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%), *hlb* (72%), *sdrG* (39%), *sdrF* (28%), *nuc* (28%), and *lip* (13%). Also, 10 isolates (55%) were resistant to cefoxitin (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 fluorchinolones. 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), β-hemolysin (hlb), 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.

Antimicrobial Stewardship & Healthcare Epidemiology 2023;3(Suppl. S1):s1–s2
doi:10.1017/ash.2023.6

Subject Category: Antibiotic Stewardship
Abstract Number: SG-APSIC1074
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 prepandemic 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.

Antimicrobial Stewardship & Healthcare Epidemiology 2023;3(Suppl. S1):s2
doi:10.1017/ash.2023.7

Subject Category: COVID-19
Abstract Number: SG-APSIC1208
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 ≥18 years old with positive SARS-CoV-2 RT-PCR results from respiratory samples (naso-oropharyngeal 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.

Antimicrobial Stewardship & Healthcare Epidemiology 2023;3(Suppl. S1):s2
doi:10.1017/ash.2023.8

Subject Category: COVID-19
Abstract Number: SG-APSIC1053
Detection of SARS-COV-2 in nasopharyngeal swags 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