



Evolution of rotifers in saline and subsaline lakes: A molecular phylogenetic approach

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ABSTRACT: Evolutionary relationships within the phylum Rotifera are poorly understood despite the important role that they play in freshwater ecosystems. Phylogenetic analyses of DNA sequences from two mitochondrial genes, 16S rDNA and cytochrome oxidase I (COI), were employed to examine the extent of genetic divergence within populations of several common taxa. This work sought to verify the role of phenotypic plasticity versus genetic variation in explaining the morphological variation in some taxa. Deep genetic divergence (4.4% COI nucleotide sequence divergence) was detected between spined and unspined forms of *Keratella cochlearis*, which suggests that they represent different species. However, morphological variation in *K. hiemalis* appeared to be environmentally induced. The study also sought to ascertain the role of one environmental variable, salinity, in the patterning of sequence variation. Greater haplotype diversity and genetic divergence were observed among populations of halophilic *Brachionus plicatilis* than among freshwater *Keratella quadrata* populations from northern Canada. When COI DNA sequences for *B. plicatilis* haplotypes were compared with those from Spain, there was evidence for considerable genetic diversity within this species among closely located saline lakes in northern Canada.

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