

COVID-19 hospitalisation during period of delta and omicron predominance in Malaysia: A descriptive study

Syarifah Nurul Ain Syed Badaruddin¹, Swarna Lata Krishnabahawan¹, Shafiq Eiman Abdul Razak¹, Satya Tamilselvam¹, Suriya Kala Balachandran¹, Tharmini Ravi¹, Aminiril Anisah Abdul Hamid¹, Nur Suriana Mah Hassan¹, Liew Boon Seng¹, Kalaiarasu M. Peariasamy², Chew Chun Keat², Low Ee Vien²

¹Clinical Research Centre, Hospital Sungai Buloh, ²Institute for Clinical Research, National Institute of Health

ABSTRACT

Introduction: Hospital Sungai Buloh is the main COVID-19 referral centre since the pandemic started. Having a large database of COVID-19 patients, this study describes the demographic characteristics of patients who were admitted to Hospital Sungai Buloh during periods of Delta and Omicron predominance. **Materials and Methods:** Medical records of COVID-19 patients who were hospitalized in Hospital Sungai Buloh during the period of Delta and Omicron predominance were reviewed retrospectively and analyzed. **Results:** Patient admissions during the period of Delta predominance from May-July 2021 (5815 patients) are higher than during the period of Omicron predominance from January-April 2022 (3144 subjects). Among 8959 COVID-19 patients, 55.6% of them were in the age group 60-79 years old (4977 patients). Majority were male (50.7%), Malaysian (98.5%) and diagnosed as Category 4 COVID-19 upon admission (48.6%). A total of 935 (10.4%) patients died during hospitalisation. **Conclusion:** This descriptive study serves as a baseline research for more studies in future using the same dataset. Rigorous data cleaning is currently being performed to produce more robust and reliable results.

Keywords: COVID-19, Hospitalisation, Omicron, Delta

Serotypes and beta-lactamase-producing Haemophilus influenzae isolated from children attending childcare centres in Kuala Lumpur post vaccination era

Salina Mohamed Sukur, Saraswathiy Maniam, Fashihah Sherina Abdul Hadi Sabri

Infectious Diseases Research Centre, Institute for Medical Research, National Institutes of Health (NIH)

ABSTRACT

Introduction: Despite widespread and routine immunisation of children, HI remains a significant pathogen and colonisation of the upper respiratory tract is a risk factor for developing disease. This study aimed to identify the serotype distribution and determination of ampicillin resistance genes of HI strains that are asymptotically carried by healthy children post vaccination. **Materials and Methods:** Twenty-four HI isolates were obtained from oropharyngeal swabs of healthy Hib vaccinated children aged 2-4 years old (n = 436) attending registered childcare centres (n = 30) in Kuala Lumpur (August 2018-May 2019). HI isolates were characterised by serotyping using standard slide agglutination test, ampicillin susceptibility testing and resistance associated gene sequencing. **Results:** The rate of ampicillin resistance was 25% (6/24). All ampicillin resistant strains were also beta-lactamase positive (BLPAR). Out of these, 2 were serotype Hib strains, one each from serotype a and f, and 2 were NTHi. Of these 6 BLPAR isolates, 4 strains possess the TEM-1 β -lactamase gene. **Conclusion:** The findings that 21% of HI isolates were Hib and only 2 out of 5 Hib strains were BLPAR and possessed TEM-1 β -lactamase gene shows that despite routine immunisation of children, they still carried Hib asymptotically and not many strains showed reduced susceptibility to β -lactam antibiotic.

Keywords: serotype, beta-lactamase, haemophilus, influenza, childcare, ampicillin