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Author(s)	MOHAMED, Wessam Mohamed Ahmed
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氏名：WESSAM MOHAMED
AHMED MOHAMED

Name

学位論文題名
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Studies on the spread of H5N1 influenza viruses in Egypt

(エジプトにおけるH5N1インフルエンザウイルスの伝播に関する研究)

In 2014 and 2015, the number of human cases of H5N1 avian influenza virus infections had increased dramatically in Egypt. This increase might be related to increase in the transmission potential of the virus among humans. To clarify the cause of the increase in H5N1 human cases, I investigate the transmissibility of H5N1 viruses among humans via estimating the basic reproduction number R_0 using nucleotide sequences and sampling dates of viruses. To this end, full-length hemagglutinin gene sequences of human and avian H5N1 influenza viruses isolated from 2006 to 2016 in Egypt were obtained from the NCBI influenza virus resource. Taking into account the phylogeny, genetic distance, sampling time difference among viruses, R_0 was estimated to be 0.05 (95% CI: 0.01, 0.13) assuming that human-to-human transmissions occurred within a city, 0.23(95% CI: 0.14, 0.35) assuming human-to-human transmissions among cities. These results indicate that human-to-human transmission of H5N1 viruses in Egypt is limited, and the large increase in human cases is likely attributed to other factor than increase in human-to-human transmission potential.

Spatio-temporal distributions of infectious diseases are crucial for understanding the evolution, transmission, spread of pathogens. Phylogeography is a mathematical framework that can combine the geospatial data of an infectious disease with the genetic information of the pathogen, and it has become a powerful tool for analyzing outbreaks of the infectious diseases. I use phylogeography to investigate the transmission of the H5N1 viruses in Egypt and its neighboring countries from 2006 to 2016. I conducted a discrete states phylogeographical analysis with Bayesian statistical framework using time-stamped, geographically referenced sequences of H5N1 viruses. Analysis of the phylogeographic tree

revealed that Egyptian viruses were the main source of the outbreaks that occurred in the neighboring countries including Gaza, Israel, and Qatana. Spatial projection of the H5N1 viruses detected long-range migration events among Egypt, Gaza, and Qatana. Statistical analysis of the phylogeographic tree's trunk supported the Nile delta region as the common ancestor of the viruses circulating in poultry in Egypt.

These results suggested that a strategy containing virus transmissions in avian populations in Egypt, especially in Nile delta region is a key to control H5N1 infections among both human and avian populations in Egypt and its neighboring countries.