SARS-CoV-2 RBD [Elecsys® Anti-SARS-CoV-2 S (ECLIA), Roche Diagnostics]

Results: Out of 806 sera collected from the blood donors, qualitative screening of antibodies against SARS-CoV-2 virus showed 37 samples (4.59%) were positive for total antibodies against RBD, while 25 (3.10%) were positive against N proteins. 28 samples (3.47%) were tested positive by the quantitative determination of the antibodies.

Conclusion: Our study revealed similar seroprevalence rate found in an identical study conducted in Los Angeles whereby 4.06% out of 865 collected sera were positive. While the blood donor population may not represent the Malaysian population in general, the finding of the seroprevalence in this group could indicate the rate of people infected with this virus is far more than reported and could aid public health decision making.

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PS04.27 (1000)

Mortality Among COVID-19 Patients in the Intensive Care Unit (ICU): A Single-Centre Study from a Malaysian Perspective

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Purpose: This study investigated the prevalence of mortality among COVID-19 patients admitted to an intensive care unit (ICU) at a single centre hospital in Klang Valley, Selangor, Malaysia. Besides, adverse clinical events (ACE) among COVID-19 patients admitted to ICU who died and were alive were compared, and the factors associated with mortality were explored.

Methods & Materials: Patients admitted to a single centre ICU with polymerase chain reaction (PCR) confirmed of SARS-CoV-2 virus within February 2020-2021 were included in this study. Adverse clinical event (ACE) consists of the presence of pulmonary embolism (PE), deep vein thrombosis (DVT), line-related thrombosis, stroke, myocardial infarction (MI) and peripheral artery disease (PAD) during their ICU admission. A composite of ACE comprised $\geq$ 1 PE, DVT, line-related thrombosis, stroke, MI and PAD. Mortality is defined as COVID-19 patients who died during ICU admission throughout data collection.

Results: Mean (SD) age was 56.6 (13.7) with 63.5% male and 61.6% Malay. Median (IQR) 7 (3-14) days of ICU admission, 64.2%, 53.2 % and 20.9% had underlying hypertension, diabetes, and obesity, respectively. Out of 534 patients included in the study, 122 patients died, with 64.8% developed $\geq$ 1 ACE compared to 39.1% patients who survived the infection. Higher proportion of deceased patients developed PE (47.5% vs. 34%; p=0.006), MI (16.4% vs. 4.6%; p<0.001), stroke (12.3% vs. 1.5%; p<0.001) and DVT (2.5% vs. 0.2%; p=0.04) than those who survived. Significant predictors of mortality on multivariate logistic regression model include age [OR 1.05 (95% CI 1.03 – 1.07)], length of ICU stay [OR 1.05 (1.02 – 1.07),

chronic kidney disease [OR 2.30 (1.32 – 4.01), and presence of $\geq$ 1 ACE [OR 2.32 (1.45 – 3.72)].

Conclusion: The overall mortality of COVID-19 patients admitted to a single centre ICU is high (22.8%), with greater proportion of patients who developed $\geq$1 ACE. Key factors associated with the mortality were age, length of ICU stays, underlying chronic kidney disease and presence of $\geq$ 1 ACE. This finding might be helpful to the healthcare providers in the early detection and prevention of ACE associated with mortality among COVID-19 patients admitted to the ICU.

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Feasibility and accuracy of variant PCR assays for low- and middle-income countries in SARS-CoV-2 surveillance

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Purpose: Surveillance of different SARS-CoV-2 variants of concern (VOCs) is a crucial aspect in control of the pandemic. Although sequencing is the gold-standard to detect VOCs, it is labor intensive and is costly. We compared a cost-effective real-time PCR assay that detects single nucleotide polymorphisms (SNPs) of VOCs, with next generation sequencing (NGS) in surveillance of VOCs.

Methods & Materials: A total of 782 SARS CoV-2 PCR positive samples From May – August 2021 were screened using two variant RT-qPCR assays (Seegene Allplex[TM] SARS-CoV-2 Variant Assay I and II), which detects 7 SNPs in the spike protein assigning them to one of the VOCs. We compared the results of the variant RT-qPCR with Illumina (n=97) and Oxford Nanopore (n=53) platforms in a subset of samples (n=150). Sequences with > 25x coverage were used and assigned to a Pangolin lineage.

Results: 516 samples amplified for N501Y and HV69/70 deletion of the spike protein were assigned as alpha (B.1.1.7). Two samples with spike K417N mutation along with N501Y and E484K were considered to be beta (B.1.351) and 175 samples which are only positive for spike L452R mutation were considered to be delta (B.1.617). 120/156 samples designated as alpha, 22/175 designated as delta and 2 samples designated as beta by RT-qPCR were sequenced either by Illumina or Oxford nanopore platforms. The sequencing results showed a 100% accuracy with the variant RT-qPCR for identification of VOCs.

Conclusion: RT-qPCR that detected SNPs specific for VOCs, appear to be highly sensitive and specific in detection of VOCs and had a similar specificity of genomic sequencing. Therefore, this could be a rapid and less expensive method for surveillance of VOCs, in lower income countries. However, as it only detects specific SNPs, any emerging mutations of concern in these VOCs or newly emerging variants, will not be detected.

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