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***Ceratomyxa bohari* sp. n. (Myxozoa: Ceratomyxidae) from the gall bladder of *Lutjanus bohar* Forsskål from the Red Sea coast off Saudi Arabia: morphology, seasonality and SSU rDNA sequence**

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Abstract: A new myxozoan, *Ceratomyxa bohari* sp. n., infecting the gall bladder of two-spot red snapper, *Lutjanus bohar* Forsskål, in the Red Sea off Saudi Arabia, is described using light microscopy and characterised genetically. The infection was recorded as mature spores floating free in the bile. The overall prevalence of infection of the type host was 19% (67 fish infected of 360 examined), with the highest prevalence in autumn (31%; 28/90) and the lowest in winter at 12% (11/90). Mature spores are slender and slightly crescent-shaped in the frontal view, with anterior and posterior margins tapered gradually to rounded valvular tips. Spore valves are unequal with a prominent sutural line. The spore dimensions are 3–4 µm (mean 3.5 µm) in length and 16–19 µm (mean 17 µm) in thickness. Two polar capsules are spherical, equal in size, 1.5 µm in diameter. Coils of the polar filament are indiscernible. The sporoplasm is binucleated and fills nearly one third of the extracapsular space restricted to the area below the capsules. The molecular analysis based on the small subunit rDNA (SSU rDNA) sequence revealed a close relationship with majority of species of *Ceratomyxa* Thélohan, 1892 and phylogenetic clustering with species from different geographical location. Thus, the shorter spore of the present *Ceratomyxa* species and the divergence of the SSU rDNA sequences were the distinctive features that separate it from all previously described species and identified this parasite as a new species of *Ceratomyxa*.

Keywords: Myxosporea, fish parasites, Bivalvulida, spore, coelozoic infection, phylogeny, Lutjanidae

Members of the myxozoan genus *Ceratomyxa* Thélohan, 1892 are predominantly parasites of the gall bladder of teleosts and elasmobranchs (Gunter et al. 2009). Species of *Ceratomyxa* have elongated, generally crescent-shaped or arcuate, sometimes subspherical or ovoid, spores. Shell valves are frequently conical or subhemispherical and exceed significantly in length one half of the axial diameter of the spore (Gunter et al. 2010). Since the establishment of *Ceratomyxa* Atkinson, Foott et Bartholomew, 2014, which includes *C. shasta* (Noble, 1950) (syn. *Ceratomyxa shasta* Noble, 1950) and *Ceratomyxa gasterostea* Atkinson, Foott et Bartholomew, 2014 (see Atkinson et al. 2014), all species accommodated in *Ceratomyxa* are coelozoic and occur in the gall bladder of marine teleost fish.

All *Ceratomyxa* species with known SSU rDNA sequences cluster in the single large clade within the marine myxosporean lineage (Gunter et al. 2009, Fiala et al. 2015). Although this clade contains more than 70 species of *Ceratomyxa*, the presence of *Palliatius indecorus* Shulman,

Kovaleva et Dubina, 1979 and *Myxodavisia bulani* Fiala, Hlavničková, Kodádková, Freeman, Bartošová-Sojčková et Atkinson, 2015 caused the paraphyletic character of the *Ceratomyxa* clade (Fiala et al. 2015, Rocha et al. 2015).

The fish genus *Lutjanus* Bloch contains 70 species and a review of the available literature revealed that this genus is known to be infected with seven myxozoan species belonging to four genera. These species are *Kudoa hypoepicardialis* Blaylock, Bullard et Whipps, 2004; *Kudoa lutjanus* Wang, Huang, Tsai, Cheng, Tsai, Chen, Chen, Chiu, Liaw, Chang et Chen, 2005; *Kudoa lemniscati* Miller et Adlard, 2012; *Unicapsula andersenae* Miller et Adlard, 2013; *Sphaerospora motemarinii* Holzer, Pecková, Patra, Brennan, Yanes-Roca et Main, 2013 and *Henneguya jocu* Azevedo, Rocha, Matos, Matos, Oliveira, Al-Quraishy et Casal, 2014 (see Miller and Adlard 2013, Azevedo et al. 2014, Holzer et al. 2013). To our knowledge, however, only one *Ceratomyxa* species has been reported from fish of this genus, namely *C. milleri* Gunter, Whipps et Adlard,

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2009 described from the gall bladder of *Lutjanus fulviflamma* Forsskål collected in the Helena Island, Moreton Bay, Queensland, Australia (Gunter et al. 2009).

