

*Staphylococcus epidermidis* isolates from blood cultures of newborns with sepsis were investigated from January to December 2021. The frequency of detection of virulence genes was distributed as follows: *atl* (94.5%), *sspB* (94.5%), *sspA* (89%), *gehD* (89%), *ebh* (89%), *hly* (72%), *sdrG* (39%), *sdrF* (28%), *nuc* (28%), and *lip* (13%). Also, 10 isolates (55%) were resistant to ceftazidime (MRSE). Furthermore, 72% of *S. epidermidis* isolates showed resistance to azithromycin and 33% were resistant to clindamycin and gentamicin. Also, 39% of strains were resistant to fluoroquinolones. All isolates were susceptible to vancomycin, linezolid, and fusidic acid. **Conclusions:** *S. epidermidis* strains isolated from blood cultures had high rates of exoenzymes *sspB*, *sspA*, *gehD*, autolysin (*atl*),  $\beta$ -hemolysin (*hly*), and cell-wall-associated fibronectin-binding protein (*ebh*). Among 18 neonatal sepsis pathogens, 10 (55%) were MRSE, so it is necessary to pay attention to antibiotic therapy adjustment.

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**Subject Category:** Antibiotic Stewardship

**Abstract Number:** SG-APUSIC1074

**Trend of 'ESKAPE' and their susceptibility changes for meropenem and levofloxacin during the pandemic at Sardjito Hospital Yogyakarta Indonesia**

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**Objectives:** The bacteria in the 'ESKAPE' group are monitored due to their ability to resist antibiotic action. During the COVID-19 pandemic at our hospital, the usage of meropenem and levofloxacin as the empirical treatment for bacterial pneumonia increased and might have contributed to the antimicrobial resistance problem. In this study, we evaluated the ESKAPE group infection rates and their susceptibility to antibiotics in Dr. Sardjito Hospital, a referral and academic hospital in Yogyakarta, Indonesia. **Methods:** Data for ESKAPE pathogens in 2019–2021 were taken from the microbiology laboratory of Dr. Sardjito Hospital and were evaluated. **Results:** The proportion of ESKAPE isolates among positive cultures during 2019–2021 slightly increased from 49.4% to 48.4% to 50.7% each year ( $P > .05$ ). The dominant ESKAPE infections were pneumonia, bloodstream infection, and urinary tract infection by *K. pneumoniae*, and wound infection by *P. aeruginosa*. The susceptibility pattern of ESKAPE to meropenem decreased from 72% in 2019 to 68% in 2020 but increased to 84% in 2021. To levofloxacin, the susceptibility pattern was decreased in a fluctuating trend from 68% in 2019 to 33% in 2020 and to 39% in 2021. During the COVID-19 pandemic (2020–2021), the pattern of ESKAPE infections was similar to that of 2019. In descending order, the frequency rank was *K. pneumoniae*, *P. aeruginosa*, *A. baumannii*, *Enterobacter spp*, and *S. aureus*. The proportions of MDR isolates increased from the pre-pandemic period to the COVID-19 pandemic era for *E. faecium* (from 5% to 24.4%), for *A. baumannii* (from 9.6% to 38.5%), and for *P. aeruginosa* (from 7.4% to 13.5%) ( $P < .05$ ). These patterns did not differ between non-COVID-19 patients and COVID-19 patients. These results highlight the general impact of overused antibiotics beyond COVID-19 patients. Usage of watched and restricted antibiotics must be more controlled because bacterial coinfection and superinfection in COVID-19 patients was relatively low. **Conclusions:** During the COVID-19 pandemic, ESKAPE infections increased and their susceptibility to meropenem and levofloxacin decreased. Tight control of antibiotic usage is needed.

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**Association between severity of COVID-19 pneumonia and vaccination status in a tertiary-care teaching hospital in Malaysia**

