

**SPECTRUM, ANTIMICROBIAL SUSCEPTIBILITY PROFILES, AND
MOLECULAR CHARACTERISTICS OF BACTERIAL PATHOGENS
FROM SEVERELY ILL COVID-19 PATIENTS IN KENYATTA NATIONAL
HOSPITAL, KENYA**

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DECLARATION

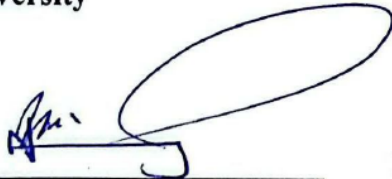
This thesis is my original work and has not been previously submitted for the purpose of obtaining a degree or any other accolade in any academic institution.

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ABSTRACT

Bacterial infections are among the leading causes of morbidity and mortality among patients with viral respiratory infections. Because it is difficult to differentiate viral from bacterial pneumonia based on clinical presentation and bacterial pathogens' epidemiology varies geographically, Coronavirus Disease 2019 patients are prescribed antibiotics frequently, even without laboratory-based evidence of bacterial infection. This has a serious negative implication on antimicrobial resistance situation that is expected to worsen causing approximately 10 million deaths and 100 billion USD economic loss by 2050. Information on bacterial infections among Coronavirus Disease 2019 patients in many developing countries, including Kenya, is limited. This study aimed to determine the spectrum, antimicrobial susceptibility profiles and molecular characteristics of pathogenic bacteria among patients with COVID-19 at Kenyatta National Hospital, Kenya. An analytical cross-sectional study design was adopted and a total of 120 participants purposively recruited among laboratory-confirmed severely ill Coronavirus Disease 2019 patients who gave informed consent through a legally authorized representative. Socio-demographic, clinical and outcome data were gathered using case report forms and structured sample collection forms. Nasopharyngeal and oropharyngeal swabs, tracheal aspirates and blood samples were collected, transported to KNH microbiology laboratory, and analyzed following the standard bacteriological methods. Bacterial isolation was done on selected culture media, whereas isolates identification and susceptibility testing were done using MALDI-TOF (VITEK[®] MS) and VITEK[®] 2 COMPACT system, respectively. The AST data was interpreted based on 2021 CLSI standards. The screening for ESBL-production was conducted using the Double-Disc Synergy Tests, which was subsequently confirmed through Phenotypic Confirmatory Disc Diffusion Test. ESBL-resistant genes were PCR-detected from all ESBL-producers at the Centre for Microbiology Research, KEMRI. An overall prevalence of 44.2% (53/120) bacterial infections was found among the study participants, with a 31.7% (38/120) mortality rate. Isolates of Gram-negative bacteria (GNB) exhibited greater prevalence, (73.1%, 49/67). Majority (69.6%, 32/46) of multidrug resistant (MDR) bacteria were GNB. *K. pneumoniae* (45.5%, 15/33) was the dominant ESBL producer and most of MDR-GNB harboring the TEM (83%, n=10/12) and SHV resistance gene (100%, n=7/7) were resistant to beta lactamase inhibitors including amoxicillin/clavulanate but susceptible to piperacillin/tazobactam (60%, n=6/10). Male patients were more likely to have bacterial infections (aOR = 2.61, 1.2 – 5.65), including those caused by ESBL producing bacteria (aOR=0.21, 0.06 - 0.68). Individuals with pre-existing comorbidities were found to have a five-fold increased likelihood of harboring ESBL-producing bacteria (cOR=5.46, 1.37 - 21.67). Patients: aged 25 to 44 years (aOR = 0.13, 0.02 – 0.6), hospitalized in the IDU ward (aOR=3.27, 1.08– 6.89), vaccinated for Coronavirus Disease 2019 (aOR = 0.2, 0.05 – 0.83) and hospitalized for short duration (0 -5 days) (aOR=14.28, 3.25 - 62.76) had a positive hospitalization outcome. These results highlight a significant burden of bacterial infections among Coronavirus Disease 2019 patients, with males at higher risk. Those: not vaccinated, admitted to CCU, aged over 60 years, and with pre-existing comorbidities had poor outcome. There is urgent need for systematic and continuous AMR surveillance at KNH and beyond to inform prevention interventions in accordance with national and global action plans.