Although there is considerably exhaustive information on the ceratomyxan parasites from different parts of the world, little is known about the distribution and diversity of species of this genus in the Red Sea fishes. Research on these parasites is restricted to light microscopic description of just five species from the entire extent of the Red Sea coastline, all of which having been described from Egypt: *Ceratomyxa ghaffari* Ali, Abdel-Baki et Sakran, 2006 from *Tylosurus chorum* Rüppell, *C. bassoni* Abdel-Ghaffar, Ali, Al Quraishy, Al Rasheid, Al Farraj, Abdel-Baki et Bashtar, 2008 from *Plectorhynchus gaterinus* Forsskål, *C. entzerothi* Abdel-Ghaffar, Ali, Al Quraishy, Al Rasheid, Al Farraj, Abdel-Baki et Bashtar, 2008 from *Valamugil seheli* Forsskål, *C. hurghadensis* Abdel-Ghaffar, Ali, Al Quraishy, Al Rasheid, Al Farraj, Abdel-Baki et Bashtar, 2008 from *Fistularia commersonii* Rüppell, and *C. swaisi* Abdel-Ghaffar, Ali, Al Quraishy, Al Rasheid, Al Farraj, Abdel-Baki et Bashtar, 2008 from *Saurida undosquamis* Richardson (see Abdel-Ghaffar et al. 2008, Ali et al. 2008).

Here, we describe a new species of *Ceratomyxa* from the gall bladder of the two-spot red snapper, *Lutjanus bohar* Forsskål, based on morphological and molecular data. We ascertain the phylogenetic position of this species among congenetic taxa and describe the seasonal variation in prevalence of its infection.

MATERIALS AND METHODS

A total of 360 specimens of fresh two-spot red snapper, *Lutjanus bohar* (Teleostei: Lutjanidae), were bought from the fishermen at the boat landing sites of the Red Sea coast off Jizan City in Saudi Arabia. The collection was carried out in a period from April 2013 to April 2014, at a rate of 90 fish per season, of both sexes ranging from 20–40 cm in length. Upon necropsy, the gall bladder of each specimen was removed and examined for myxosporean infection with light microscopy. Fresh spores were measured and photographed using an Olympus BX51 microscope equipped with an Olympus DP71 camera. Descriptions and measurements of spores followed guidelines of Lom and Arthur (1989). Measurements were based on 30 fresh spores and data were given as range with mean in parentheses. All measurements are in micrometres (µm) and drawings were made with the help of a camera lucida. For permanent preparation, air-dried smears were stained with Giemsa after fixation in acetone-free absolute methanol. For DNA analysis, heavily infected gall bladders were preserved in ethanol.

Genomic DNA was extracted from three gall bladders with detected myxosporean infection preserved in 85% ethanol. After washing three times with phosphate buffer saline solution, extraction was carried using the QIAGEN DNeasy kit (QIAGEN Inc., Valencia, California). The small subunit partial sequence was amplified by PCR using the primers Myxospec F (Fiala 2006) and 18R (Whipps et al. 2003). PCR reactions were performed

in a personal thermocycler apparatus (Techne TC-Plus Satellites, Staffordshire, UK) with an initial denaturation at 94 °C for 5 min, followed by 30 cycles of denaturation at 94 °C for 20 s, annealing at 52 °C for 30 s and extension at 72 °C for 120 s with a final extension at 72 °C for 5 min. Three different positive PCR products from three different individual gall bladders were obtained. These products were then purified and quantified, and sequence reactions were conducted by Macrogen Inc. (Seoul, South Korea). Two additional primers, MYXF1338 and MyxR1437 (Mansour et al. 2013), were also used for sequencing reactions in order to obtain overlapping sequences.

