Structural aberration in R282K genetic mutation and antiviral drug-resistant H7N9 bird flu

Sir,

The emerging H7N9 influenza is a significant infectious disease.[1] This infection is classified as an atypical cross-species influenza infection. It is belongs to the bird flu group and can result in mortality. The underlying genetic pathological disorder in this new influenza is very interesting. The topic of focus is the emerging problem of antiviral drug resistance. The drug resistance problem has just been referred to since July 2012.[2,3] The newly discovered genetic mutant, R282K, is a new issue in infectious genetics.[3] Here, the authors perform a study to assess the structural aberration in the R282K genetic mutation. A significant aberration in the secondary structure can be seen and this is believed to be the underlying pathological process for the antiviral drug-resistance in H7N9 bird flu.

This is a structural genetics study. The basic concept of structural genomics has been applied here. The authors use a standard bioinformatics technique, NNPREDICT, for assessing the secondary structure of the studied molecules, the naïve neuraminidase and the R282K genetic mutant. The protocol of this study follows the standard protocol published in previous structural genetic studies.[4,5] The naïve neuraminidase (Accession: AGI60300.1, GI: 475662452) and the assigned R282K genetic mutant have been studied for their secondary structures. At the mutant site, within the R282K genetic mutant, an additional helix can be seen.

To manage the new emerging H7N9 bird flu, the use of an antiviral drug becomes an important tool for the prevention and treatment of the disease.[1] Similar to other emerging influenza infections, oseltamivir is the first-line drug of choice.[1] Emergence of the drug-resistance problem is usually an important episode that can make control of the new emerging influenza outbreak more difficult.[6,7] Focusing on the H7N9 bird flu, the drug resistance due to R282K mutation is presently widely discussed.[2,3] The use of new laboratory investigation for determining this genetic mutation has become the new approach for cases with poor response to antiviral drug treatment. Although it is known that R282K contributes to resistance, there is no report on its pathomechanism.

Here, the authors use the bioinformatics approach to study the secondary structures of naïve to compare them with mutant neuraminidase. It can be clearly demonstrated that the mutant form has an additional pathological helical portion. This portion may cause difficulty in the interaction between the neuraminidase and the drug, and further result in drug resistance. Further studies for verification of the exact pathobiology form the subject of the ongoing research.

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