**INVESTIGATION OF CARRIAGE AND ANTIBIOTIC SUSCEPTIBILITY OF PATHOGENIC BACTERIA IN THE NOSE AND OROPHARYNX AMONG STUDENTS OF UNIVERSITI TUNKU ABDUL RAHMAN KAMPAR CAMPUS**

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Some members of the normal microbiota of the human upper respiratory tract can be potentially pathogenic when they overgrow or translocate to other body sites; the latter could lead to pneumonia and meningitis. The presence of these pathogens can be investigated via respiratory carriage studies, which have been recognised as a pragmatic solution to gaining large real-time epidemiological data on their carriage at the population level. This study aimed to investigate the upper respiratory carriage of *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Neisseria meningitidis*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* among the students of UTAR Kampar Campus. Nasal and oropharyngeal swabs from 100 students aged 18-28 years were collected and cultured onto various media, which include the chocolate agar, Columbia blood agar, MacConkey agar, mannitol salt agar, and King’s A medium. Identification of the *S. aureus*, *K. pneumoniae*, and *P. aeruginosa* isolates obtained was done through assessment of their growth characteristics, Gram stain, biochemical tests, and 16S rDNA sequencing. They were isolated from 39%, 12%, and 1% of subjects in this study, respectively. In the Kirby-Bauer assay, 19 *S. aureus* isolates were resistant to penicillin while 11 were intermediately resistant to quinupristin-dalfopristin. All the *K. pneumoniae* isolates were resistant to ampicillin as expected. Two *S. aureus* isolates were *mecA*-positive but only one showed methicillin resistance and was determined to be methicillin-resistant *S. aureus* (MRSA). Nine and two *K. pneumoniae* isolates were *blaSHV*- and *blaTEM*-positive in the multiplex extended-spectrum beta-lactamase (ESBL) PCR, respectively; however, these did not correspond to the findings of the combination disc test. In this study, the presence of *S. pneumoniae*, *H. influenzae*, and *N. meningitidis* was assessed via multiplex PCR on total DNA extracts from the chocolate agar sweeps. Among the 44 subjects screened, 9.1%, 20.5%, and 2.3% were positive for these target bacteria, respectively. All these were from the oropharyngeal swabs except for the sole *N. meningitidis*-positive sample, which was of nasal origin. The outcomes of this study contributed to better understanding of the respiratory carriage of bacterial pathogens, which will be of value to help inform the immunisation and antibiotic prescription policies.