The obtained sequences were assembled and edited using BioEdit version 7.2.5 (Hall 1999). A consensus sequence of 1 562 bp was obtained and then used for comparison with previously published sequences through a standard nucleotide-nucleotide BLAST (blastn) (Altschul et al. 1997). Fifty SSU rRNA sequences belonging to species of *Ceratomyxa* and one sequence of *Tetracapsuloides bryosalmonae* Canning, Curry, Feist, Longshaw et Okamura, 1999 were extracted from GenBank and used for phylogenetic analysis. Alignment was performed using ClustalX 2.1.0.12 software with the default parameters (gap opening penalty of 10 and gap extension penalty of 4 for paired and multiple alignments) (Larkin et al. 2007). Phylogenetic trees were constructed using maximum likelihood (ML), maximum parsimony (MP) and Bayesian inference. ML and MP analyses were conducted in Mega 5.0 software (Tamura et al. 2011) with inferred nodal support based on 1 000 bootstrap replicates. ML analysis was performed based on the General Time Reversible model with Gamma distributed rate and Invariant sites (GTR + G + I) selected on the basis of the lowest score of Bayesian Information Criterion and corrected Akaike Information Criterion (AICc) with the MEGA package. Estimates of evolutionary divergence between sequences was conducted in MEGA5 using the Kimura 2-parameter model (Kimura 1980).

For MP, tree was obtained using the Subtree-Pruning-Regrafting algorithm with search level 4 in which the initial trees were obtained by the random addition of sequences (4 replicates). Bayesian analyses were conducted by MrBayes v3.2.5 (Ronquist and Huelsenbeck 2003) under the GTR + I + Γ model, selected by Modeltest v. 3.7 (Posada 2008) with parameters setting to 4 000 000 generations (ngen = 4 000 000) with 2 runs each containing 4 simultaneous Markov Chain Monte Carlo chains (nchains = 4) and every 100th tree saved (samplefreq = 100). Each run was considered to have reached a stationary distribution based on split frequencies reported in MrBayes and by plotting the log likelihood values (the value 0.009 of the split frequency was reached after 450 000 generations). A total of 36 667 trees per run were generated. The first 25% of sampled trees of each Bayesian run were discarded as burnin, the remaining trees in each analysis were used to calculate the posterior probabilities and the final 95% of trees were used to produce a majority rule consensus tree. Fisher's exact test was carried out to compare prevalences using Quantitative Parasitology web software Version 1.0.9 (Reiczigel et al. 2014). The results were considered significant at $p < 0.05$.

Fig. 1A–D. Fresh spores of *Ceratomyxa bohari* sp. n. during their movement from the gall bladder of *Lutjanus bohar* Forsskal.

Fig. 2. Schematic drawing of a mature spore of *Ceratomyxa bohari* sp. n. from the gall bladder of *Lutjanus bohar* Forsskal.

RESULTS

Ceratomyxa bohari sp. n.

Figs. 1–3

ZooBank number for species:

urn:lsid:zoobank.org:act:69119BC8-19E3-480A-83AB-DACC630FD6C9

Vegetative stages

Vegetative stages were not observed. The infection was detected as free mature spores floating in the bile.

Mature spores

Mature spores slender and slightly crescent-shaped in frontal view, with convex anterior end and slightly bent posterior one (Fig. 1). Anterior and posterior margins tapered gradually terminating in rounded valvular tips (Fig. 1). Spore valves unequal. Sutural line prominent and clearly seen passing between two polar capsules. Spores 3–4 (3.5) long and 16–19 (17) thick. Two polar capsules equal in size, spherical in shape and 1–2 (1.6) in diameter. Polar filament coils indiscernible. Sporoplasm binucleate and nearly filling one third of extracapsular space restricted to area beneath two polar capsules (Fig. 2).