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**Background and objectives:** Since the introduction of the COVID-19 vaccine through the National COVID-19 Immunization Program in Malaysia in February 2021, the number of cases of severe COVID-19 and mortality have progressively decreased. We explored the association between vaccination status, type of vaccine, and the highest COVID-19 clinical category. **Methods:** Patients were recruited via the electronic medical record (EMR) at University Malaya Medical Centre (UMMC) from July 2021 onward. Included patients were aged  $\geq 18$  years old with positive SARS-CoV-2 RT-PCR results from respiratory samples (nasopharyngeal swab, saliva, or sputum). Patient demographic data, COVID-19 clinical category, vaccination status, and type of vaccine received were recorded. **Results:** In total, 1,391 positive SARS-CoV-2 PCR results were reviewed; 1,188 patients (85%) with complete data were analyzed. These patients' median age was 50 years. The proportions of patients COVID-19 clinical categories were as follows: category 1 (4.04%), category 2 (28.37%), category 3 (10.7%), category 4 (30.6%), and category 5 (2.6%). The mortality rate was 21.5%. As of July 2021, only 16.8% of patients were fully vaccinated, 30.3% were vaccinated, 31.5% unvaccinated, and 21.5% had unknown vaccination status. In total 364 patients with category 4 COVID-19 (4.4%;  $P < .001$ ) were fully vaccinated and no patients who were fully vaccinated had category 5 COVID-19 ( $P = .011$ ). Furthermore, 40.8% of patients who died had unknown vaccination status ( $P < .01$ ); 28.1% of patients who died were unvaccinated ( $P = .015$ ); 25.3% of patients who died were partially vaccinated ( $P = .036$ ); and 0.4% of patients who died were fully vaccinated ( $P < .001$ ). For category 4 and 5 illness and death, there were no significant differences between the type of vaccine received (Pfizer-BioNTechR, Astra ZenecaR and Coronavac/SinovacR) and severe COVID-19. **Conclusions:** The completion of 2 doses of government-approved COVID-19 vaccination is paramount in preventing severe COVID-19 disease and death. Rapid rollout and equitable distribution of vaccination should be initiated. Vaccine hesitancy should be promptly addressed to ensure vaccination uptake.

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**Detection of SARS-COV-2 in nasopharyngeal swabs with MALDI-TOF MS and machine learning**

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**Objectives:** The widespread distribution of SARS-CoV-2 and its high contagiousness pose a challenge for researchers seeking to develop a rapid and cost-effective screening method to identify carriers of this virus. RT-PCR is considered the gold standard for detecting viral RNA in nasopharyngeal

swabs, but it is time-consuming and requires constant changes in the primer composition due to the mutation of SARS-CoV-2 strains. We propose a method for the detection of SARS-CoV-2 in nasopharyngeal swabs using MALDI-TOF MS and machine learning. **Methods:** Nasopharyngeal swabs from patients with PCR-confirmed COVID-19 and control participants were tested (130 and 80 swabs, respectively) with MALDI-TOF MS MicroFlex LT using the HCCA matrix. MALDI spectra were preprocessed in R version 4.1.2 software with the MALDIquant R package using the workflow: sqrt transformation, wavelet smoothing, SNIP-based base removal, and PQN intensity calibration. Peaks were detected with MAD algorithms with following Peak alignment on the following parameters: minFreq 70% and tolerance 0.005. Machine learning was performed with the rtemis r package on GLM, random forest, and XGBoost models. **Results:** These models were characterized by specificity, sensitivity, and F1 score. GLM models (specificity 1 and sensitivity 0.5) showed a low F1 score of 0.71. However, the random forest and XGBoost models demonstrated sensitivity, specificity, and F1 score equaling 1. **Conclusions:** We propose a screening method for SARS-CoV-2 detection (sensitivity 1 and specificity 1). This methodology combines the analysis of nasopharyngeal swab samples using MALDI-TOF-MS with machine learning. It is suitable for screening patients with COVID-19 at the first stages of diagnosis. Random forest and XGBoost models demonstrated sensitivity, specificity, and F1 scores equaling 1.

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**COVID-19 vaccine acceptance and hesitancy among primary healthcare workers in Singapore**

