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Mite DNA in Mantle Clips

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Gene sequencing as a tool for the conservation of freshwater mussels is finally taking off, although the majority of studies are systematic in nature, rather than investigations of populations, for which many samples are required. One limitation for population-scale studies is harm to mussels. Several low-impact options are available, however, notably mantle clips (Berg et al., 2005), use of a swab rubbed across the mantle and foot (Henley et al., 2006), and even grinding fresh shells (Geisti et al., 2008). While each of these approaches progressively decreases risk to live individuals, DNA yields decline. For that reason, mantle clipping has remained the most commonly used non-lethal sampling protocol.

We discovered a caveat to sampling DNA via mantle clips. Parasitic or commensal organisms associated with unionid mussels may occasionally contaminate genetic samples taken from along the margins of individuals. Following DNA extraction from two *Pyganodon grandis* individuals for which a mantle-clip was taken during surveys throughout the Lake Erie-Lake St. Claire watersheds, a non-

unionid fragment of the mitochondrial CO1 gene was amplified (Accession numbers JQ425161-JQ425162). While these sequences barely aligned with the known haplotypes from *P. grandis*, a blast search in GenBank tentatively identified them as coming from *Unionicola* mites. Mites are symbionts with mussels, and are likely to be very common. Gangloff et al. (2008) reported all 29 *Pyganodon grandis* from a tributary of the Talllapoosa River, Alabama, possessed both unionicolid mites and aspidogastrid trematodes.

While the frequency of obtaining a non-mussel sequence from a mantle clip is not high, at about 1%, that number suggests to us that others have occasionally obtained DNA of parasites and probably done nothing further with them. Water mites are currently placed in one genus, *Unionicola* Haldeman 1842 (Acari: Unionicolidae), which presently contains some 238 named species in 57 subgenera of which limited phylogenetic analysis suggests very deep divergence levels (Edwards et al., 2010). GenBank contains even fewer water mite sequences; a search on *Unionicola* gave just 97 (some of which are expanded sequences of the same species). For a perspective on how understudied this mite system is, no GenBank sequences were more than 83% similar to either of the two recently submitted sequences, which also differed at 94 of 645 base pairs (14.6%), although base pair variation generated just seven amino acid substitutions. Clearly, any new discoveries of *Unionicola* mites, even by accident, should be uploaded to the public domain to enable future work on the diversity of this less studied group, and potentially, investigations of a relationship between parasitic unionicolid mites and their unionid hosts (Edwards and Vidrine, 2006).

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