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Rapid Communication

Range expansion of the invasive hydroid, *Cordylophora caspia* (Pallas, 1771), in Colorado River reservoirs

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Abstract

Cordylophora caspia (Pallas, 1771) colonies have significant biofouling potential at hydropower facilities, which can increase maintenance and cause system failure. In 2015, *C. caspia* colonies were observed at dams along the Lower Colorado River system in Lake Powell UT, Lake Mead NV/AZ, Lake Mohave AZ/NV, and Lake Havasu AZ/CA. The hydroid was serendipitously found on settlement plates deployed for invasive dreissenid mussel monitoring. Species identification was confirmed by taxonomy and molecular analysis, and phylogenetic reconstruction was performed to identify the relationship of sequenced COI fragments relative to those from *C. caspia* specimens collected at other geographic locations.

Key words: colonial hydroid, *Cordylophora*, biofouling, benthic predator, biofilm

Introduction

Cordylophora caspia (Pallas, 1771) is a colonial hydroid originating from the Black and Caspian Seas. This hydroid occurs in brackish and freshwater environments globally (Arndt 1989; Folino-Rorem 2015; Smith 2001). *C. caspia* has a global distribution due to transport in ballast water, increased boat travel and water connectivity, and the ability to acclimate and proliferate in varying salinities (Roos 1979; Folino-Rorem 2015; Bij de Vaate et al. 2002) ranging from 0–30 ppt (Arndt 1989). *C. caspia* colonies grow on hard surfaces and consist of polyps specialized for feeding (hydranths) and for reproduction (gonophores). Mature ova are retained in the female gonophores, and male gonophores release sperm that penetrate the female gonophore and fertilize the eggs. The embryos develop in the gonophore and are released as free-swimming, ciliated planulae which disperse from the parent colony before attaching to substrates and forming new colonies. *C. caspia* does not have a medusoid stage (Pennak 1991). Colony growth and dispersal also occurs via asexual budding, via body fragments (hydrorhiza and hydrocauli), and via temperature and drought resistant menonts (Roos 1979).

C. caspia is carnivorous, and is considered a benthic predator that feeds on small crustaceans, worms, insect larvae, watermites and other zooplankton and benthic invertebrates (Bij de Vaate et al. 2002; Smith et al. 2002). Folino (2000) suggests that *C. caspia* may contribute to a restructuring of benthic and pelagic freshwater communities. Colonies also have serious negative economic impacts associated with biofouling (Folino-Rorem 2015), as they prefer solid substrates for settlement. *C. caspia* has been found colonizing and clogging intake tunnels, filters, condenser tube sheets, power plant pipes, and drinking water treatment plants in Europe and the United States (Lipsey and Chimney 1978; Jenner and Janssen-Mommen 1993; Moreteau and Khalanski 1994; Folino-Rorem and Indelicato 2005).

Since its introduction into the United States, *C. caspia* has been documented in at least 17 states (USGS and the World Register of Marine Species). Although Peck et al. identified this hydroid in Lake Mead, NV in 1987; this location is not commonly recognized in many range distribution maps and lists for the species. This paper describes the discovery of *C. caspia* in additional reservoirs along the Colorado River and genetically confirms identification.

