Molecular characterization of *Plasmodium juxtanucleare* in Thai native fowls based on partial cytochrome C oxidase subunit I gene

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Abstract: Avian malaria is one of the most important general blood parasites of poultry in Southeast Asia. *Plasmodium (P.) juxtanucleare* causes avian malaria in wild and domestic fowl. This study aimed to identify and characterize the *Plasmodium* species infecting in Thai native fowl. Blood samples were collected for microscopic examination, followed by detection of the *Plasmodium* cox I gene by using PCR. Five of the 10 sampled fowl had the desired 588 base pair amplicons. Sequence analysis of the five amplicons indicated that the nucleotide and amino acid sequences were homologous to each other and were closely related (100% identity) to a *P. juxtanucleare* strain isolated in Japan (AB250415). Furthermore, the phylogenetic tree of the cox I gene showed that the *P. juxtanucleare* in this study were grouped together and clustered with the Japan strain. The presence of *P. juxtanucleare* described in this study is the first report of *P. juxtanucleare* in the Thai native fowl of Thailand.

Keywords: fowl, cytochrome C oxidase subunit I, *Plasmodium juxtanucleare*

**Introduction**

Avian malaria, caused by *Plasmodium* spp., is an important blood parasite disease of poultry because it results in poor meat quality and egg production [1]. The clinical signs of avian malaria in host birds vary from no apparent signs to severe anemia and death, and the mortality rate associated with avian malaria has been reported to be as high as 80%–90% [2]. *Plasmodium* spp. have been reported to infect in various domestic fowl; *Plasmodium (P.) gallinaceum* occurs in jungle fowl and domestic fowl, while *P. juxtanucleare* has been detected in domestic fowl and turkeys. Avian malaria is common in tropical countries such as Asia, East and South Africa, and Central and South America [3]. *P. juxtanucleare* was first described in Brazil [4] and has since been reported in Asian countries such as Malaysia [5], Vietnam [6], and Thailand [7].

Generally, detection of *Plasmodium* in infected birds can be performed by Giemsa staining of a thin blood smear, which may reveal erythrocytes with trophozoites, merozoites, and/or gametocytes of *Plasmodium* spp. [8]. That method is performed by specialist workers familiar with detecting and identifying parasites in blood samples. In addition, a DNA-based detection method for identifying avian malaria parasites in blood samples has been reported [9]. The mitochondrial genome of apicomplexan parasite encodes three protein-encoding genes (cytochrome b [cyt b], cytochrome c oxidase subunits I [cox I] and III [cox III]) and six fragments of large subunit rRNA genes. The cyt b and cox I genes have been widely used in the molecular detection of avian malaria parasites such as *P. gallinaceum* [10,11]. The cox I gene is the target region used for species identification and phylogenetic analysis because it is the most highly conserved mitochondrially encoded protein [12-14]. In Thailand, a molecular characterization study of *P. juxtanucleare* reported only a partial sequence of the cyt b gene of Burmese red jungle fowls [7]. To date, there are no cox I gene-based reports on *P. juxtanucleare* infection in Thai native fowl. Therefore, the aim of this study was to identify and characterize the malaria parasites infecting Thai native fowl by using molecular tech-
niques based on the partial cox I gene.

Materials and Methods

Blood sample collection
In 2016, ten of 50 Thai native fowl that had been raised in a backyard in northeast Thailand exhibited paleness and emaciation. These 10 fowl were suspected to be exhibiting sub-clinical signs of a blood parasite infection. Thus, blood samples were collected and submitted to the Veterinary Diagnostic Laboratory, Faculty of Veterinary Medicine, Khon Kaen University, Thailand.

Blood smear analysis
The collected blood smears were prepared as thin blood films and fixed with absolute methanol for 10 min, left to dry, and then stained with 10% Giemsa solution for 30 min. The stained slides were then washed with tap water and air-dried. Each slide was examined under a light microscope (Olympus, Tokyo, Japan) using 1,000× magnification with oil immersion. Avian malaria parasites were observed and identified as described by Valkiunas [11].

