthropus* infestation in the examined *Moolgarda seheli* was the highest in the winter (50%) followed by spring (46.67%) then autumn (12%), while the lowest was the summer (10%). This result was disagreed with that obtained by **Hassanin (2016)** which recorded the highest season was summer (12%) followed by spring (7%) then autumn (4%) and absent in winter in *M. seheli*. this different because locality difference and the climatic change over year. Regarding to the seasonal prevalence of *Caligus* infestation in examined *M. seheli* was the highest in the spring (33.33%) (*Lepeophtheirus* was 26.67% and *Caligus* species was 6.67% while disappeared in the other seasons. This result was closer to that obtained by **El-Deen et al. (2013)** which recorded the highest season was the spring (90%) followed by summer (71.3%) and disappeared in other season in the *Mugil cephalus* and **Abdel-Mowla et al. (2015)** which recorded the highest season was summer (12%) followed by spring (8%) and not present in the other season in other fish species. This result was disagreed with that obtained by **Hassanin (2016)** which recorded the highest season was summer (44%) and the lower was winter (12%) in *M. seheli* this

different because locality difference. Regarding to the seasonal prevalence of monogenean (*Benedenia* species) infestation to the total examined *M. seheli* was the highest in the spring (43.33%) followed by winter (32.5%) then autumn and the summer (0%) was the lowest. This result was agreed with the result recorded by **Qorany (2020)** were the spring was the highest season of the infestation in other fish species. Also, this result was disagreed with **Mohamed *et al.* (2015)** where the highest season of infestation was the summer and the lowest infestation rate was recorded at the winter. This difference could be because of different geographical areas and/or host factors in additional to the nature of benedenia species The cycle of life is affected by the temperature when the heat was higher and salinity higher. In contrast, cool, hypersaline conditions increased the longevity and the success of infection (**Brazenor & Hutson, 2015**) . Temperature is considered an important factor in the control of monogene reproductive and survival rates (**Bakke *et al.*, 2007; Winger *et al.*, 2007; Luo & Yang, 2010**). Some monogene species tend to reproduce more quickly at higher water temperatures, while others favor cool water temperatures (**Ozturk & Altunel, 2006; Luo & Yang, 2010**). Concerning the histopathological change in gills of *M. seheli* naturally infested with *Lernanthropus* species in the revealed severe atrophy of the gill lamellae along with mechanical destruction of some secondary and primary lamellae. Some cases revealed focal infiltrations with leukocytes, in addition to congestion of the gill arch blood vessels, along with congestion. This result agreed with that obtained by **Manera and Dezfuli (2003); Abdel-Mowla *et al.* (2015); Qorany (2020)**. Concerning the histopathological change in gills of *M. seheli* naturally infested with *Caligus* species revealed sever destruction and complete loss of gill lamellae filaments, degeneration and massive atrophy filaments due to attachment and feeding of copepods. This result agreed with that obtained by **Ghobashy (2000); Nike F. Aladetohun *et al.* (2014)**.Concerning the histopathological change in gills of *M. seheli* infested with monogenetic trematodes showing branchitis, marked congestion and hemorrhages at the base of the gill arch as well as the primary lamellae along with destruction of gill lamellae. This result agreed with that obtained by **El-Lamie (2007); Abdelmonem *et al.* (2009); Clarke *et al.* (2012); Eissa *et al.* (2017 a)**

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CONCLUSION

We can conclude this work as *Caligus lichiae*, *Lepeophtheirus lichiae* and *Benedenia sekii* consider as new species founded in this area as well as in this fish. The highest infestation of ectoparasites in *Moolgarda seheli* fish was *Lernanthropus* followed by monogenea and the lowest was *Caligus* Species The highest seasonal prevalence of ectoparasitic parasites was the winter and the lowest was summer. Molecular identification of *Benedenia* species using PCR analysis of the 28SrRNA (mix of C1/D2 pairs) was a useful and confirmed way for solving the problem of identification of this confusing parasite. The partial sequencing and phylogenetics of the positive sample revealed that our sample were closer related to *Benedenia sekii* from Australia followed by *Benedenia sciaenae* from Australia. Therefore, the molecular methods established and give valuable tools for future research of specimens of fish species and geographical origins.

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