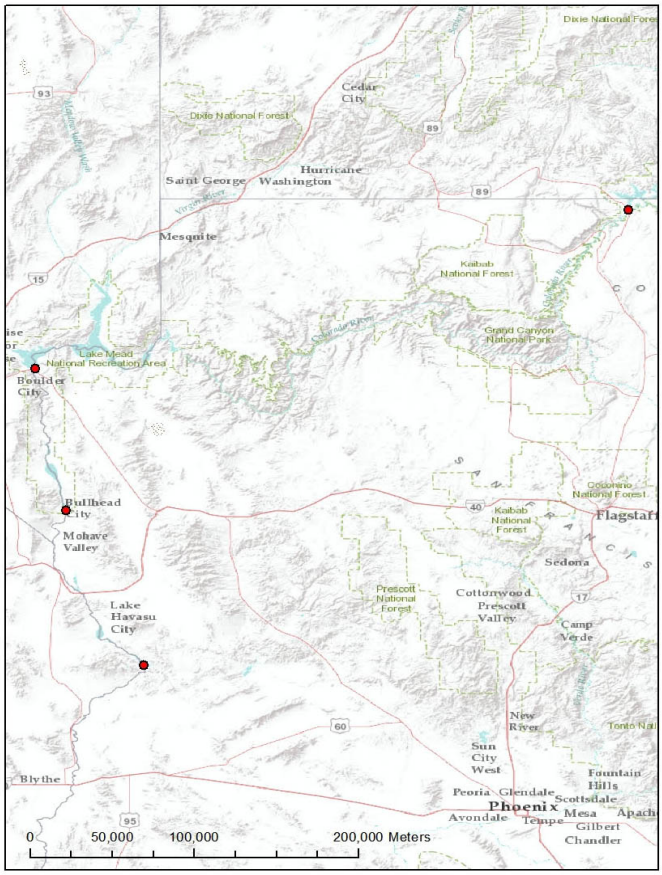

Figure 1. Dots indicate locations along the Colorado River where quagga mussel settlement plates were deployed and where *Cordylophora caspia* colonies were collected.

Methods

Cordylophora caspia was collected serendipitously on settlement plates that were deployed to monitor invasive quagga mussel (*Dreissena rostriformis bugensis,* Andrusov, 1897) settlement at dams along the Lower Colorado River system. Black PVC plates (14.7 cm × 14.7 cm) were installed at Glen Canyon Dam, Lake Powell UT (36.9375 N, 111.4837 W), Hoover Dam, Lake Mead NV/AZ (36.0163 N, 114.7372 W), Davis Dam, Lake Mohave AZ/NV (35.1967 N, 114.5683 W), and Parker Dam, Lake Havasu AZ/CA (34.2966 N, 114.1394 W) in 2014 (Figure 1). Plates were positioned at depths of approximately 10, 20, and 30 m below the surface in the forebay at each dam, and were analyzed for quagga mussel settlement monthly.

C. caspia colonies were visually (Figure 2) and microscopically (Figure 3) observed on plates. Taxonomic identification of specimens was confirmed by John Beaver and Thomas Renicker at BSA Environmental Services, INC. DNA barcoding for genetic identification of tissue samples was performed by the Reclamation Detection Laboratory for Exotic Species (RDLES) using established protocols (Keele et al. 2014).

DNA was isolated using the DNEasy Blood & Tissue Extraction Kit (Qiagen Inc., Valencia, CA USA), and a 710 bp fragment of the mitochondrial cytochrome oxidase 1 (COI) gene was PCR amplified using the primers LCO1490: 5′-GGTCAACAAAT CATAAAGATATTGG-3′ and HCO2198: 5′-TAAA CTTCAGGGTGACCAAAAAATCA-3′ (Folmer et al. 1994). PCR amplification was performed with AmpliTaq Gold DNA Polymerase (ThermoFisher Scientific, Grand Island, NY, USA), with an initial denaturation of 10 minutes at 95°C, followed by 40 rounds of amplification with 1 minute at 95°C, 1 minute at 40°C, and 1.5 minutes at 72°C, and a final extension of 10 minutes at 72°C. Resulting PCR products were sent to a commercial laboratory for DNA sequencing. The forward and reverse DNA sequences from each amplified fragment were aligned to each other and to on-line databases (DNA Bold and NCBI Blast) to identify the source organism (Supplementary material Table S1).

Phylogenetic reconstruction was performed to identify the relationship of sequenced COI fragments relative to those previous published (Folino-Rorem et al. 2009; Wollschlager et al. 2013) for *C. caspia* specimens collected at other geographic locations. COI sequences collected in the study were aligned to sequences retrieved from GenBank (Table S2) using MUSCLE (Edgar 2004). Phylogenetic reconstruction was performed using MrBayes version 3.2.1 (Ronquist et al. 2012). The analysis was run for 5,000,000 generations, with 4 runs of 2 chains each. The analysis was run with a GTR+I+G likelihood model of sequence evolution, chosen based on analysis of the dataset with jModelTest (Posada 2008). The first 1,250,000 generations of the run were discarded as burn-in prior to calculation of a consensus tree and posterior probabilities.

Figure 2. *Cordylophora caspia* colony growth on a settlement plate at Lake Mead, NV in the forebay near the Hoover Dam. Photograph by Alexander Stephens, Bureau of Reclamation.

Results and discussion

Cordylophora caspia was taxonomically and genetically confirmed at sites along the Colorado River system in UT, NV, AZ, and CA. Colonies were first noticed on settlement plates at Lake Mead in December 2014, and once identified were regularly found at all other locations on plates at 10, 20, and 30 m. *C. caspia* was previously identified as *Cordylophora lacustris* in Lake Mead in a report by Peck et al. (1987) who commonly found this hydroid coating buoy anchor ropes, submerged tree branches, and un-sedimented rock surfaces at about 15 meters or below.