DNA extraction and polymerase chain reaction (PCR)
The DNA of each of the 10 malaria-suspected fowl was extracted from each blood sample by using a TIANamp Blood DNA Maxi Kit (TIANGEN Biotech, Beijing, China) following the manufacturer’s instruction. The PCR method described by Hellgren et al. [15] for detection of the cox I gene of Plasmodium spp. was used. A partial cox I gene with a length of 588 base pairs (bp) was amplified by using forward primer CoxI-F1 (5’-GCGTACTTTGGACCGAAAA-3’) and reverse primer CoxI-R1 (5’- CATCCAGTACCACACACAAA -3’) as described in a previous study of cox I genes of P. gallinaceum in Thailand [9]. The PCR was performed in a DNA thermocycler (Major cycler, Major Science, Taiwan) using a DreamTaq Green PCR Master Mix (2×) (ThermoFisher Scientific, USA) following the manufacturer’s instruction. Briefly, 3 µL of each DNA sample was added to 22 µL of the PCR mixture, which was composed of 12.5 µL of DreamTaq Green PCR Master Mix solution, 0.5 µL of 10 µM of each forward and reverse primer, and 8.5 µL of nuclease-free water. Thermal cycling was carried out under the optimized conditions of 95°C for 5 min, followed by 40 cycles of 95°C for 30 sec, 55°C for 30 sec, and 68°C for 60 sec, followed by a final period at 68°C for 10 min. The PCR products were analyzed by electrophoresis using 1.2% agarose gels containing 1× of GelRed™ Nucleic Acid Gel Stain. Each gel was electrophoresed at 100 volts for 30 min and then visualized by using ultraviolet light in the Gel Doc™ XR+ Gel Documentation System (BioRad, USA).

Nucleotide sequence analysis of the cox I gene
The PCR products were purified for sequencing by using a NucleoSpin Gel and PCR Clean-up (Macherey-Nagel, Germany) kit following the manufacturer’s instructions. Sequencing was performed by First BASE Laboratories Sdn Bhd, Malaysia). The obtained nucleotide sequences were analyzed to determine sequence identities by using the BLASTN program (https://www.ncbi.nlm.nih.gov/BLAST) and were assembled by using BioEdit software version 7.1.11 [16]. The BankIt tool was used for analysis of the sequence data of the 588 bp fragment submissions in the GenBank database (https://www.ncbi.nlm.nih.gov/WebSub/?tool=genbank). The

<table>
<thead>
<tr>
<th>Plasmodium species</th>
<th>Host species</th>
<th>Geographic origin</th>
<th>GenBank accession number</th>
</tr>
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<tbody>
<tr>
<td>P. juxtanucleare-KKUTH02</td>
<td>Chicken</td>
<td>Thailand</td>
<td>KY930301</td>
</tr>
<tr>
<td>P. juxtanucleare-KKUTH03</td>
<td>Chicken</td>
<td>Thailand</td>
<td>KY930302</td>
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<td>KY930303</td>
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<tr>
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<td>Thailand</td>
<td>KY930304</td>
</tr>
<tr>
<td>P. juxtanucleare-KKUTH10</td>
<td>Chicken</td>
<td>Thailand</td>
<td>KY930305</td>
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<tr>
<td>P. juxtanucleare</td>
<td>n.a</td>
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<td>AB250415</td>
</tr>
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<td>P. gallinaceum</td>
<td>n.a</td>
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<td>AB250690</td>
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<td>n.a</td>
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<td>Troglodytes troglodytes</td>
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<td>Leucocytozoon caulleryi</td>
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<td>Leucocytozoon sabrazesi</td>
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<td>Malaysia</td>
<td>AB299369</td>
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</tbody>
</table>

P. juxtanucleare, Plasmodium juxtanucleare; n.a, not available; P. gallinaceum, Plasmodium gallinaceum; P. relictum, Plasmodium relictum; P. circumflexum, Plasmodium circumflexum; P. elongatum, Paramonostomum elongatum.
sequences of KKUTH02, KKUTH03, KKUTH04, KKUTH07, and KKUTH10 have been deposited in GenBank databases with the accession numbers KY930901, KY930902, KY930903, KY930904, and KY930905, respectively.

**Phylogenetic analysis**

The identified partial cox I gene sequences were analyzed by comparison with other *Plasmodium* spp. sequences obtained from the GenBank database. GenBank accession numbers for the mitochondrial sequences (Table 1) were used during the analysis. The nucleotide and deduced amino acid sequence identities and multiple sequence alignment analyses were analyzed by using ClustalW of BioEdit software [17]. Distance analyses of and phylogenetic tree generation from the nucleotide sequences were performed by applying the neighbor-joining and maximum likelihood methods by using MEGA6 software version 6.06 [18] based on the Kimura 2-parameter model with 1,000 replications of bootstrap values. *Leucocytozoon caulleryi* and *Leucocytozoon sabrazesi* sequences were used as out-of-group members to root the tree.

