



Title	Prediction of amino acid substitutions on the hemagglutinin molecules of influenza A viruses
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Citation	2010年度科学技術振興機構ERATO湊離散構造処理系プロジェクト講究録. p.190.
Issue Date	2011-06
Doc URL	http://hdl.handle.net/2115/48453
Type	conference presentation
Note	ERATO 세미나 2010 : No.30. 2011年1月7日
File Information	30_all.pdf



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ERATO セミナ 2010 - No. 30

Prediction of amino acid substitutions on the hemagglutinin molecules of influenza A viruses

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2011/1/7

概要

Human influenza viruses mutate from time to time, causing annual epidemics worldwide. Given the high mutation rate of the viral gene, it is difficult to select an effective vaccine strain prior to each influenza season. In order to elucidate the pattern of viral evolution, we introduce a bioinformatics technology that analyzes a large number of epidemic strains in a multidimensional space. We found that the relative sequence distances among past epidemic strains could be predicted by a mathematical model. Retrospective tests for 12 years showed that the model could predict the direction of viral evolution with high accuracy. Through these technologies, we investigate the past, current and future evolution of influenza A viruses.