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**Master Thesis Defense**

Entitled

*DOMINANCE OF bla<sub>OXA-48</sub>-LIKE AMONG CARBAPENEM-RESISTANT KLEBSIELLA PNEUMONIAE  
ISOLATED FROM ABU DHABI HOSPITALS*

By

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**Join with ZOOM or 872 3156 7742**

Abstract

[*Brief introduction:* Antibiotic resistance is a major concern for public health worldwide due to its associated morbidity and mortality, which is primarily attributed to the inappropriate use of antibiotics. This, in turn, leads to the evolution of bacteria which can develop genetic mechanisms to combat antibiotics. Despite the discovery of various antibiotics with different mechanisms of action, many have become ineffective due to the development of resistance over time. Carbapenems, in particular, are considered the last line of defense against bacterial infections, making their resistance a major concern. Among the various carbapenem-resistant bacteria, Carbapenem-resistant *Klebsiella pneumoniae* (CRKP) is of utmost concern due to its diverse resistome and mobilome. With the limited development of new antibiotics, it is crucial to understand the genetic relatedness of CRKP to facilitate antibiotic stewardship and enable the timely monitoring of any potential outbreaks.]. [*Aims:* Several studies have been performed for the prevalence and characterization of carbapenem resistance in *Klebsiella pneumoniae* in the UAE, but they rarely used advanced molecular typing methods to uncover the clonality of the strains. Therefore, this study aimed to employ whole genome sequencing (WGS) to study the genetic relatedness of CRKP isolates collected from Abu Dhabi hospitals.]. [*Method:* The study involved the collection of 162 *Klebsiella pneumoniae* strains from four hospitals in Abu Dhabi Emirate. The isolates were subjected to whole genome sequencing using the Illumina NovaSeq platform, and online bioinformatics tools were employed for the subsequent analysis.]. [*Results:* Our study revealed an alarming rate of extremely drug-resistant CRKP isolates and a high incidence of colistin resistance among XDRs. The most commonly found carbapenemase gene was *bla<sub>OXA-48-like</sub>*, with the most frequent ST being ST231, followed by ST2096, ST14, and ST147. ST231 clone was significantly associated with *bla<sub>OXA-232</sub>* production. The prevalence of ST231, ST2096, and ST14 was mainly restricted to one hospital, while ST147 was detected in all participated hospitals. The study also found a low prevalence of *bla<sub>KPC</sub>*-producing CRKP strains but identified ST11 clone carriers of the gene. Our findings suggest a localized spread of a high-risk *Klebsiella pneumoniae* clone in Abu Dhabi Emirate, highlighting the urgent need for surveillance and epidemiological investigations to monitor the antibiotic resistance situation across the United Arab Emirates.]

**Keywords:** Antibiotic resistance, Carbapenem-Resistant *K. pneumoniae*, Whole Genome Sequencing (WGS), high-risk clones, surveillance