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No structural change due to G228S substitution of haemagglutinin in emerging H6N1 influenza virus

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To the editor,

Sir, in later 2013, the newest emerging influenza infection is firstly reported from Taiwan[1,2]. This newest cross species influeza is called H6N1 bird flu[1,2]. Genetic mutation is believed to be the cause of cross species infection and the G228S substitution of haemagglutinin is proposed for increasing the mutant affinity for the human α2–6 linked sialic acid receptor[3]. This mechanism is believed to contribute to human infection. However, the remained question is why the mutate virus has never caused human infection. If the genetic mutation is the exact underlying cause of cross species infection, it should cause previous infection because the mutated type in avian has been detected for a long time. Here, the authors tried to study the structural change in G228S mutant comparing to wild type of H6N1 influenza virus. The secondary structure prediction by standard bioinformatics analysis (DASTM filter technique[4]) was performed using the previously published protocols[5,6]. Based on the present study, it can be seen that there is no structural change due to G228S substitution of haemagglutinin in emerging H6N1 influenza virus. Hence, it should be concluded that the structural change should not be the factor that contribute to human infection in mutated G228S H6N1 influenza virus. Further studies are required to determine the exact pathomechanism that the mutated G228S H6N1 influenza virus causes human infection.

Conflict of interest statement

We declare that we have no conflict of interest.

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