



BACTERIAL DIVERSITY IN TERMAL SPRINGS IN DESERT ZONES: OJO DE DOLORES, JIMENEZ, CHIHUAHUA, MEXICO

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Introduction. The desert of Chihuahua is one of the largest in the world covering 362,600 km2 (140,000 square miles). Wells of water presented the possibility of unique habitats that favor the presence of endemic or exclusive species of the place. El Ojo de Dolores located in the region of Bolsón de Mapimí, in Jimenez, Chihuahua State, North of Mexico, is a tourist thermal spring also presenting physical features such as an average temperature of 37 ° C and a high concentration of sulfated and arsenicated compounds and also presents the output of 4 wells within a same spring. The aim of this work was to study the diversity of bacterial biota through isolation by culture and PCR-DGGE.

Results.

To know the chemical composition of the water samples thermal and physical characteristics were analyzed some parameters of interest (Table 1), these indicate a high mineral salts content according to Norma Oficial Mexicana NOM-127-SSA1-1994.

 Table 1. Parameters - physico-chemical analysis

Parameter	Value
Chloride mg/L	11.34
pH at 25 ° C	8,09
Sulphates mg/L	332,66
Arsenic mg/L	0,082
Iron mg/L	0.043
Sodium mg/L	27,28

the six samples arose only fifteen different morphologies, dominating the Gram negative on the Gram positive.

DGGE studies that showed diversity among the different sampling sites although little diversity of banding in genera

Based on 16S rDNA analyses showed a domain of the phyla proteobacteria and firmicutes (Fig. 1).



Fig.1 Relations of some samples of specimens (red) with sequences reported in GenBank (bold access number). With 1300 pb gene 16S rDNA using Kimura 2 parameter with 1000 repetitions type bootstrap using the MEGA 5 software

Conclusions. Morphological analyses show a great diversity of microorganisms while molecular analyses indicate specialized bacterial and probable new species. by which recommended more analysis.

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References.

1.-Muyzer, G.; DeWaal, E., 1993, Profiling of microbial population by denaturing gradient gen electrophoresis analysis of polymerase chain reaction amplified genes coding for 16S rRNA, volumen 59, páginas 695-700.