Morphometric criteria and partial sequence of the 18S rRNA gene of *Ceratomyxa sultani* n. sp. from the gallbladder of *Upeneus margarethae* in the Arabian Gulf, with a note on its seasonal prevalence

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**A B S T R A C T**

This paper describes a new coelozoic myxosporean parasite named *Ceratomyxa sultani* n. sp. isolated from the gallbladder of *Upeneus margarethae* sourced from the Arabian Gulf off Saudi Arabia. Of 104 *U. margarethae* specimens examined, 27 (26%) were infected, with the highest prevalence in winter and lowest in autumn. The pseudoplasmodia were disporous and irregularly elliptical in shape, with an average size of $22 \times 17 \mu m$. Mature spores were mostly elliptical with symmetrical valves and equal spherical polar capsules. Spores were $9 \mu m$ in length and $25 \mu m$ in thickness, while polar capsules were $4 \mu m$ wide with four filament coils. The paper further provides a morphological comparison with closely related *Ceratomyxa* spp. together with phylogenetic analysis based on the partial 18S rRNA sequence, which revealed that *C. sultani* n. sp. clustered within a robust clade of *Ceratomyxa* species from the Arabian Gulf and Red Sea or nearby geographic regions.

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1. Introduction

Myxozoans are typical and occasionally highly suspicious parasites of fish that have been known since the 1800s and which have a very convoluted biphasic life cycle, epitomised by the formation of multicellular spores (Okamura et al., 2015). It has progressively become clear that myxozoans are widespread, with more than 2400 species in 62 genera now known, an incredible level of species diversity representing about 18% of currently known cnidarian species (Lom and Dyková, 2006; Okamura et al., 2015; Laamiri, 2017; Liu et al., 2017).

The identification of some of these species has been predominantly based on the shape and structure of their spores, however; which is a generally inadequate taxonomic approach, sometimes making identification very problematic (Lom and Dyková, 2006; Gunter and Adlard, 2010). Nowadays, molecular techniques based on sequence variations of the 18S rRNA gene have become an extremely useful complementary tool for differentiating closely related myxosporeans, especially cryptic species (Heiniger and Adlard, 2014; Abdel-Baki et al., 2017). The combination of spore morphometry with the greatly expanded use of molecular-genetic methods therefore provides a powerful tool for ascertaining the taxonomy of recently described species, and also for the clarification of the taxonomy and phylogeny of the myxozoan genera (Heiniger and Adlard, 2014; Zhang et al., 2017). The Arabian Gulf is home to rich and diversified fish fauna, with nearly 500 species of bony and cartilaginous fish having been reported from its various coasts (Krupp and Muller, 1994). Until recently, little attention has been paid to the myxosporean...
parasites of these Arabian Gulf fish, and thus very little is known about these parasites. Most of the previous studies that have done on Arabian Gulf fish have concentrated mainly on the helminthes (Kardousha, 2016), and although sporadic work has been carried out on myxosporean parasites (Kardousha and El-Tantawy, 2002; Mansour et al., 2014, 2015a,b; Zhang et al., 2014; Abdel-Baki et al., 2015, 2017; Al-Qahtani et al., 2015), there is clearly a need for more extensive work to get a better idea of the species infecting fish in the Arabian Gulf in general and those off Saudi Arabia in particular. Here we present a minor contribution to this assemblage of work by describing a new species of Ceratomyxa from the gallbladder of Upeneus based on the morphometric criteria of its spores and the partial sequence of the 18S rRNA gene.

2. Materials and methods

During a survey of myxosporean parasites in fishes collected from the Arabian Gulf off Dammam city (26° 26’ 0”N, 50° 6’ 0”E) in Saudi Arabia, 104 specimens of Upeneus margarethae, Uiblein and Heemstra, were collected during monthly visits between March 2014 and March 2015. Immediately after collection, the fish were dissected and their organs and body fluids were examined for the presence of myxosporean infection. Fresh spores were examined and photographed with the aid of an Olympus BX51 microscope equipped with an Olympus DP71 digital camera (Olympus, Japan). Parasite identification and measurements were taken from 30 randomly selected fresh spores according to Lom and Arthur (1989). Measurements are in micrometres (μm) and data are expressed as range (mean ± SD). Gallbladders that were heavily infected with spores were preserved in 85% ethanol for molecular analysis.