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**Objectives:** Factors affecting COVID-19 vaccine acceptance and hesitancy among primary-care healthcare workers (HCWs) remain poorly understood. We sought to identify factors associated with vaccine acceptance and hesitancy among HCWs. **Methods:** A multicenter online cross-sectional survey was performed across 6 primary-care clinics from May to June 2021, after completion of the vaccination rollout. The following data were collected: demographics, profession, years working in healthcare, residential status, presence of chronic medical conditions, self-perceived risk of acquiring COVID-19, and previous influenza vaccination. HCWs who accepted the vaccine were asked to rank their 5 best reasons for vaccine acceptance. HCWs who were vaccine hesitant completed the 5C scale on psychological antecedents of vaccination. **Results:** Of 1,182 eligible HCWs, 557 responded (response rate, 47.1%) and 29 were excluded due to contraindications. Among 557 respondents, the vaccine acceptance rate was 94.9% (n = 501) and 5.1% were hesitant (n = 27). COVID-19 vaccine acceptance was not associated with sex, age, ethnicity, profession, number of years in healthcare, living status, presence of chronic diseases, self-perceived risk, or previous influenza vaccination. The 3 most common reasons for COVID-19 vaccine acceptance as ranked by 501 HCWs were (1) to protect their family and friends, (2) protect themselves from COVID-19, and (3) the high risk of acquiring COVID-19 because of their jobs. The 15-item questionnaire from the 5C psychological antecedents of vaccination was completed by 27 vaccine hesitant HCWs. The mean scores for the components of the 5Cs were ‘confidence’ (3.96), ‘complacency’ (3.23), ‘constraint’ (2.85), ‘calculation’ (5.79) and ‘collective responsibility’ (4.12). **Conclusions:** COVID-19 vaccine hesitancy is a minute issue among primary-care HCWs in Singapore, where the acceptance rate is 95% with a 5% hesitancy rate. Future studies can focus on other settings with higher hesitancy rates and acceptance of booster vaccinations with the emergence of

the SARS-CoV-2  $\delta$  (delta) variant. Trial Registration: This study was approved by the National Healthcare Group (NHG) Domain Specific Review Board (DSRB), Singapore on April 26, 2021 (Reg No. 2021/00213).

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**Descriptive study on COVID-19 exposures in Singapore General Hospital**

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**Objectives:** The highly transmissible SARS-CoV-2 has swept across the globe, causing large swaths of COVID-19, displacing medical resources and attention from patients with other life-threatening illnesses, and overwhelming healthcare institutions. Shifting toward endemicity, the Singapore Ministry of Health ceased issuing quarantine orders to close contacts of infected cases on October 11, 2021. However, contact tracing and exposure management within SGH continued with the same risk criteria. We have examined COVID-19 exposures in different hospital locations to determine the effectiveness of surveillance in breaking the chain of transmission. **Methods:** Contact tracing of COVID-19 exposures among Singapore General Hospital (SGH) staff and patients has been conducted since the first COVID-19 diagnosis in January 2020. The information collected is used to identify those at higher risk of infection for enhanced surveillance or isolation. The data analyzed in this study were collected during later periods of the SARS-CoV-2  $\delta$  (delta) pandemic wave between August 1, 2021, and December 31, 2021. **Results:** During the 4-month study period, there were 1,686 SARS-CoV-2 exposures in SGH. Among these 1,686 exposures, 1,157 (69%) were contacts with an infected patient. Among these infected source patients, 915 were emergency department patients, 210 were ward inpatients, and 32 were clinic outpatients. The remaining 524 exposure events (31%) were contacts with infected staff, of whom 441 were SGH employees and 83 were employees from other SingHealth institutions. The remaining 5 index cases were visitors to SGH. Of the 1,686 exposure events, 330 had associated at-risk contacts requiring exposure management. Among 330 patient index cases, 213 (64.5%) resulted in 699 exposed contacts (patients vs staff), whereas 117 staff index cases resulted in 435 exposed contacts (patients vs staff). For 434 exposed contacts who were staff, 204 (47%) of their exposures occurred in inpatient ward settings, followed by 153 (35.3%) that occurred in outpatient clinics, 36 (8%) that occurred common lounging areas, 16 (3.6%) that occurred in office sites, 15 (3.4%) that occurred in the community, 8 (1.8%) that occurred in occupation therapy, and 2 (0.5%) that occurred in the emergency department. For 688 exposed contacts who were patients, 579 (84.1%) exposures occurred in inpatient wards, 70 (10.2%) occurred in DEM, 19 (2.7%) occurred in other SingHealth institutions, 16 (2.3%) were exposures to roving porters, and 3 (0.4%) occurred in the community. During the study period, 3 hospital clusters were identified and investigated, one of which included secondary cases. **Conclusions:** Most SARS-CoV-2 exposures in SGH occurred in inpatient settings where patients were index cases. Despite intensive contact tracing and stringent surveillance and isolation measures, inpatient clusters could not be prevented.

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**COVID-19 vaccine booster hesitancy among healthcare workers: A retrospective observational study in Singapore**

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