LETTER TO THE EDITOR

Reply to the letter concerning the published article entitled “Using combinatorial bioinformatics methods to analyze annual perspective changes of influenza viruses and to accelerate development of effective vaccines”

We thank Professor Viroj Wiwanitkit for his interest in our article recently published in the Journal of the Formosan Medical Association. Google Flu Trends is a web program, developed by using logarithmic linear correlation and least square estimate to appropriate Google’s accumulated databank of online search query keywords to the information collected by the traditional surveillance systems, such as US Centers for Disease Control and Prevention (CDC). This online system theoretically is beneficial for direct monitoring of local as well as global epidemic development to help the related medical units to control disease. It is an ideally powerful tool, and several similar web sites in the USA, e.g., Flu Near You and Twitter, have hence been established; however, fine tuning of user’s querying behavior and web-adjustable knowledge conversion with time-amendable algorithms could have enriched the program to predict the unexpected. The unexpected is sometimes devastating and lethal. A proper prevention strategy is therefore urgently required for the unexpected, in particular, one that would not produce more harm than the disease itself. The goal of our study was to amend such inadequacy and to supplement the procedure of the World Health Organization for vaccine development, using more benevolent viruses as vaccines to combat fatal viruses. We used Unweighted Pair-Group Method Using Arithmetic averages (UPGMA), Maximum Likelihood Estimate (MLE) and Needleman-Wunsch (N-W) Dynamic Programming to evaluate evolutional closeness of viral proteins. For instance, H3N2 is close to H1N2, and H7N7 is close to H7N9. Following determination of best viral strain similarities, we then used DNA Maximum Likelihood of PHYLIP 3.69 (written by Joe Felsenstein of the Department of Genome Sciences and the Department of Biology at the University of Washington. (http://evoluyion.genetics.washington.edu/phylip.html)) and CLUSTALX2 (written by M.A. Larkin group of the Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Ireland (http://www.clustal.org/clustal2/)) to analyze the structural differences among various viral strains and to find the most appropriate immune response foci, which would be suitable for inducing protective antibodies. As noted in our study, one of our aims was to effectively improve the current reverse genetic procedure of vaccine development. We speculated that the combined information of global surveillance, including data from the CDC (Taiwan), CDC (USA), World Health Organization, and Google Flu Trends, might speed up vaccine development and in turn save more lives.

References


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http://dx.doi.org/10.1016/j.jfma.2015.07.008
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19 June 2015