Prevalence and seasonal variation

Of the 360 examined specimens of *Lutjanus bohar*, 67 (19%) have gall bladders infected with *C. bohari*. The highest prevalence was observed in autumn, with 31% fish (28 infected of 90 examined) but the prevalence then declined sharply to 17% (15/90) in spring followed by another decline to 14% (13/90) in summer, with the lowest

Fig. 3. Phylogenetic tree resulting from Bayesian analysis inferred from the SSU rRNA dataset. Support values at branching nodes are listed as: bootstrap values from maximum likelihood / bootstrap values from parsimony analyses / Bayesian posterior probabilities from Bayesian analysis. *Tetracapsuloides bryosalmonae* Canning, Curry, Feist, Longshaw et Okamura, 1999 was used as outgroup. Values below 50% or not supported by the analysis are indicated by dashes. Scale bar is probability of nucleotide change.

level of 12% (11/90) being recorded in the winter. The data revealed a highly significant seasonal pattern of prevalence ($p = 0.0079$) fundamentally due to the significant differences between autumn and spring ($p = 0.0352$), autumn and summer ($p = 0.0123$) and autumn and winter ($p = 0.0034$) samples; no other significant differences in prevalence were found (all $p > 0.05$).

Molecular analysis

Three partial SSU rRNA gene sequences were obtained from myxozoans in three gall bladders. These sequences were identical and the consensus nucleotide sequence of

Table 1. Comparative data for *Ceratomyxa bohari* sp. n. and morphologically similar species (measurements in micrometres).

