ISOLATION AND CHARACTERISATION OF ACTINOMYCETE ISOLATED FROM SEDIMENT AND WATER AT THE MONTH OF OUED CHELIFF IN MOSTAGANEM (ORAN)

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Abstract
The emergence of drug resistance among pathogenic bacteria due to the excessive uses of antibiotics has made the search for novel bioactive compounds from natural and unexploited habitats a necessity. The objective of this study is the isolation and characterization of an actinomycete strain by their 16S rRNA sequences. Eight isolates of actinomycetes were isolated from sediment and water at the month of oued Cheliff in Mostaganem. DNA was extracted and the 16S rDNA gene of the eight isolates was amplified by polymerase chain reaction (PCR). The sequences obtained were compared for similarity with genomic database banks, using the NCBI BLAST.

Keywords: Bacteria, Algerian Sea, Genetics, Estuaries

Estuaries are the most productive ecosystem on earth. They contain more organic material than most other types of environments. All of this organic matter creates a nutrient-rich ecosystem which promotes the development of a large diversity of microbial community including actinomycetes. They are filamentous, antibiotics producing bacteria and are found in soil, freshwater and marine water habitats [1]. Aquatic actinomycete produce several novel bioactive compounds. Species of Streptomyces, account for more than 70% of the total antibiotic production and Micromonospora was less than one-tenth as many as Streptomyces [2]. Eight actinomycetes were isolated from sediment mud and water at the month of oued Cheliff (fig 1).

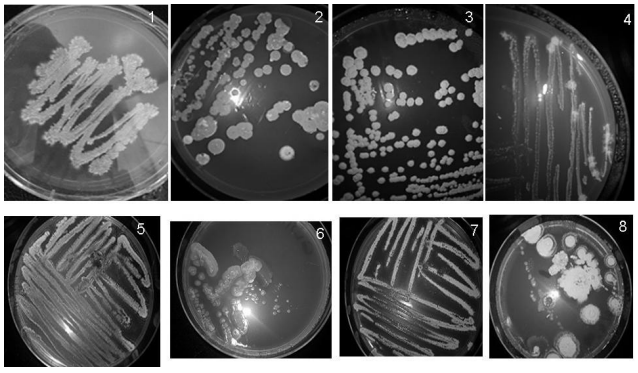

Fig. 1. Eight isolated strains of actinomycetes from Oued Cheliff. 1, ,2, 3, 4 & 5: *Streptomyces sp*. – 6: Isolate SSO – 7: isolate SS V – 8: Nocardia sp.

It's located in North West coast of Mostaganem and is the longest river in Algeria.The chromosomal DNA of each isolates was extracted using different methods (CTAB, boiling with CTAB, boiling with TE, simple boiling) 3].The 16S rRNA genes (1500 bp, partial sequence) of 5 representative isolates from morphologically different groups were analyzed by PCR method with 2 pairs of primers 9F (5'GAGTTTGATCMTGGCTCAG3') and SQ6 (5'CGGTGTGTACAAGGCCC3') [4].The PCR product obtained was sequenced. The same primers as above were used for this purpose. The sequence was compared for similarity with the reference species of bacteria contained in genomic database banks, using the NCBI BLAST. The 16S rRNA sequences allow us to identify 4 *Streptomyces sps* and one is *Nocardia sp*.The sequences obtained were compared with the corresponding sequences of other strains obtained from the GenBank database to evaluate phylogenetic diversity and taxonomic position of these isolates (fig 2).

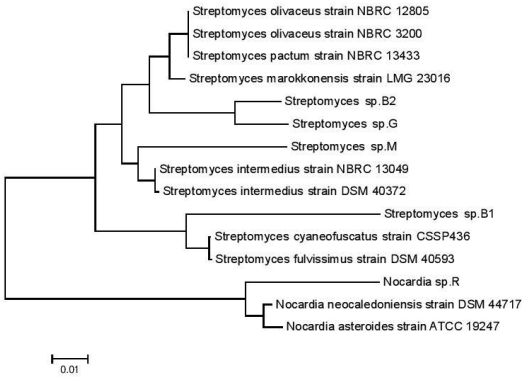

Fig. 2. Phylogenetic tree based on 16S RNA sequences.
Tree was constructed using the Neighbor Joining method. Strains B1, B2, G, M and R were isolated from sediments mud and fresh water.

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