

Isolation and Characterization of Fungi from Lake Magadi of the  
Kenyan Rift Valley

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## ABSTRACT

Lake Magadi is the southernmost lake in the Kenya Rift Valley, lying in a catchment of faulted volcanic rocks, north east of Lake Eyasi. Lake Magadi is a saline, alkaline lake, approximately 100 square kilometers in size that lies in a graben. Soda lakes harbor diverse groups of microorganisms that have developed mechanisms to thrive at different temperature ranges according to their optimal growth requirements. The objectives of this study were to isolate, characterize and identify fungi from Lake Magadi, a soda Lake of the Kenyan Rift Valley and then screen the isolates for the production of useful metabolites. Samples from the lake were isolated on malt extract agar, potato dextrose agar and Sabourand dextrose agar media at pH 10, 30°C. Thirty isolates were isolated, characterized using cultural, biochemical and molecular approaches, and screened for production of extracellular enzymes as well as potential for production of bioactive metabolites. The fungi grew at pH ranging from 5 – 10, temperature range of 25 – 35 °C and sodium chloride range of 5- 30 %.

All the thirty isolates produced different extracellular enzymes such as amylases, lipases, proteases and esterases. Antimicrobial assays done to determine the isolates range of *in vitro* activity against test organisms; *Staphylococcus aureus* (NCTC 10788), *Escherichia coli* (NCTC 10418), *Pseudomonas aeruginosa* (ATCC 27853), *Bacillus subtilis* (ATCC 55732), and fungi; *Candida albicans* (ATCC 90028) exhibited a range of inhibitory effects. Isolate LM13 produced coloured pigments into the media.

Analysis of partial sequences using Blast showed that about 60% of the isolates were affiliated to microorganisms belonging to the genus *Penicillium* and *Aspergillus* .7% and 10% belonged to the genus *Polyzellus* and *Fusarium* respectively while 7%

affiliated to the genus *Neurospora* and 16% clustered closely with uncultured fungus. The DNA sequences of LM3 showed identity of 95 % similarity with the previously known sequences in the GenBank database. These could represent a novel species of organisms within the lake's ecosystem. Isolates LM12 and LM17 showed DNA sequence identity of 89 % and 82% respectively and could represent novel genera of organisms.