



Prevalence of Klebsiella Pneumoniae Sequence type 258 in clinical isolates from Fayoum University Hospitals

Thesis

Submitted in partial fulfillment of the master degree in
Medical Microbiology and Immunology

Presented by

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(M.B.B.Ch)

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gene, *prp* gene**

Background:

Carbapenem-resistant *K. pneumoniae* (CRKP) has emerged as a serious clinical challenge in health care facilities worldwide. The vast majority of the global KPC-



producing *K. pneumoniae* isolates are associated with a single multilocus sequence type ST258. *K. pneumoniae* ST258 emerged as a notable clinical problem in the middle 2000s and remains the main ST everywhere.

Objective:

To detect the prevalence of *Klebsiella pneumoniae* sequence type 258 in the clinical isolates collected from patients at Fayoum University Hospitals as recommended by the infection control unit and to detect the antibiotic resistance patterns, the phenotypic and genotypic characterizations of these isolates.

Methods:

Bacteriological samples were collected then we did bacteriological isolation and identification of *K. pneumoniae* isolates. Then we screened the *K. pneumoniae* isolates for detection of carbapenem resistant



K. pneumoniae Strains. Then the (CRKP) isolates were subjected to antibiotic susceptibility testing and genotypic and phenotypic characterization. Finally, we detected the prevalence of *K. pneumoniae* ST 258 by polymerase chain reaction technique through detection of *pilv-1* and *prp* genes.

Results:

In our Study we detected (16.3%) of the CRKP isolates harboring both *pilv-1* and *prp* genes. These 8 isolates were *bla_{KPC}* positive and so we considered them as KPC-producing *K. pneumoniae* ST 258.

Conclusion:

Antibiotic resistance is a rising threat in Egypt.