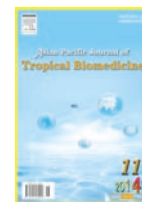




Contents lists available at ScienceDirect

## Asian Pacific Journal of Tropical Biomedicine

journal homepage: [www.elsevier.com/locate/apjtb](http://www.elsevier.com/locate/apjtb)

Document heading doi: 10.12980/APJTB.4.2014APJTB-2014-0459 © 2014 by the Asian Pacific Journal of Tropical Biomedicine. All rights reserved.

## New Ebola virus in 2014: do identified mutated amino acids in the viral sequences sense?

Somsri Wiwanitkit<sup>1</sup>, Viroj Wiwanitkit<sup>2,3,4,5\*</sup><sup>1</sup>Wiwanitkit House, Bang Khae, Bangkok 10160, Thailand<sup>2</sup>Hainan Medical University, China<sup>3</sup>Faculty of Medicine, University of Nis, Serbia<sup>4</sup>Joseph Ayobabalola University, Nigeria<sup>5</sup>Dr DY Patil Medical University, India

To the editor,

The problem of new Ebola virus outbreak in 2014 is the present big consideration of medical society. The new infection occurs in West Africa and causes infection in thousands of local people, and the trend of the worldwide expansion leads to serious concerns of the medical society. The reason why the disease rapidly progresses and be more severe than previous outbreak is still unknown and this topic should be discussed. For several reasons, the genetic change within the circulating virus can be an answer. According to the preliminary report from Guinea, there are some detected mutations that lead to amino acid substitutions in the derived sequences from the patients, such as positions 2185 (A→G, NP552 glycine→glutamic acid) and 6909 (A→T, sGP291 arginine→tryptophan)[1]. Whether those amino acid substitutions are sense or non-sense is the topic to be investigated. Here, the authors try to study the effect of amino acid changes in the identified mutations. A standard prediction tool, Protein Variation Effect Analyzer[2], was used for assessment and

prediction. Of interest, the studied mutations can result in deleterious effects, which mean sense mutations. This finding can support the hypothesis that the mutation within viral genome is the cause of serious clinical severity and strong contagious ability of the problematic new Ebola virus.

### Conflict of interest statement

We declare that we have no conflict of interest.

### References

- [1] Baize S, Pannetier D, Oestereich L, Rieger T, Koivogui L, Magassouba N, et al. Emergence of Zaire Ebola virus disease in Guinea. *N Engl J Med* 2014; doi: 10.1056/NEJMoa1404505.
- [2] Choi Y, Sims GE, Murphy S, Miller JR, Chan AP. Predicting the functional effect of amino acid substitutions and indels. *PLoS One* 2012; doi:10.1371/journal.pone.0046688.

\*Corresponding author: Professor Viroj Wiwanitkit, Wiwanitkit House, Bang Khae, Bangkok 10160, Thailand.  
E-mail: [wiroj@yahoo.com](mailto:wiroj@yahoo.com)

Article history:  
Received 4 Sep 2014  
Accepted 29 Sep 2014  
Available online 7 Oct 2014