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PARASITES IN A CHANGING WORLD

**ABSTRACT
BOOK**





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Genetic diversity in *Cryptocotyle lingua* (Digenea: Heterophyidae): expanding a dataset to its geographical limits

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Intraspecific genetic diversity in digeneans was shown to follow several patterns, largely depending on the number and vagility of hosts in their life cycle. Better understanding of these patterns requires information on more species, and larger sample sizes. We contributed to this topic with research on *Cryptocotyle lingua* (Heterophyidae) from its first intermediate hosts, *Littorina littorea*. This topic has some important background.

In a 2008 study, April Blakeslee and her colleagues used information on the genetic structure of *C. lingua* as one of the sources of evidence to resolve the origin of *L. littorea* in North America. In this study, a large *cox1* dataset for *C. lingua* was collected, covering 20 North American and 16 European locations. In Europe, sampling spanned from the Atlantic coast of France in the south to the Oslo region in the north. High genetic diversity was detected, and even more expected, if sampling effort increased.

In our study, we aimed to expand the available European *cox1* dataset for *C. lingua*, covering the north-eastern limits of its distribution range. In summer 2020, we collected 37 isolates of *C. lingua* from periwinkles at the White and Barents Sea shores, and sequenced a *cox1* gene fragment for them. These new data and 196 sequences from GenBank were aligned, and analyzed together in PopART and DnaSP6. In our material, we detected both new unique haplotypes and those that were shown to dominate in a 2008 study. These and other results of the current study prove and expand previous findings.