GenBank blastn alignment of COI sequences from hydroids sampled from Lake Powell, Lake Mead, and Lake Mohave showed highest similarity to *C. caspia* sequences for all specimens. All sampled sequences showed 99% identity to a reference *C. caspia* COI sequence (GenBank accession number: KC489509.1). Phylogenetic analysis of COI sequences isolated from *C. caspia* in the Colorado River placed all the specimens sampled within the previously identified clade 1A (Figure 4; Folino-Rorem et al. 2009; Wollschlager et al. 2013). This clade includes samples collected from a wide variety of geographic locations, including Virginia, Panama, Lake Michigan, Lake Erie, and the Illinois River and tributaries. Although the limited geographic sampling and resolution within the tree do not allow a definitive identification of the source population for *C. caspia* in the Colorado River, the presence of specimens from the Upper Mississippi River and Great Lakes watersheds in the 1A clade suggests possible origins for the invasion. It is also intriguing that all other specimens in this clade were collected from exclusively freshwater habitats, like that of the Colorado River. This is in contrast to the other *C. caspia* clades

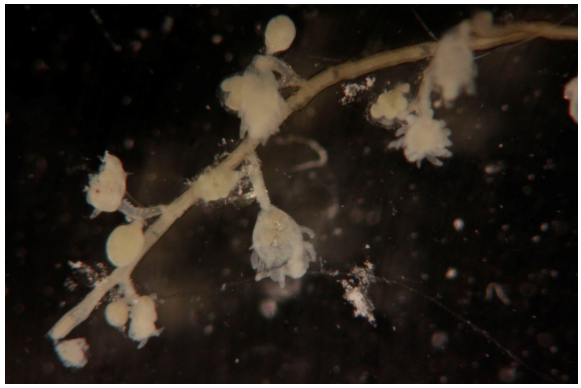

Figure 3. Microscopic view (30× magnification) of *Cordylophora caspia* collected from Lake Mohave, NV/AZ. Photomicrograph by BSA Environmental Services, INC.

(1B, 2A, and 2B), which contain representatives collected from waters with a range of salinities. The possibility that "*C. caspia*" is a complex of genetically distinct species or subspecies with different ecological tolerances has been suggested previously (see Folino 2000), and bears further investigation.

During microscopic examination of *C. caspia*, feeding polyps were regularly observed to contain dreissenid mussel larvae (Figure 5). Dense quagga mussel populations are found in the Lower Colorado River (Mahon 2011), and it is possible that *C. caspia* is benefiting from the high numbers of mussel veligers available as prey, facilitating range expansion and increased population densities. *C. caspia* has previously been reported to co-occur with invasive populations of dreissenid quagga and zebra mussels, feeding on mussel larva and using mussel shells as a substrate (Olenin and Leppäkoski 1999; Folino-Rorem