3. Phylogeny

Ethanol-preserved gallbladders were washed three times with saline buffer in order to remove alcohol. Then, DNA was extracted using a DNeasy® Blood & Tissue Kit (QIAGEN Inc., Valencia, CA) according to the manufacturer’s recommendations. Two commonly recommended primers were used for the amplification of the partial 18S rRNA gene of the myxozoan parasite: MyxospecF 5’ TTCTGCCGTATCAACTWGTTG 3’ (Fiala, 2006) and reverse 18R 5’CTACGGAAACCTTGTTACG3’ (Whipps et al., 2004). The PCR amplifications were conducted in 30 μl of final volume following the same protocol reported by Mansour et al. (2015a). Briefly, 50–100 ng of DNA template was mixed with 0.5 μM of each primer, 2 mM dNTPs (0.5 mM each), and 0.5 U of iProof™ High-Fidelity DNA polymerase, purchased from Bio-Rad (Hercules, CA, USA), 1X iProof™ HF buffer, and 1.5 mM MgCl2. Amplifications were performed in a Techne TC-Plus Satellites personal thermocycler apparatus (Staffordshire, UK) following the program reported in Mansour et al. (2015a). Sequencing of the extracted fragments was carried out by Macrogen Inc. (Seoul, South Korea), using the same primers as for SSU rDNA amplifications. The sequences were visualized, assembled and edited using BioEdit 7.2.5.0 (Hall, 1999).
A consensus sequence was obtained and then used to extract the most closely related sequences among *Ceratomyxa* species using the BLASTn search (Altschul et al., 1997). Alignments were produced for phylogenetic analyses using ClustalX 2.1.0.12 software (Larkin et al., 2007) with default parameters. Phylogenetic trees were constructed with maximum likelihood (ML) and Neighbour joining (NJ) methods using MEGA software, version 7 (Kumar et al., 2016). For ML, we used the General Time Reversible with invariant sites and gamma distributed rates approach (GTR + I + G) as the model for nucleotide substitution. The NJ method was based on the Kimura 2-parameter model (Kimura, 1980). Both trees were constructed based on 1000 replicates.

### 3.1. Statistical analysis

Statistical analyses were performed using the One-way ANOVA and the Holm-Sidak methods within the Sigma Plot statistical
package, version 11.0. All P values are two-tailed and results were judged to be statistically significant difference when $P \leq 0.001$.

4. Results

4.1. Vegetative stages

The infection was reported as pseudoplasmodia mixed with a large number of free spores. The pseudoplasmodia were disporous, free floating in the bile, and irregularly elliptical in shape (Fig. 1A), with an average length of 19–24 (22 ± 0.8) $\mu$m and width of 15–19 (17 ± 0.7) $\mu$m.

4.2. Spore description

Mature spores were almost elliptical with a slightly convex anterior margin and a usually flat posterior one. Spores were 7–11 (9 ± 0.2) $\mu$m in length and 22–27 (25 ± 0.3) $\mu$m in thickness (n = 30) (Fig. 1). The spore valves were symmetrical and smooth with a slightly curved suture (Fig. 2). Polar capsules were spherical, equal in size and 3–5 (4 ± 0.2) $\mu$m wide (n = 30). Polar filaments had four turns, perpendicular to the longitudinal axis of the capsule. The sporoplasm was binucleated, filling most of the extracapsular space (Figs. 1 and 2).

4.3. Phylogeny

A consensus sequence of 985 bp was produced and submitted to GenBank under the accession number (MG266049). The GC content of this sequence was 51.7%. Pairwise alignment with sequences in the database shows a maximum similarity (96.8%) with C. mehlhorni (Mansour et al., 2015a) (31 substitutions and 7 gaps) followed by C. dennisi (Gunter and Adlard, 2008) with 96.6% and C. arabica (Al-Qahtani et al., 2015) with 95.8% (14 substitutions and 1 gap). The lowest similarity was observed with C. tunisiensis (62.8%) (Thabet et al., 2016). Ceratomyxa arabica and C. mehlhorni have both been reported from fish in the Arabian Gulf (Mansour et al., 2015a,b; Al-Qahtani et al., 2015). Forty SSU rRNA Ceratomyxa spp. were selected for the construction of the phylogenetic tree based on having the highest BLAST scores and identity, with some similarities in their spores or due to their geographical distribution. The sequence of Tetracapsuloides vermiciformis was used as an outgroup. The trees generated by ML and NJ had similar topologies with slight differences in the nodal support values in favour of the ML tree. As shown in Fig. 3, the phylogenetic analysis reveals clustering of C. sultani with C. mehlhorni, C. arabica, C. cardinalis, C. diamanti, C. gunterae and C. dennisi with a high level of bootstrap support.

