Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

hospital against medical advice. The outcome of secondary infections is depicted in Figure 1.

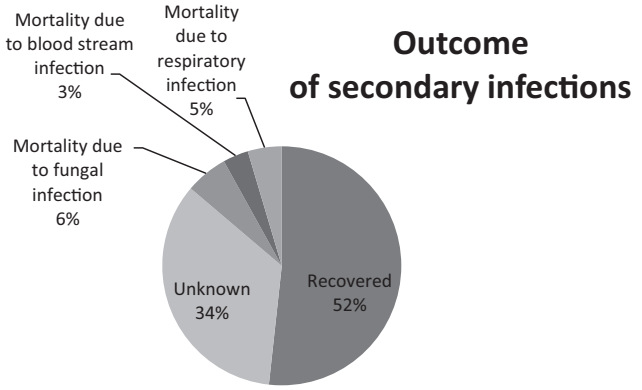

Figure 1. Outcome of secondary infections.

Conclusion: Secondary infections play a vital role in increasing the morbidity and mortality in COVID-19 patients. The common isolates were Carbapenem Resistant *Klebsiella pneumonia* and Multidrug resistant *Acinetobacter baumanii*. Based on the time taken between COVID-19 positivity and development of secondary bacterial infection we can say that these pathogens could be nosocomial. Most of the bacterial isolates identified are multidrug resistant implying that empirical antimicrobial therapy might not be useful in such cases. Adhering to antimicrobial stewardship guidelines and strict infection control practices can help reduce the transmission such resistant pathogens in healthcare settings. The most common fungal isolate was *Rhizopus spp.* The primary reason for dissemination of fungal infection could be improper glycemic control and rampant use of corticosteroids and immunomodulators. Picking up the sentinel signs of mucormycosis early and employing multimodal therapy with antifungals and surgical debridement can play a vital role in reducing this fungal menace.

PCO-008

Identification of daclatasvir as a repurposed drug against Nsp15 of SASR-CoV2 (COVID-19) by using in silico approaches

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Background: In December 2019, SARS-Cov-2 epidemic was reported in Wuhan, China and then it spreads widely affects millions of people around the world. Nsp15 is one of the key members of EndoU family which perform several biological functions like RNA endonuclease activity which generate 2'-3' cyclic phosphodiester termini. In viruses, Nsp15 is conserved among nidoviruses and absent in other RNA viruses which makes it potential target for recent coronavirus outbreak.
Methods: In this study, we have used earlier studied Benzopurpurin B which has inhibition property against Nsp15 protein of SARS virus (0.2 μM). Next, we have developed structure-based pharmacophore model with the help of Benzopurpurin B and crystal structure of Nsp15 endoribonuclease NendoU from SARS-CoV-2 (6vww). For pharmacophore development, we have employed two different software, viz., Discovery Studio 4.0 and Ligandscout. The selected pharmacophore was used to screen FDA approved drugs from DrugBank Database. The hits retrieved were next subjected to molecular docking analysis followed by molecular dynamics studies.
Results: The best pharmacophore model A with 6 features (2 hydrogen bond acceptor, 2 hydrogen bond donor and 2 hydrophobic group, AADDHH) was selected based on highest selectivity score of 11.155. the validated hypo model 1 able to screen out 136 drugs out of 2454 FDA approved drugs from DrugBank Database. These drugs were further filtered out using molecular docking to remove any false-positive hits. Finally, 3 top hits were selected for MD simulation to confirm their binding stability.
Conclusion: Daclatasvir (DB09102), an antiviral approved drug was identified as possible candidate for designing the potent inhibitor against Nsp15 of SARS-CoV-2 virus, although further evaluation via wet lab is required to measure its efficacy.

Abstract withdrawn

PCO-010

Real-time PCR detects 4 rapid transmission variants of SARS-CoV-2

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Background: Currently in the world there are many variants of SARS-CoV-2, among which there are 4 variants: Alpha (B.1.1.7), Beta (B.1.351), Gamma variant (P.1), and Delta variant (B.1.617.2) has a faster transmission rate than the original strain by 82%, 161%, 50% and 198%, respectively. To detect the SARS-CoV-2 variants circulating in a certain endemic area, the method that the researchers are currently using is to sequence the entire genome

of the viruses detected in the samples. However, the sequencing method has the limitation that it cannot be applied in clinical laboratories.

Aim of the study: Design a test kit using multiplex real-time PCR that can be performed in diagnostic laboratories to detect 4 variants Alpha, Beta, Gamma and Delta and two mutations that help the virus to spread rapidly (D614G) and can escape the action of specific antibodies (E484 K).