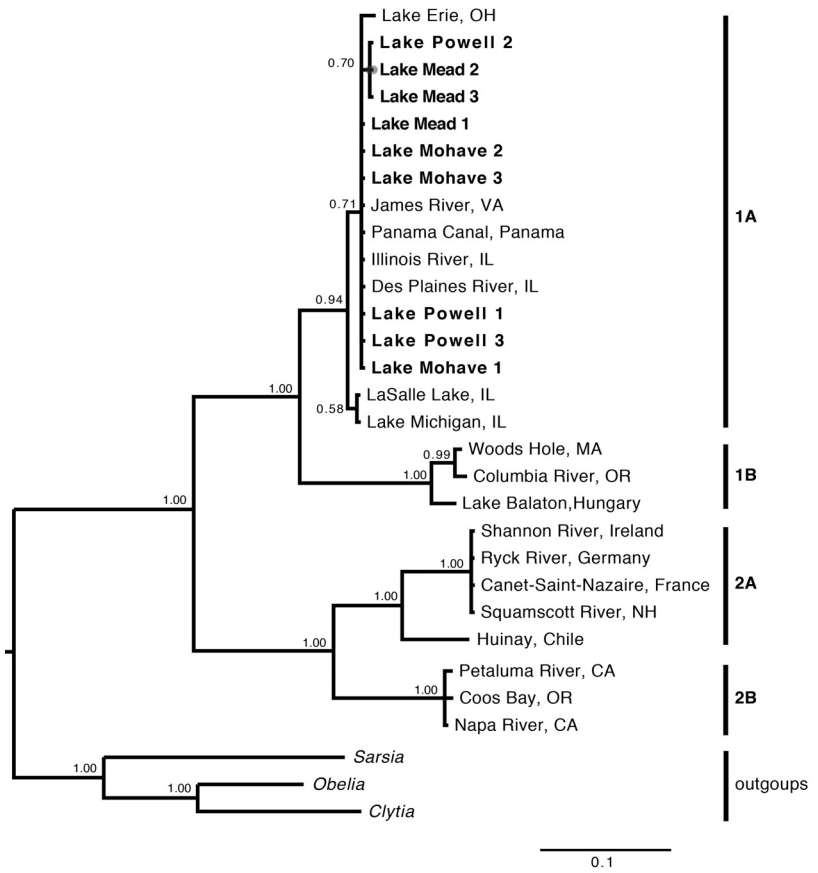

Figure 4. Phylogenetic analysis in of *Cordylophora caspia* COI sequences. Phylogram from Bayesian likelihood analysis with 4 independent runs of 5,000,000 generations each. Posterior probabilities are shown for nodes with values greater than 0.50. Scale bar below the tree represents 0.1 nucleotide substitutions per site. Clade names are presented to the right of the tree.

et al. 2006). The hydroid's filamentous structure may enhance or facilitate recruitment of dreissenid mussels by providing additional surface area for settlement (Dean and Hurd 1980; Moreteau and Khalanski 1994), although it is possible that the two species compete for suitable substrate for colonization (Walton 1996; Folino-Rorem 2015). Given that the native range of *C. caspia* overlaps with those of zebra and quagga mussels, it may be that hydroid colonies have translocated with, and have benefitted from, the range expansion of invasive dreissenid mussels.

C. caspia growth rates have been found to increase non-linearly with temperature, suggesting that a small increase in temperature can result in a large increase in growth rate (Meek et al. 2012). Positive growth rates occur at temperatures above 14°C and the peak growth rate occurs above 19°C (Meek et al. 2012). Temperatures at lower Colorado River Reservoirs are commonly above 20°C during the summer months, suggesting that *C. caspia* growth

Figure 5. Microscopic view (105× magnification) of *Cordylophora caspia,* collected from Lake Havasu AZ/CA with two quagga mussel veligers (arrows) inside a feeding polyp. Photomicrograph by Sherri Pucherelli, Bureau of Reclamation.

rate has the potential to be maximized. The presence of *C. caspia* in the Colorado River system may be of concern to local facility managers as there are several hydropower facilities located along the Colorado River, and *C. caspia* has the potential to cause significant biofouling issues at these sites.

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References

Arndt EA (1989) Ecological, physiological and historical aspects of brackish water fauna distribution. In: Ryland JS, Tyler PA (eds), Reproduction, genetics and distributions of marine organisms (1989) International Symposium Series. European Marine Biological Symposium, Swansea (U.K.) Olsen & Olsen, Fredensburg, Denmark, pp 327–338

Bij de Vaate A, Jazdzewski K, Ketekaars HAM, Gollasch S, Van der Velde G (2002) Geographical patterns in range extension of Ponto-Caspian macroinvertebrate species in Europe. *Canadian Journal of Fisheries and Aquatic Sciences* 59: 1159–1174, http://dx.doi.org/10.1139/f02-098

Dean TA, Hurd LE (1980) Development in an estuarine fouling community: the influence of early colonists on later arrivals. *Oecologia* 46: 295–301, http://dx.doi.org/10.1007/BF00346255

Edgar RC (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Research* 32: 1792–1797, http://dx.doi.org/10.1093/nar/gkh340

Folino-Rorem NC, Indelicato J (2005) Controlling biofouling causes by the colonial hydroid *Cordylophora caspia*. *Water Research* 39: 2731–2737, http://dx.doi.org/10.1016/j.watres.2005.04.053

Folino-Rorem NC, Stoeckel J, Thorn E, Page L (2006) Effects of artificial filamentous substrate on zebra mussel (*Dreissena polymorpha*) settlement. *Biological Invasions* 8: 89–96, http://dx.doi.org/10.1007/s10530-005-0330-1

Folino-Rorem NC, Darling JA, D'Ausilio CA (2009) Genetic analysis reveals multiple cryptic invasive species of the hydrozoan genus *Cordylophora*. *Biological Invasions* 11: 1869–1882, http://dx.doi.org/10.1007/s10530-008-9365-4