Species	Host	Locality	Spore size	PC size	Spore shape	References
<i>C. anko</i> Freeman, Yokoyama et al (Jordan) Ogawa, 2008	<i>Lophius litulon</i>	Japan (Pacific Ocean)	9.7–11.9 × 36.9–47.2 (10.8 × 41.9)	4.1–5.3 (4.6) in diameter	SP: arcuate to crescent V: equal with rounded PC: spherical	Freeman et al. 2008
<i>C. arabica</i> Al-Qahtani, Mansour, Al-Quraishy et al Abdel-Baki, 2015	<i>Acanthopagrus bifasciatus</i> (Forsskål)	Saudi Arabia (Arabian Gulf)	7–9 × 10–14 (8 × 12)	2.5–3.5 × 1.5–2.5 (3 × 2)	SP: stubby-shaped V: unequal PC: subspherical, unequal	Al-Qahtani et al. 2015
<i>C. choerodonae</i> Heiniger, Gunter et al Adlard, 2008	<i>Choerodon cyanodus</i> (Richardson)	Heron Island, Queens land, Australia	4.2–5.8 × 15.8–26.7 (5 × 21.4)	1.7–2.8 × 1.4–2.5 (2.2 × 2)	SP: crescent-shaped V: equal	Heiniger et al. 2008
<i>C. choleospora</i> Landsberg, 1993	<i>Centropomus undecimalis</i> (Bloch)	USA (Atlantic Ocean)	4–5 × 15–23 (4.5 × 18.3)	2 in diameter	SP: elongate V: equal with rounded ends PC: circular	Landsberg 1993
<i>C. dissostichi</i> Brickle, Kalavati et al MacKenzie, 2001	<i>Dissostichus eleginoides</i> Smitt	Falkland Islands (Atlantic Ocean)	3.2–4.5 × 15.4–22.8 (3.8 × 17.8)	2.3–3.6 (2.6 × 1.8)	SP: crescent-shaped V: equal with round ends	Brickle et al. 2001
<i>C. hamour</i> Mansour, Al-Qahtani, Al-Quraishy et al Abdel-Baki, 2015	<i>Epinephelus coioides</i> (Hamilton)	Saudi Arabia (Arabian Gulf)	6–8 × 15–18 (7 × 16.5)	2–4 × 3–5 (4 × 3)	SP: crescent shaped V: equal PC: pyriform	Mansour et al. 2015
<i>C. heinigeriae</i> Gunter, Whipps et al Adlard, 2009	<i>Choerodon cephalotes</i> (Castelnau)	Helena Island, Moreton Bay, Queensland	16.7–32.3 × 4.8–6.3 (5.6 × 24)	1.8–2.4 (2) diameter	SP: crescent-shaped V: unequal	Gunter et al. 2009
<i>C. husseini</i> Abdel-Baki, Mansour, Al-Qahtani, Al Omar et Al-Quraishy, 2015	<i>Cephalopholis hemistiktos</i> (Rüppell)	Arabian Gulf (off Saudi Arabia)	8–10 × 14–18 (9 × 16)	4.0–5.0 (4.5) diameter	SP: arched V: equal, with rounded ends PC: spherical	Abdel-Baki et al. 2015
<i>C. intexua</i> Meglitsch, 1960	<i>Jordanidia solandri</i> Cuvier <i>Plagiogonion rubiginosus</i> (Hutton)	New Zealand (Pacific Ocean)	3.4–5.4 × 9.3–20.1 (4.4 × 15.4)	1.2–2.2 (1.8) diameter	SP: slightly curved V: equal PC: spherical	Eiras 2006
<i>C. koieae</i> Gunter, Burger et al Adlard, 2010	<i>Sphyrna forsteri</i> Cuvier	Lizard Island, Australia	4.9–6.7 × 28.6–41.2 (5.5 × 36.7)	2.5–2.9 × 2.3–2.9 (2.8 × 2.6)	SP: crescent-shaped V: equal	Gunter et al. 2010
<i>C. milleri</i> Gunter, Whipps et al Adlard, 2009	<i>Lutjanus fulviflamma</i> (Forsskål)	Lizard Island (Australia)	4.1–5.4 × 11.4–20.9 (4.7 × 16.4)	1.3–2.0 × 1.1–2.0 (1.6 × 1.5)	SP: slightly crescent V: unequal	Gunter et al. 2009
<i>C. pantherini</i> Gunter, Burger et al Adlard, 2010	<i>Bothus pantherinus</i> (Rüppell)	Lizard Island, Australia	7.3–9.1 × 17.9–24.6 (8.1 × 21.6)	2.3 × 2.2 (1.8–2.6 × 1.7–2.6)	SP: crescent-shaped V: equal	Gunter et al. 2010
<i>C. sprengi</i> Moser, Kent et al Dennis, 1989	<i>Chaetodon aureofasciatus</i> Macleav	Australia (Coral Sea)	4–8 × 14–23 (5.7 × 16.3)	2–3 (2.4) diameter	SP: stubby V: equal, slightly tapered with rounded ends	Eiras 2006
<i>C. subtilis</i> Meglitsch, 1960	<i>Coelorhynchus australis</i> (Richardson)	New Zealand (Pacific Ocean)	3.4–4.5 × 15.7–26 (3.9 × 21.5)	1.5–2 (1.8) diameter	SP: slender V: equal or somewhat unequal	Eiras 2006
<i>Ceratomyxa bohari</i> sp. n.	<i>Lutjanus bohar</i> Forsskål	Saudi Arabia (Red Sea)	3–4 × 16–19 (3.5 × 17)	1–2 (1.6) diameter	SP: slender shape V: unequal PC: spherical	Present study

SP – spores; PC – polar capsules; V – valves.

1562 bp was deposited in GenBank database under the accession number KP893567. BLAST search using the obtained SSU rRNA sequence revealed no identical myxosporean sequence deposited in GenBank.

The maximum level of similarity was obtained with myxosporidia belonging to the genus *Ceratomyxa*. Comparison of the 50 selected sequences of species of *Ceratomyxa* revealed the percentages of identity varying between 86.2% with *C. heinigeriae* Gunter, Whipps et al, 2009 and 76.9% with *C. aegyptica* Yemmen, Marton, Eszterbauer et Bahri, 2012. The sequence differs from the aligned sequences of *Ceratomyxa* spp. at 158–310 bp over 1240 nucleotide alignment.