4.4. Prevalence and seasonality of infection

The overall prevalence was 26% (27/104), with the highest infection rate in winter (42.3%, 11/26) followed by spring (30.8%, 8/26) and summer (23.1%, 6/26), and lowest infection rate in autumn (7.7%, 2/26) (Table 1; Fig. 4). Analysis of this data revealed a significant difference between winter and autumn ($P < .001$), winter and summer ($P < .001$), spring and autumn ($P < .001$), sumer and autumn ($P = .001$), winter and spring ($P = .007$) and spring and summer ($P = .050$).

4.5. Taxonomic summary

Type host: Upeneus margarethae Uiblein and Heemstra, 2010 (Teleostei, Perciformes, Mullidae).

Type locality: Saudi Arabian coast off the Arabian Gulf.

Site of infection: Gallbladder.

| Seasons    | No. examined fish | No. infected fish | Percent of infection |
|------------|-------------------|-------------------|----------------------|
| Spring     | 26                | 8                 | 30.8%                |
| Summer     | 26                | 6                 | 23.1%                |
| Autumn     | 26                | 2                 | 7.7%                 |
| Winter     | 26                | 11                | 42.3%                |
| Total      | 104               | 27                | 26%                  |

Prevalence: 26% (27/104).

Type-material: Gallbladder in 70% ethanol was deposited in the parasitological collection of the Zoology Department Museum, College of Science, King Saud University, Saudi Arabia, with number (C/11/2017). SSU rDNA sequence was deposited in the GenBank database with the accession number MG266049.

Etymology: The specific epithet is given after the common name of the fish host “Sultan Ibraheem”.

4.6. Remarks

Although no species of the genus Ceratomyxa Thelohan, 1892 have yet been described from members of the family Mullidae, some species can be compared with the present form either due to some similarities in their spores or due to their geographical location and habitat (Table 2). Species with apparently close similarities are: C. laxa (Meglitsch, 1960), C. chromis (Lubat et al., 1989), C. peculiaria (Yurakhno, 1991), C. syacii (Kpatcha et al., 1996), C. azonusi (Aseeva, 2003) and C. moseri (Gunter and Adlard, 2008). Ceratomyxa laxa differs in having shorter and more bent spores with a higher number of polar filament coils (5–6 vs. 4). In the same way, C. chromis differs in having crescent-shaped and shorter spores with tapered extremities and small polar capsules. Also, C. peculiaria could be differentiated by its shorter spores and small pyriform polar capsules. The shorter spores with unequal valves and smaller polar capsules of C. syacii easily differentiate it from Ceratomyxa sultani n. sp. Similarly, C. azonusi could be differentiated by its shorter and arch-like spores with pyriform polar
Table 2
Comparative data for Ceratomyxa sultani sp. n. and morphologically similar species.

| Species                  | Host                      | Locality       | Spore size       | PC size         | Spore shape               | References              |
|--------------------------|---------------------------|----------------|------------------|-----------------|---------------------------|-------------------------|
| Ceratomyxa sultani n. sp.| Upenes margarethaet       | Saudi Arabia   | 7–9 (7–11) × 24.5| 2.5–3.5 × 1.5–2.5 (3 × 2) | PC: spherical with 4PF     | Present study           |
| Ceratomyxa sultani       | Aeoliscus rehmi           | Arabian Gulf   | 7–9 × 10–14 (8 × 12) | 2–3 (2.5)       | PC: spherical              | Al-Qahtani et al. (2015) |
| Ceratomyxa sultani       | Ceratomyxa aurichichi     | Arabian Gulf   | 5–7 × 10–14 (6 × 12) | 2–3 (2.5)       | PC: spherical              | Abdel-Baki et al. (2017) |
| Ceratomyxa sultani       | Pleurogrammus azonus      | Sea of Japan   | 7–9 × 23–30 (3 × 1.8–2.5) | 3–5             | PC: spherical              | Aseeva (2003)           |

