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An update on the *Acanthamoeba* DNA sequence database at the Ohio State University:
A resource for the study of clinical and environmental isolates

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The genus *Acanthamoeba* has a worldwide distribution, inhabiting a wide range of environmental niches. It has been isolated from soil, fresh and saltwater, humans, domestic and feral animals. The genus includes opportunistic pathogens responsible for the sight threatening disease *Acanthamoeba* keratitis (AK) in otherwise healthy individuals. *Acanthamoeba* is also responsible for life threatening infections in immunocompromised patients. Variation in the pathogenicity of *Acanthamoeba* strains has been observed, but the relevance of these results to human disease is unclear. Lack of a reliable subgeneric classification system has complicated analysis. *Acanthamoeba* traditionally has been classified using morphological markers such as cyst morphology and trophozoite size and shape. Questions regarding the reliability of morphological methods led our laboratory to examine molecular methods to determine whether more definitive subgeneric classifications could be accomplished. Our initial studies focused on the nuclear small subunit ribosomal RNA gene (*Rns*). Subsequent studies added mitochondrial loci as additional markers and as a test of the consistency of conclusions drawn from the *Rns* studies. The data collected over the previous decade now allow us to quickly examine a clinical or environmental sample using molecular methods and determine and classify the sequence genotype for an unknown specimen. Twelve *Rns* sequence types were originally identified and designated T1-T12. Several more may exist. The database currently includes ~190 "nearly complete" sequences (defined as sequences of 2000 or more nucleotides). Of these, 133 (70%) are classified as sequence type T4. In addition, more than 200 isolates have been examined for which partial *Rns* sequences have been reported, including 135 isolates with sequences of 400-1000 nucleotides and 20 isolates with sequences of 1000-2000 nucleotides. While mitochondrial *rns* sequences have been less extensively analyzed, there are over 80 sequences that have been reported, spanning almost all nuclear sequence types. (Supported by grants from NIH)