he bite was evaluated.

References


Introduction
Avian influenza (A) is a highly contagious virus disease affecting several species of domestic producing birds (chickens, turkeys, quails, guinea fowl, etc.), as well as pet birds and wild birds (OIE, 2008b). According to WHO, AI refers to a large group of different influenza viruses that primarily affect birds. On rare occasions, these bird viruses can infect other species, including pigs and humans. The vast majority of avian influenza viruses do not infect humans. An influenza pandemic happens when a new subtype emerges that has not previously circulated in humans. For this reason, avian H5N1 is a strain with pandemic potential, since it might ultimately adapt into a strain that is contagious among humans (WHO, 2005).

Despite of the information on their susceptibility to the highly pathogenic AI virus by experimental infections (Kuiken, 2001; Rimmelzwaan, 2001), very little is known about its natural infection in long tail macaques (Macaca fascicularis). A report by C. Brien and T. Quan (1973) described the high incidence of antibodies to H2 and H3 subtypes of type A influenza virus in African non-human primate species.

The objective of the study was to trace and confirm the indication of AI virus natural infection in long tail macaques by antibody detection against the H5 antigen of the AIV.

Materials and Methods
This study utilized 132 serum samples from long tail macaques that are in the archive collection of Microbiology and Immunology Laboratory at IPB Primate Research Center (IPB PRC). Serum samples were grouped based on the type of breeding colony from which they were taken from. Three types of breeding colony were categorized as type A breeding colony for one managed as semi-free breeding colony on an island, type B breeding colony is outdoor captive breeding colony managed on area with the presence of poultry farms within the radius of two kilometers, while type C breeding colony is outdoor captive breeding colony managed on area with the absence of poultry farm within five kilometer range and direct contact with wild bird.

The detection of antibodies against H5 antigen of the virus was based on the beta method of Hemagglutination Inhibition (HI) Test described by OIE with minor modifications (OIE, 2008b) using inactivated reference H5N1 of AI virus purchased from BiBlitv (Balai Besar Penelitian Veteriner, Bogor-Indonesia) as standard virus.

Results
The results showed strong indication of natural infection by H5 subtype of AI virus in long tail macaques, as shown that out of 132 serum samples, 124 (94%) were tested positive by HI, while only eight (6%) were tested negative. When analyzed based on their breeding type of origin, positive HI tested serum samples were found at 97.7% in type A breeding colony, 100% in type B breeding colony, and 89.4% in type C breeding colony. The summary of the results is presented in Table 1.

<table>
<thead>
<tr>
<th>Breeding source type</th>
<th>HI tested positive</th>
<th>HI tested negative</th>
<th>% positive</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>44</td>
<td>1</td>
<td>97.7</td>
</tr>
<tr>
<td>B</td>
<td>21</td>
<td>0</td>
<td>100</td>
</tr>
<tr>
<td>C</td>
<td>59</td>
<td>7</td>
<td>89.4</td>
</tr>
<tr>
<td>Total</td>
<td>124</td>
<td>8</td>
<td>94</td>
</tr>
</tbody>
</table>

Discussion
The high percentage of positive HI test results indicates that natural infection by H5 subtype of AI virus might have occurred naturally in long tail macaques. The samples tested in the study were made available from the archive collection of Microbiology and Immunology Laboratory at IPB PRC during the period of November 2007 to May 2008. Interestingly, when grouped into three different groups based on the type of breeding colony from which they were taken from, samples obtained from an outdoor captive breeding colony situated in an area close by to poultry farms (within the radius of two kilometers) showed 100% tested positive by HI test, while samples from an open free ranging island breeding showed 97.7% tested positive by HI test, and samples from an outdoor captive breeding colony at minimum five kilometers
away from poultry farms showed the lowest speculations about source of transmission are easily to be made based on these data, but the source of transmission is still unclear and remains undetermined. Further investigation is needed to reveal better information on the source of transmission. In comparison with samples taken from an indoor breeding colony, we have included 13 serum samples from the juveniles (ranging from one to one and a half years of age) born in the colony and the results interestingly showed that nine out of 13 samples (69.23%) were tested negative by HI test. We have not followed up on the mothers of the juveniles from which the samples were HI positive to see if a maternal antibodies might have been the case in the juveniles.

Conclusions
Based on the results we obtained, a conclusion that natural infection by H5 subtype of AI virus in long tail macaques (Macaca fascicularis) is very likely to have occurred. To reveal a better information on the source of transmission is still unclear and remains undetermined. Further investigation will be necessary.

Introduction
Jembrana disease virus (JDV) is a lentivirus causing an acute debilitating disease in Bali cattle. JDV appears to have undergone multipoint changes in multiple strains. However, spread of the virus to cattle in South Kalimantan has been accompanied by a more divergence strain which has 88% identity in env compare to the type strain Tabanan strain (H5N1). JDV has two separate Tat coding exons, and the first exon (Tat-1) has been shown to produce a functional Tat protein.

Lentiviruses use alternative splicing to generate viral mRNAs for protein production, including Tat- an early regulatory protein for replication. The tat transcription and expression was investigated in 3 strains of virus infecting the native host, Bali cattle. Sequences were analysed to determine splice sites and amino acid variation.

Materials and Methods
Animals and infection. Bali cattle were infected with either JDV Tabanan strain, Pulukan or Kalimantan strains. Peripheral blood mononuclear cells (PBMCs) were obtained every 2 days and spleens were taken on the 2nd-day fever when virus spread peaked.

Transcripts detection. Total RNAs from spleens were subjected to RT-PCR, cloning and sequencing to identify 5' and 3' splice sites.

Protein detection. PBMC lysates were electrophoresed, blotted and probed with affinity purified sheep antiserum against prokaryotic recombinant Tat, and developed using chemiluminescence system.

Sequence Analysis. Sequences were obtained from proviral DNAs. The deduced amino acids of Tat-1 were aligned and displayed using PileUp and Prett programs, respectively.

Results and Discussion
Amplification with J129 and junction primers revealed various tat mRNAs. Sequence defined the composition of each transcript and Tat-1 above. Transcripts major species in 3 prior to disease on Alignment of from mRNA an showed variation identified Kalimantan strain. However, residues in the coding regions are essential.

References

Jembrana Disease Virus tat Gene Expression in Bali Cattle
Surachmi Setiyaniangish
Virology, Department of Infectious Disease and Veterinary Faculty of Veterinary Medicine, Bogor Agricultural University.


OIE. 2008b. OIE Terrestrial Manual 2008. Chapter 2.3.4. – Avian influenza


Bogor, Indonesia, August 19th – 22nd
percentage at 89.4% HI positive. Although References


OIE. 2008b. OIE Terrestrial Manual 2008. Chapter 2.3.4. – Avian influenza
