

**ABSTRACTS**  
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64 - Mitochondrial DNA variation: A basis for the taxonomy of *Acanthamoeba*. THOMAS J. BYERS, LINDA L. BURIANEK, VALERIE STEWART, and BYEONG G. KIM, Department of Microbiology, The Ohio State University, Columbus

Difficulties in identifying species within the genus *Acanthamoeba* have led several laboratories to more extensive use of molecular methods of classification. Analysis of mitochondrial DNA organization by use of restriction endonucleases is one of the more promising approaches. We previously reported comparisons of different strains based on agarose gel electrophoresis of DNA restriction fragments. The most striking observation was the extensive diversity of fragment patterns obtained for different strains. In most pairwise comparisons of strains, there were very few identically sized, and presumed homologous, fragments. The diversity among strains within a species was as great as among species and was comparable to that among sibling species of other organisms. Our more recent studies have concentrated on comparing the mtDNA restriction site maps for various strains. These studies suggest that quantitative comparisons based on fragment size differences, as used in the earlier studies, overestimate actual differences among strains. Similarities in size among homologous fragments from different strains appear to be absent due to insertions and deletions that are present in some of the fragments. Thus, it appears unlikely that measures of genetic distance based solely on fragment sizes will provide an adequate measure of relatedness. Rather, it will be necessary to perform the more detailed work of comparing restriction site maps and, possibly, nucleotide sequences. (Supported by NIH grant A1 17526).