| Species                  | Host                      | Locality       | Spore size       | PC size         | Spore shape               | References              |
|--------------------------|---------------------------|----------------|------------------|-----------------|---------------------------|-------------------------|
| Ceratomyxa sultani       | Ceratomyxa sultani        | Arabian Gulf   | 7–9 × 15–18 (7 × 16.5) | 2–4 × 3–5       | PC: spherical              | Mansour et al. (2015a)  |
| Ceratomyxa sultani       | Ceratomyxa sultani        | Arabian Gulf   | 9 (8–10) × 16 (14–18) | 4.5 (4–5)       | PC: spherical              | Abdel-Baki et al. (2015) |
| Ceratomyxa sultani       | Ceratomyxa sultani        | New Zealand    | 8.7 (7.8–9.8) × m (25.6 (20.8–30.3)) | 3.4 (2.9–3.9)   | PC: spherical              | Meglitsch (1960)        |
| Ceratomyxa sultani       | Ceratomyxa sultani        | Arabian Gulf   | 8 (7–9) × 12 (10–14) | 3 (2–4)         | PC: spherical              | Mansour et al. (2015b)  |
| Ceratomyxa sultani       | Ceratomyxa sultani        | Australia      | 4.5 (3.5–6) × 11.9 (9–14.3) | 1.6 (1.3–2.2)   | PC: spherical              | Gunter and Adlard (2008) |
| Ceratomyxa sultani       | Ceratomyxa sultani        | Ukraine        | 6.5–8.5 × 21–29.3 (2.4–2.7 × 1.9–2.4) | 1.6 (1.5–2.0)  | PC: spherical              | Yurakhno (1991)         |
| Ceratomyxa sultani       | Ceratomyxa sultani        | Senegal        | 9.3 (9–9.5) × 23.6 (22.5–25) | 1.9 (1.5–2.0)  | PC: spherical              | Kpatcha et al. (1996)   |

Abbreviations: SP, spores; PC, polar capsules; PF, polar filament.

Capsules. Ceratomyxa moseri, meanwhile, has shorter and thinner spores with rather smaller pyriform polar capsules. It is worth mentioning that our team recently reported five Ceratomyxa spp. in the Arabian Gulf. These species are C. arabica (Al-Qahtani et al., 2015), C. hamour (Mansour et al., 2015a), C. husseini (Abdel-Baki et al., 2015), C. mehlhorni (Mansour et al., 2015b) and C. azvedoi (Abdel-Baki et al., 2017), all of which have shorter and thinner spores. In addition, C. arabica and C. mehlhorni have unequal valves. Moreover, C. arabica and C. hamour have pyriform polar capsules.

5. Discussion

Ceratomyxa Thélohan, 1892, is the second largest genus among the myxozoan groups, comprising 300 known species, which is about 8% of the myxozoan diversity (Fiala et al., 2015; Abdel-Baki et al., 2017; Zatti et al., 2017). Members of the genus Ceratomyxa are mainly coelozoic, inhabiting the gallbladders of their fish hosts, although a few species have been reported from other organs, including the digestive tract, urinary bladder and kidney tubules (Eiras, 2006). The majority of ceratomyxan species have been reported from marine fish hosts, with a few species being described from freshwater teleosts (Zatti et al., 2017). The morphometric features of mature spores in fish hosts are commonly used for the identification and differentiation of Ceratomyxa spp., as is common for all the myxosporean genera. This is due three reasons: (i) this is the most readily accessible stage in field studies; (ii) the lack of uniform characterization of vegetative stages (when available) and; (iii) because differences may exist in the other parasite life cycle stages, which are usually unknown and/or potentially inaccessible (Gunter et al., 2009).

Sometimes, however, the dimensions of the spore components overlap between species and may even vary within a single species due to the spore plasticity at the light microscope level (Heiniger and Adlard, 2013). Also, life cycles for marine Ceratomyxa spp. are poorly resolved, with only one having been described, for Ceratomyxa aurichichi (Kodádková et al., 2014). Consequently, in order to arrive at more reliable identifications, it is always worthwhile to take into account as many additional criteria as possible, such as the partial sequence of the SSU rDNA gene, host specificity and the geographical location (Fiala, 2006; Heiniger and Adlard, 2013; Kalatzis et al., 2013). In order to establish species novelty, therefore, it is now considered
to be beat practice to use SSU rDNA data in combination with morphological and/or biological data (Heiniger and Adlard, 2013; Rocha et al., 2016). Following this perspective, we have here described a new species of Ceratomyxa using a combination of spore morphometric characters and 18S rRNA sequence data. Additionally, Heiniger and Adlard (2013) confirmed that marine Ceratomyxa are highly host specific and typically confined to a single host species. The fact, therefore, that no Ceratomyxa spp. have previously been described from the family Mullidae, gives an initial indication of the potential importance of the Arabian Gulf as a source of new information on this field of science.

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