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学位論文内容の要旨
Abstract of the dissertation

博士の専攻分野の名称：博士（獣医学）

氏名：Nipawit Karnbunchob
Name

学位論文題名
The title of the doctoral dissertation

A study on the avian-to-swine transmission of influenza A viruses
(A型インフルエンザウイルスの鳥豚間伝播に関する研究)

Interspecies transmissions of influenza A viruses from avian to swine play important role for the emergence of new pandemic influenza strains. Human influenza pandemics have historically been caused by genetic reassortment of human and avian influenza A viruses, and this reassortment typically occurs among viruses circulating in swine. Thus, the avian-to-swine transmission of influenza A viruses is an important factor contributing to the emergence of new pandemic strains.

In this dissertation, I traced viral transmissions between avian and swine hosts by using nucleotide sequences of avian viruses and swine viruses registered in the NCBI GenBank. BLAST and reciprocal best hits technique were introduced to find pairs of avian and swine nucleotide sequences that may be associated with transmissions between avian and swine hosts.

First, I investigated the evolution of polymerase gene during avian-to-swine transmission of influenza A viruses. I found 32, 33, and 30 pairs of avian and swine nucleotide sequences that may be associated with avian-to-swine transmissions for PB2, PB1, and PA genes, respectively. On average, avian-to-swine transmission pairs had 5.47, 3.73, and 5.13 amino acid substitutions on PB2, PB1, and PA, respectively. However, amino acid substitutions were distributed over the positions, and few positions showed common substitutions in the multiple transmission events. Statistical tests on the number of repeated amino acid substitutions suggested that no specific positions on PB2 and PA may associated with avian-to-swine transmissions. I also found that avian viruses that transmitted to swine tend to possess I478V substitutions on PB2 before interspecies transmission events. Statistical tests suggested that the I478V substitution may be beneficial for avian viruses to transmit to swine.

Next, I investigated interspecies transmission of influenza A viruses focusing on the HA gene. Using nucleotide sequences of HA gene of influenza A viruses isolated from avian and swine, my method detected 57 sequence pairs associated with interspecies transmissions

between avian and swine. Out of 28 H5 HA genes registered in NCBI database, 15 were associated with avian-to-swine transmissions, and other 13 genes were considered to be swine-to-swine transmissions. Out of 20 H9 HA genes registered in NCBI database, 11 were associated with avian-to-swine transmissions, and others 9 genes were considered to be swine-to-swine transmissions. Using this proportion, the reproduction number in swine population was estimated as 0.46 for H5 viruses and 0.45 for H9 viruses. The 95% CI of reproduction number was estimated as [0.280, 0.649] and [0.232, 0.668] for H5 and H9 respectively. These results suggested that the transmissibility of H5 and H9 viruses among swine population is limited.