

Sarawak Covid-19 Genomic Surveillance Statement

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Statement

The Institute of Health & Community Medicine (IHCM) in Universiti Malaysia Sarawak has been tracking the SARS-COV-2 variants circulating in Sarawak. To date, the IHCM laboratory has completed genomic sequencing of over 484 samples and the genomic sequence data is shared in the GISAID global SARS-COV-2 sequence database.

We recently reported that our variant surveillance study has identified the B.1.470 and B.1.524 lineages as the circulating variants in the third wave (Sept – Nov, 2020) and lineages B.1.470, B.1.524 and B.1.466.2 as the circulating variants in the fourth wave (December 2020 onwards) in Sarawak. Notably, the B.1.466.2 variant is related to the ‘Pasai’ cluster in Sarawak and this variant shares the P681R mutation with the UK B.1.1.7 variant that is associated with increased transmissibility.

Today, we would like to report the detection of a ‘Variant of Interest (VOI), the B.1.1.28.3 or P.3 variant. This variant was first reported in the Philippines in March this year and was recently identified in import cases in the UK. This P.3 variant is characterized by 2 key mutations; the E484K mutation shared with the B.1.351 variant (South African variant) and the N501Y mutation shared with the B.1.1.7 variant (UK variant). These mutations have been associated with immune-escape from both vaccine-induced and natural infection protection, and greater transmissibility.

Uncontrolled intense transmission of the virus will lead to emergence of more virus variants that may have important impact on the vaccine efficacy and possibly severity of the disease. The continuous evolving of new SARS-COV-2 variants strongly emphasizes the need for the public to continue adhering to the Standard Operating Procedures (SOPs) and guidelines, particularly mask-wearing, hand hygiene and physical distancing and the need to achieve herd-immunity through the vaccination program. These efforts will help slow virus transmission and reduce the chance of future variants evolving in the community.

¹ Other members of the Sarawak Covid-19 Vaccine Advisory Group are: Prof Dato Dr Andrew Kiyu, Dr Alan Fong, Dr Charlie Yeo, Dr Chin Zin Hing, Dr Chua Hock Hin, Dr Ivan K.S. Yap, Dr Jane Cardoso, Prof Jamilah Hashim, Dr Ooi Mong How and Dr Radziah Mohamad.

Report on SARS-CoV-2 Genomic Surveillance in Sarawak

Report date: 28 April 2021

Reporting laboratory: Institute of Health & Community Medicine, Universiti Malaysia Sarawak

Number of sequences completed: 484

Viral lineages identified:

Lineages	Location													Import cases	Total
	Kuching	Sibu	Betong	Bintulu	Samarahan	Sri Aman	Miri	Kapit	Mukah	Serian	Sarikei	Lundu	NA ¹		
B	4											1		1	7
B.1	84	1	1		4			1		2	1			12	106
B.1.1.312														1	1
B.1.260				1											1
B.1.36.19														2	2
B.1.404	1														1
B.1.438	1														1
B.1.459	2														2
B.1.466.1				1											1
B.1.466.2	46	122	9	9	1	2	4	2	3		1			6	205
B.1.470	30	1				4							1	6	42
B.1.524	55	1					1							29	86
B.1.551	5									1					6
B.6	8		1											6	15
B.1.525														1	1
P.3	4				4										8
Total	240	125	11	11	9	6	5	3	3	3	2	1	1	64	484

¹ Location not available

Variants of Concern (VOC) or Variants of Interest (VOI) detected:

Lineage	Variant designation	Spike protein mutations of interest
B.1.1.28.3 or P.3	VOI	E484K, N501Y, D614G, P681H
B.1.525.	VOI	E484K, Q677H, F888L

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