

**Microbial Diversity of Lake Elmenteita,
Kenya**

Romano Mwirichia Kachiuru

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ABSTRACT

The major goal of microbial ecology is to understand microbial diversity in natural habitats their interaction with one another and with their habitat. The soda lakes are highly productive environments and the soda lakes of the East African Rift valley have been shown to support a dense and diverse population of aerobic, organotrophic, halophilic, alkaliphilic and alkalitolerant representatives of major bacterial and archaeal phyla.

The isolation and characterization of organisms belonging to widespread but previously uncultivated groups of organisms can provide insights into the roles and functions of these organisms in their natural settings and assist in the formulation of hypotheses about metabolic interactions between microorganisms and their natural environment. Several studies have been carried out to document the microbial diversity of the Kenyan soda lakes by other researchers. However no comprehensive study has been done in Lake Elmenteita. The aim of this study was to assess the microbial diversity of Lake Elmenteita using both culture independent and culture dependent techniques. The application of both techniques was expected to provide new insights into the microbial diversity of the Lake as well as possible roles played by each group within the soda lake environment.

Application of molecular tools to study microbial ecology has widened our approximation of diversity in the environments. Clone Libraries were constructed from PCR amplicons from total environmental DNA. Primers specific for Bacteria and Archaea respectively were used. Partial sequences were generated for both the clones and the isolates. The relatedness of the Lake Elmenteita bacterial rRNA sequences to known rRNA gene sequences was determined by BLAST analysis

and by alignment to the sequences on the ARB database (Release, 1994).

Clones possessed a higher similarity to other environmental clones than to cultured microorganisms. A total of 655 clone sequences were sequenced. Of these 525 (80.15%) sequences were related to uncultured members of the Domain Bacteria. This indicates that a large proportion of deep phylogenetic groups are represented in the clone libraries. Sixteen percent of the clones had similarity values below 90% to both cultured and uncultured microorganisms. Forty three percent of the clones had similarity values between 90-95% as compared to 34.35% that had values between 96-98%. Only a mere 6.87% had values between 99-100%. However a number of factors including relatively low cell numbers of large organisms and a variable number of rRNA operons among organisms, as well as extraction and PCR bias, may lead to under-representation of phylotypes relative to their *in situ* abundance.

Cultured isolates are still very important in developing our understanding of bacterial physiology, genetics, and ecology. Isolation was done using both nutrient rich and nutrient poor media. A polyphasic approach was employed in the identification of the various strains. The majority of the isolates (36.75%) belonged to the genus *Halomonas* while 31.35% belonged to the Genus *Bacillus*. More than half of the isolates (59.45%) belonged to the *Gammaproteobacteria*. An overlap between the clone library and the isolates was observed in the Order *Bacillales* and the *Actinobacteria* only. In this study novel isolates related to *Marinospirillum*, *Idiomarina*, *Streptomyces*, *_ocardia*, *Marinilactibacillus*, *Amphibacillus* and *Vibrio* were recovered. A polyphasic approach to characterization showed they

represented novel taxa.

The study showed that the application of both culture dependent and culture independent methods gives a better picture of diversity in the environment. It can be concluded the soda lakes harbour novel uncultured groups of microorganisms and most of them are of biotechnological potential. Future work should focus on Archaeal diversity as well as the uncultured groups of bacteria.