Abstracts

Public Health Laboratory, Ministry of Health Malaysia, Sungai Buloh, SUNGAI BULOH, Malaysia ³ National Public Health Laboratory, Ministry of Health Malaysia, Sungai Buloh, 47000 Selangor D.E, Malaysia, SUNGAI BULOH, Malaysia ⁴ Institute of Pathology, Laboratory and Forensic Madizing (LDPAFEM), University Talaysia, MADA

Medicine (I-PP2erForM), Universiti Teknologi MARA, Sungai Buloh Campus, 47000 Selangor D.E., Malaysia, SUNGAI BULOH, Malaysia

⁵ Non-Destructive Biomedical and Pharmaceutical Research Center, Smart Manufacturing Research Institute (SMRI), Universiti Teknologi MARA, Puncak Alam Campus, 47000 Selangor D.E., Malaysia, PUNCAK ALAM, Malaysia

⁶ Department of Public Health, Faculty of Medicine, Universiti Teknologi MARA, Sungai Buloh Campus, 47000 Selangor D.E., Malaysia, SUNGAI BULOH, Malaysia

Introduction: The SARS-CoV-2 virus genome surveillance is important to monitor and track emerging variants. In a hospital setting, this will help identify both community and inter and intrahospital transmission and, if performed in real-time, will reduce the rate of the disease spread by immediately implementing infection control measures. The study aims to describe the COVID-19 outbreaks from the SARS-CoV-2 virus genomic surveillance by whole genome sequencing (WGS).

Methods: 101 laboratory-confirmed clinical isolates belonging to patients with COVID-19 from June 2021 to June 2022 were subjected to WGS. The sequences were assembled using Bioinformatic tools EPI2ME software by the Oxford Nanopore technology (ONT). Based on the Q10 quality score, 86 isolates were subjected to phylogenetic tree analyses using the Maximum Likelihood method in MEGA 11 software. The sequencing process reached 100% coverage within 16 hours. The sociodemographic and clinical data were retrieved from both the hospital information systems (UNIMEDS) and patients' medical records. Patients' clinical presentations were categorized into mild and severe.

Results: Phylogenetic analysis revealed 7 clusters of COVID-19 outbreaks with 24 patients showing only mild symptoms. The first three clusters (Cluster I, II and III) were found to have circulated from June to July 2021 and belonged to Clade GK (Delta variant). Cluster I showed transmission from a father to his 2 sons. Cluster II involves transmission between the 2 siblings from different families. Cluster III suggested an intrahospital transmission between medical staff and medical students. Meanwhile, from February to April 2022, four clusters were detected within Clade GRA (Omicron Variant). Cluster IV involved 3 medical students who stayed in the same residential college. Cluster V involved a group of medical staff with 1 university student. Cluster VI also involved a group of 3 university students, indicating possible transmission within their residential area. Cluster VII involved infection between family members from mother to her child.

Discussion: In our study, we were able to track 1 intrahospital transmission, 1 inter-hospital and 5 community COVID-19 transmissions based on the phylogenetic tree. No new viral variants were found. The viral evolutions were of a similar pattern to what is being described globally. This WGS technique has been shown to give a faster turnaround time.

Conclusion: The WGS has enabled laboratory scientists and epidemiologists to detect the occurrence of COVID-19 outbreaks as well as genomic surveillance. Due to its robustness and rapid sequencing results, this technique could be used in real-time in the hospital setting to prevent further transmission of the infection. International Journal of Infectious Diseases 152 (2025) 107388

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Social Contexts and Public Health Control: Addressing Vaccine Hesitancy: The TRUST Study on SARS-CoV-2 Booster Uptake in Individuals Aged 50+ in the UK

Prof Silvia Riva, Mr Samuel Lam

St. Mary's University, London, United Kingdom

Background: New strains of SARS-CoV-2 have brought to light the importance of booster jabs as a public health intervention. While individuals aged 50+ are at a heightened risk of severe disease and were prioritised for booster vaccination, uptake varied significantly among ethnic groups, socioeconomic background and education level. This highlights the importance of understanding the intentions, psychological behaviours and concerns of underrepresented populations within the broader context of social determinants of health.

Methods and Materials: The TRUST study employed a demographic pre-screen tool, to identify and invite 30 individuals aged 50+ who had declined the booster jab in London (n=15) and the West Midlands (n=15) for qualitative interviews. These interviews delved into participants' attitudes towards COVID-19 vaccine boosters and their interactions with (mis)information about COVID-19. Thematic analysis was conducted using NVivo V.12 with transcriptions generated by Otter.ai.

Results: The analysis revealed four pivotal themes: 'Vaccine production and administration', 'Health (mis)information and beliefs', 'Personal circumstances and social influences', and 'Policy and logistical factors'. Within the social context, the primary drivers of booster jab hesitancy were concerns over 'Vaccine manufacturing' and 'The role of family and friends'. Psychological constructs such as epistemic trust and the "bandwagon" effect were found to shape booster vaccination behaviour.

Discussion: The TRUST study provides critical insights into the factors influencing SARS-CoV-2 booster vaccine hesitancy among individuals aged 50+ in the UK, particularly within the framework of social contexts and public health control. The findings underscore the necessity of culturally relevant and transparent public health messaging to address vaccine hesitancy, combat healthcare misinformation, and establish trust in the safety and efficacy of booster vaccinations.

Conclusions: Tailored communication strategies, encompassing diverse channels and focusing on education regarding vaccine safety, are essential to engage effectively with diverse populations and mitigate concerns. Implementing robust monitoring and adaptation mechanisms is crucial to align public health messaging with official guidelines and promptly address emerging concerns. These insights serve as a foundational step towards designing more effective and inclusive booster vaccination campaigns, advocating for a holistic approach that integrates scientific evidence, transparency, education, and cultural sensitivity.

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