Bayesian inference and maximum parsimony methods yielded trees with similar topology. *Ceratomyxa bohari* sp. n. was placed at the base of the clade grouping *C. choer-*

odonae Heiniger, Gunter et al, 2008, *C. koieae* Gunter, Burger et al, 2010, *C. heinigeriae* and *C. milleri* (Fig. 3).

Type host: *Lutjanus bohar* Forsskål (Perciformes: Lutjanidae), two-spot red snapper.

Type locality: Red Sea off Jizan city (16°53'21"N; 42°32'3"E), Saudi Arabia.

Type material: Syntype spores in 80% ethanol are deposited in the parasitological collection of the Hungarian Natural History Museum under the number HNHM-70639.

Site of infection: The infection was detected as large numbers of free floating spores in the bile solution. Vegetative stages were not observed.

Prevalence: 19% (overall prevalence; in 67 out of 360 fish examined).

Etymology: The specific name is given after the Arabic common name of the fish host 'bohar'.

DISCUSSION

The present species exhibits some morphometric similarities with other members of the genus *Ceratomyxa* that parasitise fish from different families and different geographical regions (Table 1). Despite the similarity of these species, they differ from *Ceratomyxa bohari* sp. n. in several characteristics. *Ceratomyxa choleospora* Landsberg, 1993 differs in having more crescentic and slightly larger spores ($4\text{--}5\text{ }\mu\text{m} \times 15\text{--}23\text{ }\mu\text{m}$ vs $3\text{--}4\text{ }\mu\text{m} \times 16\text{--}19\text{ }\mu\text{m}$), equal shell valves and a sporoplasm filling the entire extracapsular space. *Ceratomyxa dissostichi* Brickle, Kalavati et MacKenzie, 2001 is distinguished from the present species by having equal valves, triangular intercapsular thickening and a larger ellipsoidal polar capsule, compared to the rounded ones in our species ($2.3\text{--}3.6\text{ }\mu\text{m}$ vs $1\text{--}2\text{ }\mu\text{m}$). Spores of *Ceratomyxa intexua* Meglitsch, 1960 can be readily distinguished from the present species by its equal valves that terminate in narrow tips with straight posterior margins and a wide range of spore thicknesses ($9.3\text{--}20.1\text{ }\mu\text{m}$ vs $16\text{--}19\text{ }\mu\text{m}$).

Similarly, *Ceratomyxa sprengi* Moser, Kent et Dennis, 1989 has quite long spores ($4\text{--}8\text{ }\mu\text{m}$ vs $3\text{--}4\text{ }\mu\text{m}$) with straight anterior and posterior margins and equal shell valves, whereas *Ceratomyxa subtilis* Meglitsch, 1960 has thicker spores [$21.5\text{ }\mu\text{m}$ ($15.7\text{--}26\text{ }\mu\text{m}$) vs $17\text{ }\mu\text{m}$ ($16\text{--}19\text{ }\mu\text{m}$)] with equal valves. *Ceratomyxa anko* Freeman, Yokoyama et Ogawa, 2008 is quite different to our species in all its body dimensions [$(11\text{ }\mu\text{m}$ ($10\text{--}12\text{ }\mu\text{m}$) $\times$ $42\text{ }\mu\text{m}$ ($37\text{--}47\text{ }\mu\text{m}$) vs $3.5\text{ }\mu\text{m}$ ($3\text{--}4\text{ }\mu\text{m}$) $\times$ $17\text{ }\mu\text{m}$ ($16\text{--}19\text{ }\mu\text{m}$)]]. Also, *C. choerodonae* differ in having larger spores with equal valves ($5\text{ }\mu\text{m} \times 21\text{ }\mu\text{m}$ vs $3.5\text{ }\mu\text{m} \times 17\text{ }\mu\text{m}$).

