



University of Zabol

Graduate management

Autonomous Pardis

Department of Biology

**The thesis Submitted for the Degree of M.Sc
(biology, molecular genetics)**

**Genetic diversity of *Pseudomonas aeruginosa*
strains isolated from hospitalized patients in zabol**

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Abstract

Pseudomonas aeruginosa is one of the most common nosocomial pathogens often causing major problems in Intensive Care Units. This study aimed to investigate the genotypic diversity of *Pseudomonas aeruginosa* strains isolated from hospitalized patients in zabol with Random Amplified Polymorphic DNA (RAPD) method and also to determine the antibiotic resistance pattern. One Hundred *Pseudomonas aeruginosa* isolates from different specimens were analyzed. These strains were isolated from patient admitted in Intensive Care Unit (ICU), non-ICU inpatient. All strains were identified with biochemical testing and antimicrobial susceptibility testing which carried out according to National Committee for Clinical Laboratory Standards (NCCLS). Random Amplified Polymorphic DNA typing (RAPD) was used to study the genetic diversity of *Pseudomonas aeruginosa* using 2 sets of primers and electrophoretic banding patterns were analyzed by NTSYS software. Phylogenic analysis of the RAPD pattern showed rates of genetic similarity ranging from 5-80%. Five epidemiologically and genetically related isolates (clones) were identified. Most of them were from ICU. We detected high antimicrobial resistance rate to cefexime (98%) and relatively low resistance rate tobramycin(4%), Ciprofloxacin and piperacilin(7%).Although a few epidemiologically related clones are found with RAPD method, most of the isolates are probably emanate from the host itself.

Key words: *Pseudomonas aeruginosa*, Typing, Random Amplified Polymorphic DNA (RAPD), Susceptibility pattern