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Editorial

The More Precise, the Higher Efficient

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On March 22, 2021, the Translational Medicine Research Center, Prince of Songkla University received a great honour from Dr.Pilailak Akkapaiboon Okada, Department of Medical Science (DMS), Minister of Public Health, Thailand who gave us a talk entitled: 'Understanding the Pandemic through Viral Genome Sequencing'. The important message within the talk was that: within a couple of weeks after the outbreak in Wuhan City, Hubei Province, China, the first 2 COVID19 patients outside China were detected, via the screening program at the immigration service of an international airport[1]. Whole genome sequencing of the virus pointed out that patients were infected with a new SAR-CoV strain, which had significant difference in its genome sequence when compared to the SAR-CoV outbreak in 2003. As the SAR-CoV-2 genome sequence has been published on http://www.virological.org, just one day before the identification of these cases, the team compared the sequence detected in these patients and diagnosed the first 2 cases of COVID19 in our country with certainty[2]. Soon after the detection of the transmission, the team from DMS successfully developed diagnostic tests, based on real-time reverse transcription polymerase chain reaction (RT-PCR), and then passed on this technique thorough the country[3].

Precise determination of the 30Kb length viral genome not only helped in diagnosis, the information helped in tracking the spread of the outbreak. Following the detection of SAR-CoV-2 Clade L (GISAID nomenclature[4]), Clade S was predominate in the first wave of the outbreak, which originated from a huge boxing event in Bangkok[3]. In the second wave, or so-called shrimp market outbreak, Thailand was attacked by the Clade GH, which was believed to have migrated from India, through the Myanmar and the western border. The recent outbreak, the burst from nightclubs in Bangkok, or the so-called Thong Lor cluster, was proven to be the Clade GR (Lineage B.1.1.7, 20B/501Y.V1); known as the English variant. Evidence has proven that B.1.1.7 spreads quicker than other strains, because of higher affinity of 501Y in binding to ACE2 receptors[5]. Moreover, severity of the symptoms and response to the vaccination in these new strains are being questioned[6]. Information from the viral genome data is, therefore, crucial to the infection control plan and vaccination policy.

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Viral genome data has shown to us that the currently spreading SAR-CoV-2 is no longer the SAR-CoV-2 of December 2020. Just the same way in that the original SAR-CoV-2 evolved from the SAR-CoV in the previous pandemic. Precision medicine plays its role in answering the question: 'Which virus are we actually chasing?', and: 'When the virus is mutating, how can a strategy maker get ahead?.' The only way to see the virus in its details is to have a closer look in its nucleic acid sequence and use modern bioinformatic tools to annotate the 'variant of interest', which means the mutations that potentially cause higher infection rate, stronger capability in immunologic evasion and resistance to the available vaccines. At the time this issue of PSU Medical Journal is preparing, the novel Brazil lineage (B.1.1.28.3/P.3) and the India lineage (G/452R.V3/B.1.617) are knocking on our door and no one sees the end of this war.

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