

**NEW REPORT OF SOME BACTERIAL SPECIES ISOLATED FROM HUMAN
SPUTUM AMONG PATIENTS WITH RESPIRATORY TRACT INFECTIONS
USING 16SRDNA SEQUENCING**

ABDULAMEER ABDULLAH AL-MUSSAWI

College of Nursing, University of Basra, Iraq

ABSTRACT

Objective: The objectives of the study were to identification of bacteria from sputum samples in patients suffering from respiratory tract infections (RTIs) and suspected with TB infection, by using 16SrDNA sequencing.

Methods: The study was carried out to isolate and identify the common bacteria causing respiratory tract infections among 150 TB suspected patients attending to Advisory Clinic for Chest Diseases and Respiratory (ACCDR) in Basra city between March and December, 2013.

Results: During nucleotide sequences of 16SrDNA gene thirteen (20%) of bacterial isolates were isolated from 150 sputum clinical specimens identical with reference strain these are *Sporosarcina aquimarina*, *Pseudomonas putida*, *Bacillus licheniformis*, *Lautropia mirabilis*, *Mycobacterium tuberculosis*, *Streptococcus pasteurianus*, *Sporomusa sphaeroides*, *Sphingomonas paucimobilis*, *Bacillus anthracis*, *Thermotalea metallivorans*, *Streptococcus oligofermentans*, *Enterococcus faecium*, *Bacillus subtilis*.

Our study showed *Sporosarcina aquimarina*, *Pseudomonas putida*, *Bacillus licheniformis*, *Streptococcus gallolyticus*, *Sphingomonas paucimobilis* *Enterococcus faecium*, *Bacillus subtilis*, *Streptococcus oligofermentans* were recorded that isolated in RTI at the first time in world and in Basra/Iraq patients.

Conclusions: isolated different bacterial species were recognized in the present study by using the PCR nucleotide sequences as the best test for diagnosing the bacterial species among the other assays.

KEYWORDS: Bacteria, Respiratory Tract Infections (RTI), TB, 16SrDNA, Sequencing