Folino-Rorem NC (2015) Phylum Cnidaria. In: Thorp J, Rogers DC (eds), Ecology and General Biology: Thorp & Covich's Freshwater Invertebrates, Academic Press, San Diego, CA, pp 159–179, http://dx.doi.org/10.1016/b978-0-12-385026-3.00009-7

Folmer O, Black M, Hoeth W, Lutz R, Vrijenhoek R (1994) DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates. *Molecular Marine Biology and Biotechnology* 3(5): 294–299

Jenner HA, Janssen-Mommen JPM (1993) Monitoring and control of *Dreissena polymorpha* and other macrofouling bivalves in the Netherlands. In: Nalepa TF, Schloesser DW (eds), Zebra Mussels: Biology, Impacts and Control. Lewis Publishers, Boca Raton, FL, pp 537–554

Keele JK, Carmon J, Hosler D (2014) DNA Barcoding for Genetic Identification of Organisms. DNA Barcoding Standard Operating Procedure, SOP Version 1.0, Technical Memorandum No. 86-68220-14-08

Lipsey LL, Chimney MJ (1978) New distribution records of *Cordylophora lacustris* and *Craspedacusta sowerbyi* (Coelenterata) in southern Illinois. *Ohio Journal of Science* 78(5): 280–281

Mahon RF (2011) Quagga mussel (*Dreissena rostriformis bugensis*) population structure during the early invasion of Lakes Mead and Mohave January–March 2007. *Aquatic Invasions* 6: 131–140, http://dx.doi.org/10.3391/ai.2011.6.2.02

Meek MH, Wintzer AP, Wetzel WC, May B (2012) Climate change likely to facilitate the invasion of the non-native hydroid, *Cordylophora caspia* in the San Francisco Estuary. *PLoS ONE* 7: e46373, http://dx.doi.org/10.1371/journal.pone.0046373

Moreteau JC, Khalanski M (1994) Settling and growth of *D. polymorpha* in the raw water circuits of the Cattenom nuclear power plant (Moselle, France). Proceedings of the Fourth International Zebra Mussel Conference, Madison, WI, March 1994, pp 553–574

Olenin S, Leppäkoski E (1999) Non-native animals in the Baltic Sea: alteration of benthic habitats in costal inlets and Lagoons. *Hydrobiologia* 393: 233–243, http://dx.doi.org/10.1023/A:1003511003766

Peck SK, Pratt WL, Pollard JE, Paulson LJ, Baepler DH (1987) Benthic invertebrates and crayfish of Lake Mead. Available at: http://digitalscholarship.unlv.edu/water_pubs/98

Pennak RW (1991) Fresh-water Invertebrates of the United States: Protozoa to Mollusca, 3rd edition John Wiley and Sons, Inc., USA, 628 pp

Posada D (2008) jModelTest: phylogenetic model averaging. *Molecular Biology and Evolution* 25: 1253–1256, http://dx.doi.org/10.1093/molbev/msn083

Roos PJ (1979) Two-stage life cycle of a *Cordylophora* population in the Netherlands. *Hydrobiologia* 62: 231–239, http://dx.doi.org/10.1007/BF00043540

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology* 61: 539–442, http://dx.doi.org/10.1093/sysbio/sys029

Smith DG (2001) Pennak's freshwater invertebrates of the United States: Porifera to Crustacea. Wiley, New York, 638 pp

Smith DG, Werle SF, Klekowski E (2002) the rapid colonization and emerging biology of *Cordylophora caspia* (Pallas, 1771) (Cnidaria: Clavidae) in the Connecticut River. *Journal of Freshwater Ecology* 17: 423–430, http://dx.doi.org/10.1080/02705060.2002.9663916

Walton WC (1996) Occurance of zebra mussel (*Dreissena polymorpha*) in the oligohaline Hundson River, New York. *Estuaries* 19: 612–618, http://dx.doi.org/10.2307/1352521

Wollschlager J, Folino-Rorem N, Daly M (2013) Nematocysts of the invasive hydroid *Cordylophora caspia* (Cnidaria: Hydrozoa). *Biological Bulletin* 224(2): 99–109

Supplementary material

The following supplementary material is available for this article:

Table S1. Geographic and gene information for *Cordylophora caspia* samples analyzed for this study.

Table S2. Accession numbers for *Cordylophora caspia* and outgroup COI sequences retrieved from GenBank for phylogenetic analysis.

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