Ceratomyxa heinigeriae can be differentiated by their longer and thicker spores ($5.6\text{ }\mu\text{m} \times 24.0\text{ }\mu\text{m}$ vs $3.5\text{ }\mu\text{m} \times 17\text{ }\mu\text{m}$). *Ceratomyxa milleri* differs in having thicker spores ($4.7\text{ }\mu\text{m}$ vs $3.5\text{ }\mu\text{m}$) with straight posterior margins and subspherical polar capsules. *Ceratomyxa koieae* differs in having quite larger spores with equal valves ($5.5\text{ }\mu\text{m} \times 36.7\text{ }\mu\text{m}$ vs $3.5\text{ }\mu\text{m} \times 17.0\text{ }\mu\text{m}$). *Ceratomyxa pantherini* Gunter, Burger et Adlard, 2010 has rather longer and thicker spores ($7.3\text{--}9.1\text{ }\mu\text{m} \times 17.9\text{--}24.6\text{ }\mu\text{m}$ vs $3\text{--}4\text{ }\mu\text{m} \times 16\text{--}19\text{ }\mu\text{m}$).

It is worth mentioning that, recently, our research group described three ceratomyxan species from fishes in the Arabian Gulf off Saudi Arabia. These species are *Ceratomyxa arabica* Al-Qahtani, Mansour, Al-Quraishy et Abdel-Baki, 2015, *Ceratomyxa hamour* Mansour, Al-Qahtani, Al-Quraishy et Abdel-Baki, 2015 and *Ceratomyxa*

husseini Abdel-Baki, Mansour, Al-Qahtani, Al Omar et Al-Quraishy, 2015, but all of these differ from this new species in having longer spores ($7\text{--}9\text{ }\mu\text{m}$, $6\text{--}8\text{ }\mu\text{m}$, $8\text{--}10\text{ }\mu\text{m}$, respectively vs $3\text{--}4\text{ }\mu\text{m}$) (see Abdel-Baki et al. 2015, Al-Qahtani et al. 2015, Mansour et al. 2015).

Ceratomyxa bohari was present all year round with a maximum prevalence in autumn (31%) and a minimum prevalence in winter (12%). In general, many factors are involved in seasonal fluctuations of myxosporeans, including temperature, endogenous cycles of the parasites and the availability of susceptible hosts (Foott and Hedrick 1987, Alvarez-Pellitero and Sitjà-Bobadilla 1993, Alvarez-Pellitero et al. 1995, Yokoyama and Fukuda 2001). Additionally, the seasonal variation in prevalence of ceratomyxan parasites could be attributable to the variable condition of bile secretion at each sampling period (Yokoyama and Fukuda 2001).

Phylogenetic analysis based on maximum likelihood, maximum parsimony and Bayesian inference methods clusters *C. bohari* within the clade grouping the majority of species of *Ceratomyxa* within the marine lineage. Recently, a large phylogenetic reconstruction of *Ceratomyxa* resulted in distinction of five subclades (Fiala et al. 2015). The newly identified species clusters within subclade E of Fiala et al. (2015), which contains the highest number of species analysed.

The new species appears at the base of a well-supported clade grouping *C. choerodonae*, *C. koieae*, *C. heinigeriae* and *C. milleri* Gunter, Whipps et Adlard, 2009. All these species of *Ceratomyxa* were reported from fishes off Australia. Of them, *C. milleri* was described in the gall bladder of dory snapper, *Lutjanus fulviflamma* (Forsskal) Lutjanidae.

The obtained sequence has at least 8% divergence from other deposited sequences of identified species. The least sequence divergence was 7.9% with *C. heinigeriae* from *Choerodon cephalotes* (Castelnau) (Perciformes: Labridae) in Australia (Gunter et al. 2009). Sequence divergence with the three recently identified species of *Ceratomyxa* in the Arabian Gulf, *C. arabica*, *C. hamour* and *C. husseini*, was 8.5%, 15.4% and 9.6%, respectively. These data support validity of the new species from *L. bohar* in the Red Sea.

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