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Zika virus infection in Asia: Reappraisal on phylogenetic data of Asian lineage

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Dear editor,

Zika virus is the new focused virus in tropical medicine. The Zika virus infection can result in acute hemorrhagic febrile illness and the infection can also result in birth defect [1,2]. The disease has been known for several decades but the big outbreaks have just been noted for a few years and the infection becomes the present global problem. There are many ongoing researches on this new infection. An interesting aspect is on the genetic epidemiology of this disease [3]. Success in isolation of virus could be seen in several recent outbreaks and the genetic contents analyses of the isolates were also done. "Passage history of the virus" can be seen from analysis of such data [4]. The genetic epidemiology study shows that the infection has subgroups of outbreaks. The Asian lineage is an interesting group that can be seen in a wide area [4]. In this short article, the authors reappraises on the phylogenetic data of Asian lineage. The study on period, distance and phylogenetic parameter differences among isolated from several countries in the Asia lineage group is done.

The data on the phylogenetic patterns on Asian lineage of Zika virus infection appeared in the previous referencing report [5] is used for further analysis in this study. The data were from 6 countries in Asia Pacific Region including French Polynesia, Thailand, Canada, Cambodia, Micronesia and the Philippines. The differences among the studied member of the lineage are assessed. The parameters to be studied include: (1) Difference in year of merging of disease, (2) Difference in distance (km) and (3) Difference in phylogenetic parameter (Bootstrap unit). Cross tabulation analysis is used for showing the interrelationship among countries in the lineage.

According to this study, difference in year of merging of disease, difference in distance (km) and difference in phylogenetic parameter (Bootstrap unit) are shown in Tables 1–3, respectively.

The present study can successfully shows the interrelationship among countries in the Asian lineage. Focusing on time, it can be seen that some countries have the problem of emerging of disease in the same period. However, when both

Table 1

Difference in year of merging of disease (year).

Countries	French Polynesia	Thailand	Canada	Cambodia	Micronesia	The Philippines
French Polynesia	0	1	0	3	6	1
Thailand	1	0	1	4	7	2
Canada	0	1	0	3	6	1
Cambodia	3	4	3	0	7	2
Micronesia	6	7	6	7	0	5
The Philippines	1	2	1	2	5	0

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Table 2

Difference in distance (km).

Countries	French Polynesia	Thailand	Canada	Cambodia	Micronesia	The Philippines
French Polynesia	0	12577	9150	12071	6373	10329
Thailand	12577	0	11625	567	6306	2264
Canada	9150	11625	0	11855	9718	11158
Cambodia	12071	567	11.855	0	5865	1822
Micronesia	6373	6306	9718	5865	0	4048
The Philippines	10329	2264	11158	1822	4048	0

Table 3

Difference in phylogenetic parameter (Bootstrap unit).

Countries	French Polynesia	Thailand	Canada	Cambodia	Micronesia	The Philippines
French Polynesia	0	0	2	11	1	1
Thailand	0	0	2	11	1	1
Canada	2	2	0	9	3	3
Cambodia	11	11	9	0	12	12
Micronesia	1	1	3	12	0	0
The Philippines	1	1	3	12	0	0

time and distance paired parameters are focused, it cannot show any trend that the nearby countries will have an increased chance to get earlier problem. Also, when distance and phylogenetic parameter paired parameters are focused, it cannot show that the nearby countries will have a genetic closer viral sequence. It means that the infection spread independently to time and place background. Based on the present study, the time and place dimensional analysis can show that the disease distribution should be mainly induced by the international traveling. The disease might be rapidly carried from one to the other setting without expectation and the international traveler from the third party countries might be the connecting jigsaw for the disease transmission. As noted by Imperato [6], “the globalization of the Zika virus was made possible by the widespread presence in various parts of the world of *Aedes* vectors and increased human travel that facilitated geographic spread.”

Conflict of interest statement

We declare that we have no conflict of interest.

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