

Chapter 2: **Rationale and Objectives**

Rationale:

K. pneumoniae has become an increasing concern in the clinical environment owing to the increase in the incidence of fatal illnesses. Due to the increasing number of multidrug-resistant, especially carbapenem-resistant and hypervirulent pathotypes along with antibiotic resistance among strains, which can infect both immune-compromised and healthy individuals have become critical in prevention and control.

The diagnostics field is now confronted with a major obstacle in promptly identifying multidrug-resistant and/or hypervirulent strains of *K. pneumoniae*. This problem arises from the absence of any efficient, rapid, and cost-effective methods. And in the medical field, the management of *K. pneumoniae* infections have becoming increasingly difficult to manage due to the significant occurrence of capsule formation, colonization facilitated by fimbriae, and the rise in antibiotic resistance, particularly against last-resort antibiotics like carbapenems, tigecycline, and colistin. However, while being aware of the many challenges, there is a scarcity of therapy and diagnostic options, mostly due to limited research conducted at the molecular and genomes level.

Our work aims to investigate the presence of antibiotic resistance and virulence genes using next generation sequencing, in addition to conducting a phenotypic examination of certain selected isolates, it is important to establish a correlation between both the genotypic and phenotypic data for better understanding. This technique will provide significant knowledge on the determination of the frequency of antibiotic resistance and virulence genes, *K. pneumoniae* clonal groups and sequence types (STs), Capsular type, and O-types. This data will offer critical insights into the field epidemiology and frequency of the genes, genomes, and clones, and will play a role in defining the specific targets for diagnostics, treatments, and vaccinations.

Objectives:

1. Sample collection, identification, screening of antibiotic resistance (ABR) isolates, and whole genome sequencing.
2. Genotypic and phenotypic study of antibiotic resistance in *K. pneumoniae*.
3. Genotypic and phenotypic study of virulence factors in *K. pneumoniae*.