

Results report

1. Title of Research and Development :

Evaluation of the pandemic potential of H5N1 highly pathogenic avian influenza viruses circulating in Indonesia

2. Principal Investigator :

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4. Results of Research and Development:

Highly pathogenic H5N1 avian influenza viruses have caused outbreaks among poultry in Indonesia every year, leading to human infections. We urgently need to understand the current situation regarding H5N1 virus circulation in Indonesia and to characterize these viruses to assess their pandemic potential and to prepare for a potential H5N1 pandemic.

To this end, the Indonesian research team has strengthened its influenza surveillance systems to collect swab samples from poultry and pigs in outbreak areas. For example, they established a project to collect samples continually in Madura Island, East Java. Furthermore, they have strengthened their relationship with the local government of West Java province so that H5N1 viruses isolated in West Java can be promptly provided to the Indonesian team. In 2015, they conducted surveillance not only in Java Island but also in Kalimantan Island. They sent 980 swab samples (120 and 860 samples collected in 2015 and 2014, respectively) to the Tokyo research team. The Indonesian team also sent 828 swab samples collected in 2014 and 2015 and 70 swab samples collected between 2011 and 2014 to the US research team. They isolated H5N1 viruses in their BSL3 facility and 61 influenza PCR-positive samples were sent to US team.

The Japanese research team isolated viruses from the swab samples collected by the Indonesian team by using embryonated chicken eggs in their BSL3 facility. From the 980 samples, seven H5N1 viruses were isolated. Phylogenetic analysis of the hemagglutinin (HA) genes showed that all seven H5N1 viruses belonged to clade 2.3.2.1. Clade 2.3.2.1 virus were thought to have been introduced from Vietnam in 2012. Whole genome sequencing showed that all of the other segments of these seven viruses also originated from clade 2.3.2.1 viruses. Analysis of the HA and neuraminidase (NA) amino acid sequences revealed that none of the isolates have acquired any mutations that are known to be responsible for human-type receptor recognition or resistance to NA-inhibitor drugs, respectively.

The US team has conducted virus isolation on 420 of the 828 samples collected in 2014 and 2015, but no virus has been isolated so far. From the 70 samples collected between 2011 and 2014, 9 viruses were isolated and 6 samples were RT-PCR positive. None of the 61 influenza PCR-positive samples they received contained infectious virus.

In summary, we have strengthened the influenza surveillance systems and collected swab samples in Indonesia. From these samples, we have isolated currently circulating H5N1 viruses in Indonesia and molecularly characterized them. The information from this study improves our understanding of the current situation regarding H5N1 virus circulation in Indonesia.