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ISOLATION AND IDENTIFICATION OF ALGAE PRESENT IN WHATER BODIES OF CHIHUAHUA TOWNSHIP

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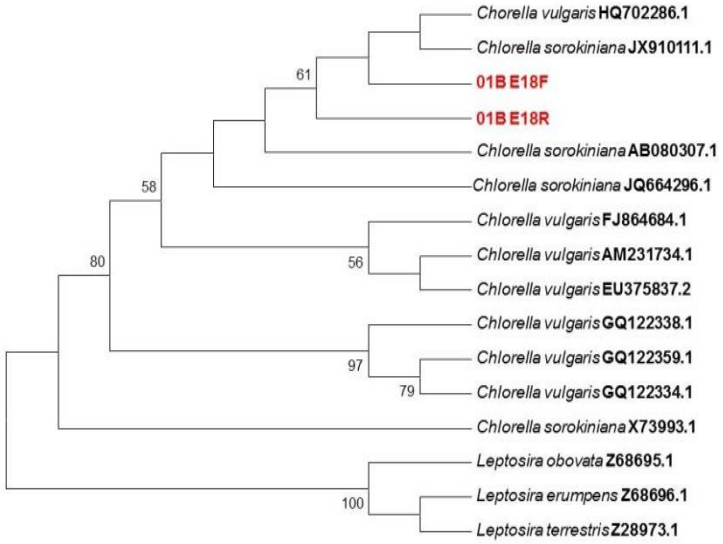
Introduction. Algae are a very diverse group in taxonomic terms, which may include the same bacteria that plants and protists. In recent times have become important by potential biotechnological use either as a source of biofuel or by managing to capture CO2. However there is very little information from them and more in areas like Northern Mexico which usually presents bodies of water located in regions that tend to be considered semi-arid as the State of Chihuahua

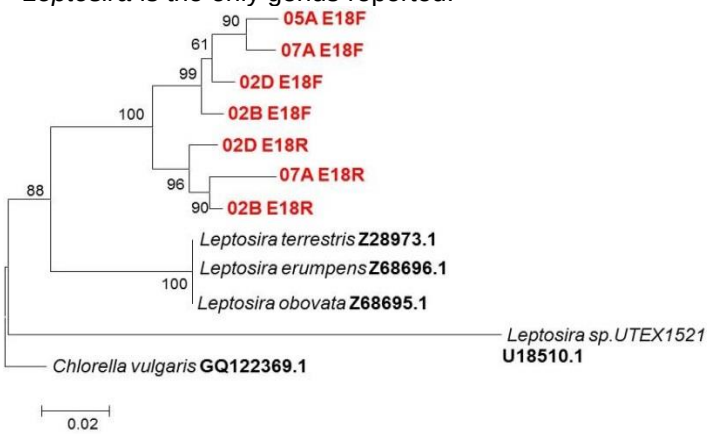
Methodology. The study was made in various water bodies in the city, rivers, streams and dams. Samples were taken in different parts of Sacramento and Chuviscar rivers. The sampling sites were chosen randomly along these rivers, in areas where the main streams converged and had good ventilation. The samples were cultivated for one month, after the samples were seeded in Petri dishes with BG-11 agar. After three weeks, the colonies with pigments characteristic of photosynthetic organisms, were selected. The colonies obtained were seeded again in Petri dishes, until uniform colonies were obtained, observed by microscope three weeks after. Once isolated colonies were seeded in "swan neck duct" with BG-11 solution, for maintain contamination free colonies and obtain sufficient biomass for extraction of DNA. The DNA of microalgae was obtained and purified using techniques previously described (Hoffman and Winston, 1987; Hoarau, Coyer, Stam and Olsen, 2006). Made slight modifications to the protocols described originally. The obtained DNA was used for amplify segments 16S and 18S ribosomal DNA, using the method PCR .The amplified products were sent for sequencing to Macrogen, in South Korea. Analysis was performed with the sequences obtained, then seeks similar sequences in the databases and aligned with the program CLUSTAL X.

Results. Seven samples were taken from different regions of Chuviscar and Sacramento rivers, the samples were taken in areas of confluence with streams and low flow sites, submit adequate aeration. They grew in 6 of 7 in Petri dishes. 17 colonies were selected. 13 of them grew, which were transferred to tubes with BG-11 solution. 5 of them were selected for growth in "swan neck duct". 4 weeks later, were observed in the microscope again and then performed for DNA extraction. There were two PCR amplifications for segments 16S bacterial and 18S eukaryote. All samples for fragments amplified 16S and 18S rDNA.

Because the 18S fragment is present only in eukaryotic organisms, it is considered that all of the amplified sequences were eukaryotic organisms. The all sequences were found in the class *Trebouxiophyceae*. The amplified sample 01B was classified in the genus *Chlorella*.



The other 4 samples (02B, 02D, 05A and 07A) were classified within the family *Ctenocladaceae*, which *Leptosira* is the only genus reported.



Conclusions. Isolated five colonies identified by colonial morphology and sequencing of the subunit 16S rRNA as members of the genus Chlorella (1), related to the species C. sorokiniana, and 4 with the Ctenocladaceae family whose only member is the genus Leptosira. This is the first report of isolation of algae for the State and municipality of Chihuahua