Material and method: Primers and probes to detect Alpha, Beta, Gamma and Delta variants are designed based on the detection of specific mutations of these variants. The Alpha, Beta and Delta variants were detected based on ARMS Taqman real-time PCR (ARMS: Amplification Refractory Mutation System) with the principle that if a mutation is present, the Taqman probe will not be hydrolyzed and will not have an amplified signal, if there is no mutation the Taqman probe will be hydrolyzed and will have an amplified signal. The Gamma variant and the D614G mutations as well as the E484 K mutations were detected based on the SNP Taqman real-time PCR with the principle that each mutation would be detected by two Taqman probes with different reporters, FAM and HEX or TexasRED and CY5 and depending on the early or late of the fluorescent signal of these two Taqman probes, it can be concluded whether or not there is a mutation. The test kit is designed with three RT multiplex real-time PCR with multiplex A (MPL-A) to detect SARS-CoV-2 based on E gene using primers and Taqman probe (FAM) according to WHO design, variant Alpha (HEX) and the internal control is the RNAseP gene (CY5); MPL-B detects Delta variant (FAM), Beta variant (HEX), and Gamma variant (TexasRED/CY5); MPL-C detects D614G (FAM/HEX) and E484 K (TexasRED/CY5). The multiplex was prepared from AgPath-ID™ One-Step RT-PCR (ThermoFisher, USA). To check the primers and probes, the corresponding DNA sequences for the mutants were also designed as controls [+]. The test kit is then tested on samples that are the RNA extracts positive with SARS-CoV-2.

Results: Testing on [+] controls showed that the detection limit for the E gene and the Alpha variant was 10-6 fm/μl, the Delta variant was 10-5 fm/μl, and the Beta and Gamma variant was 10-7 fm/μl, the D614G and E484G mutations were 10-5 fm/μl. There was no cross-detection of mutations or variants. Tested on RNA extracts that were positive with SARS-CoV-2, the results said that: In HCMC, the strain (1) taken in April 2020 is the wild type, while all strains (12) taken in June 2021 are Delta variants with additional mutations D614G and no mutations E484 K; In Quang Nam, the samples taken in June 2020 are both wild type (2) and have mutation D614G (3), while in June 2021 all strains were variants Alpha (4) and has the D614G mutation. The sample with the wild type, with the Delta variant, with the Alpha variant and the sample with only the D614G mutation were sequenced the whole S gene and the results were completely consistent with the real-time PCR results.

Conclusion: According to the laws of evolution, a rapidly spreading variant will gradually replace the original wild strain, and once community immunity to a variant is achieved, it may be susceptible to another variant and it can therefore replace the old one. Therefore, it is necessary to develop and set-up the multiplex real-time PCR test to detect 4 rapid transmission variants in diagnostic laboratories. With the collected results on the stock samples, we can conclude that at the beginning of the epidemic in Ho Chi Minh City, SARS-CoV-2 was still the original wild strain, but now it has been completely replaced by the Delta variant. In Quang Nam, the beginning of the epidemic was a wild strain but also circulating a strain with a D614G mutation, however the Alpha variant is currently circulating and has a D614G mutation. Particularly, the E484 K mutation has not appeared so far and this is an indication that SARS-CoV-2 has not yet been resistant to specific antibodies that recognize the receptor on the spike protein of the virus.

Keywords: SARS-CoV-2 variants, RT Multiplex real-time PCR.

PCO-011

Assessment of serial monitoring of inflammatory markers in hospital in-patients

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Background: Inflammatory markers such as C-Reactive Protein (CRP) and D-dimer have played a key role in prognostication, triaging of COVID-19 patients. The Ministry of Health and Family Welfare (MoHFW) India has proposed national guidance on the serial monitoring of inflammatory markers as a part of management for hospitalized COVID patients.

Objectives: We aimed to review if the serial monitoring of inflammatory markers adheres to existing national guidance.

Methods: A retrospective review of electronic patient records of 100 hospital in-patients with swab-confirmed COVID-19 was conducted as a baseline audit in which documentation on serial monitoring with CRP and D-dimer on days 1, 4, 7, 10 was checked for patients with moderate to severe COVID disease. Multiple improvement strategies were subsequently implemented and assessed via Plan–Do–Study–Act (PDSA) cycles. A need for more consistent monitoring of markers was emphasized to the treating faculty mainly in form of departmental meetings, in-house clinical seminars. Repeat survey was carried out after a gap of 4 weeks.

Results: Baseline audit highlighted two components were deemed essential: (1) Baseline record of the markers which is up to 4 days of admission; (2) Final record of the markers which is within a period of 4 days prior to discharge. The frequency of these components saw significant improvement by completion of the final PDSA cycle.

Conclusion: The serial monitoring of inflammatory markers did not fall within the existing national guidance. There is a scope for larger studies to validate the serial use of markers, cost benefit and utility of these tests and to determine the frequency of their repeatability in terms of difference it can make in terms of disease outcome.

Keywords: COVID-19, inflammatory markers.

PCO-012

Place of COVID-19 transmission in blood transmission: A case report

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A novel human coronavirus, SARS-CoV-2, has emerged from China in December 2019. It has spread worldwide, conforming to person-to-person transmission. Though the studies have found 15% to 40% of symptomatic patients had detectable RNA-emia, it is not known whether COVID-19 may be transmitted by blood transfusion. Also, according to the worldwide data, only less than 10% do annual blood donations. As Blood and blood components are essential inpatient management it is very important to know whether the SARS-CoV-2 virus is transfusion-transmitted.

Case report: A 33-year-old had donated a whole blood unit at a mobile blood donation campaign on 08/12/2020. The donor was healthy, asymptomatic, and no evidence to suspect COVID-19 infection at the time of donation. He had completed the routine pre-donation procedures including screening questionnaire, temperature check, and short medical review. It concluded without any post-donation complications.

On 19/12/2020, the donor was identified as a COVID-19 confirmed case. 11 days after the contact, all first contacts related to the blood transfusion process, remaining Fresh Frozen Plasma pack, and the