MEDWIN PUBLISHERS
Committed to Create Value for Researchers

Open Access Journal of Pulmonary & Respiratory Sciences
ISSN: 2642-1143

Phylogenetic Analysis of First Wave Outbreak of COVID-19: Thailand's Experience

Cheepsattayakorn A[1]* and Cheepsattayakorn R[2]

[1]10th Zonal Tuberculosis and Chest Disease Center, Chiang Mai, Thailand

[2]Department of Pathology, Faculty of Medicine, Chiang Mai University, Chiang Mai, Thailand

***Corresponding author:** Attapon Cheepsattayakorn, 10th Zonal Tuberculosis and Chest Disease Center, 143 Sridornchai Road, Changklan Muang, Chiang Mai 50100, Thailand, Tel: 6653140767; 66 53 276364; Fax: 6653140773; 6653273590; Email: Attapon1958@gmail.com

Editorial

Volume 5 Special Issue 1

Received Date: August 17, 2020

Published Date: September 01, 2020

DOI:10.23880/oajprs-16000s1-005

Editorial

A previous study reveals that the COVID-19 was introduced into the human population in Wuhan, China in early December 2019 and has an epidemic doubling time of about 7 days. The study demonstrated substantial heterogeneity in the number of secondary infections caused by each COVID-19-infected case that indicated by a high level of over-dispersion in the reproduction number [1]. By phylogenetic analysis, there was a common ancestor to SARS-CoV-2 (COVID-19), human SARS-CoV, and the bat SARS-CoV converge. The envelope (E), membrane (M), nucleocapsid (N), and spike (S) structural viral proteins implied a high degree of shared identity in range of 97.7-100 % between the SARS-CoV-2 (COVID-19) and bat coronaviruses that supports the animal descend of SARS-CoV-2 (VID-19) [2].

The SARS-CoV-2 (COVID-19) first wave of outbreak initiated in early March 2020 and peaked between March 22, 2020 and March 29, 2020. There was an overall huge decline in the cases since March 20, 2020 [3]. A recent study on SARS-CoV-2 (COVID-19) isolates from Thailand that investigated the genotypes of the SARS-CoV-2 (COVID-19) from February 2020 to April 2020 with basing on the genome sequences available in GIASID, nucleotide variation in the four regions of the SARS-CoV-2 (COVID-19) genome for conducting viral tracking and identifying sites of origin of outbreaks in Thailand revealed five main clusters, defined as L, S, G, V, and O types, based on genetic variations and amino acid changes by selection of the sequences of partial ORF1ab (nucleotides 8,596-8,927 and 13,259-16,269), S (nucleotides 21,320-25,541), ORF3a to E (nucleotides 25,902-26,549), and ORF9b to ORF10 (nucleotides 28,101-29,682) [3].

During the early period of the SARS-CoV-2 (COVID-19) outbreak in China, genetic variations of L and S types were identified and confirmed SARS-CoV-2 (COVID-19)-imported cases from China during January 2020 and February 2020 [3]. One specimen collected in January 2020 in this study from Thailand revealed L type that closely related to the SARS-CoV-2 (COVID-19) strain circulating in China at that time [3]. All of the specimens that related to the first SARS-CoV-2 (COVID-19) outbreak in a boxing stadium and entertainment venues in Bangkok, Thailand during March 2020 demonstrated type L (branching off from type S-originating from China) that has not been identified in other countries [3]. This finding suggested local transmission in Bangkok, Thailand [3]. After the first outbreak in Thailand in March 2020, type T was detected less frequently and limiting the imported cases. This may be due to Thai government's intervention policies, such as mandatory closure of entertainment and sporting venues, the land border closure, and suspension of all international flights (partial city-lockdown, state quarantine, local quarantine, and self-quarantine) [3]. Nevertheless, several cases who included multiple genetic variants of SARS-CoV-2 (COVID-19), such as types G1, G2, and O recently returned from outside of Thailand had positive SARS-CoV-2 (COVID-19) testing [3]. In March 2020, these cases were identified as having type O and classified as imported cases as well as returned travelers and the religious-pilgrimage group from the southern region of Thailand [4]. In May 2020, a new cohort of imported cases of a group of migrant workers in the southern region of Thailand were identified as type G2 [5]. This may be multiple introductions of SARS-CoV-2 (COVID-19) and an outbreak in

the southern region of Thailand [3].

Conclusion

In conclusion, most study cases from Thailand demonstrated mild febrile illness without sequel, but with multiple origins of SARS-CoV-2 (COVID-19) that are similar to the identified pattern in Shanghai, China [6]. Understanding SARS-CoV-2 (COVID-19) genetic variations will assist more accurate future trend prediction and the more informed Thai government's development of intervention policies.

References

1. Volz E, Baguelin M, Bhatia S, Boonyasiri A, Cori A, et al. (2020) Report 5: Phylogenetic analysis of SARS-CoV-2. Imperial College London, pp: 1-8.

2. Ramaiah A, Arumugaswami V (2020) Insights into cross-species evolution of novel human coronavirus 2019-nCoV and defining immune determinants for vaccine development. bioRxiv, pp: 1-15.

3. Puenpa J, Suwannakarn K, Chansaenroj J, Nilyanimit P, Yorsaeng R, et al. (2020) Molecular epidemiology of the first wave of severe acute respiratory syndrome coronavirus 2 infection in Thailand in 2020. Research Square, pp: 1-16.

4. Coronavirus disease 2019 (COVID-19) WHO Thailand Situation Report-20 March 2020.

5. Coronavirus disease 2019 (COVID-19) WHO Thailand Situation Report-73.

6. Zhang X, Tan Y, Ling Y, Lu G, Liu F, et al. (2020) Viral and host factors related to the clinical outcome of COVID-19. Nature 583: 437-440.