**Results**

**Microscopic examination**

Examination of the Giemsa-stained blood thin smears revealed that none of the ten Thai native fowl sampled had visible plasmodial stages in the blood smears.

**Homology analysis**

Agarose gel electrophoresis of five of the ten Thai native fowl samples revealed the presence of 588 bp amplicons (Fig. 1). The results of nucleotide sequence and amino acid analyses revealed 100% nucleotide identities of the amplicons to the cox I gene of *P. juxtanucleare*. The sequence alignment of the nucleotide and amino acid sequences (Figs. 2 and 3) of the five amplicons isolated in this study were 100% similar to each other and were closely related to the *P. juxtanucleare* Japan strain (AB250415). The amino acid sequence identity similarities among samples KKUTH02, KKUTH03, KKUTH04, KKUTH07, KKUTH10, and the Japan strain were 100%.

**Phylogenetic analysis**

The phylogenetic tree of the partial cox I gene of *P. juxtanucleare* based on including 17 sequences of the GenBank

![Fig. 1. PCR Electrophoresis gel demonstrating *P. juxtanucleare* cox I gene amplification with CoxI-F1 and CoxI-R1. M. 100 bp DNA marker ladder, Lanes: 1. KKUTH01; 2. KKUTH02; 3. KKUTH03; 4. KKUTH04; 5. KKUTH05; 6. KKUTH06; 7. KKUTH07; 8. KKUTH08; 9. KKUTH09; 10. KKUTH10. NC, negative control; PC, positive control.

![Fig. 2. Deduced amino acid sequences alignment of *P. juxtanucleare* cox I gene from Thai native fowls compared with reference sequence. Dots in the sequence signify the similarity of the amino acids. These sequences of *P. juxtanucleare* Thai native chicken isolates (KKUTH02, KKUTH03, KKUTH04, KKUTH07 and KKUTH10) were identical to that of *P. juxtanucleare* [NCBI reference number: AB250415]. Numbers indicate the amino acid positions.](image-url)
reference strains formed two major groups. *P. juxtanucleare* positive samples KKUTH02, KKUTH03, KKUTH04, KKUTH07, and KKUTH10 were closely related (100% similarity), and they also had 100% similarity with the *P. juxtanucleare* Japan strain. The five sequences obtained in this study were separated from other *Plasmodium* spp. and from the *Leucocytozoon* species outlier (Fig. 4). They had 95.7%, 95.7%, and 95.5% similarities with *P. gallinaceum* strains from Thailand, Japan, and Philippines, respectively. The greatest phylogenetic distance between our sequences and other published strains were for the partial cox I genes of *P. elongatum*, *P. circumflexum*, and *P. relictum* (95.1%, 95.7%, and 96.1% similarities, respectively) from South Africa, Lithuania, United Kingdom, and USA. The results showed that *P.*
Plasmodium juxtanucleare in Thailand are genetically related to P. juxtanucleare of Asian strain.

Discussion

The aim of this study was to identify the presence of P. juxtanucleare in Thai native fowls and to compare the partial cox I sequences obtained from our samples with those of other Plasmodium spp. isolated around the world. Included in our analyses were various GenBank sequences including one each from wren (Troglodytes troglodytes) and black-footed penguin (Spheniscus demersus) [19] and that for P. gallinaceum isolated from Gallus gallus domesticus in Japan [20]. Also included were the PCR amplicons and the percentage identity from the BLASTN software of the five positive field samples. The phylogenetic tree developed for the cox I gene revealed that the five isolates were grouped together and were most similar to the Japan strain of P. juxtanucleare. Similarly, the nucleotide and amino acid identities of the five samples (KKUTH02, KKUTH03, KKUTH04, KKUTH07 and KKUTH10) showed a close relationship with the P. juxtanucleare isolated in Japan (100% similarity).

Avian malaria is well recognized in poultry, but only a few studies on its molecular characterization have been reported. P. juxtanucleare is one of the most common species of Plasmodium to cause malaria in poultry. P. juxtanucleare has mainly been detected in quail, turkey, and domestic fowls [11,21] in several countries. Several Plasmodium spp. cannot be identified based solely on blood stage morphology via microscopic examination, thus molecular technology has to be used for accurate species identification. Moreover, microscopy-based detection of avian malaria presence is less sensitive than the molecular-based method and such sensitivity can be further reduced by low quality blood sample slides or by the inexperience of the investigator. As shown in the present study, PCR assay amplification of the cox I gene fragment can detect P. juxtanucleare from fowl blood samples even though the parasite was not detected by light microscopy of blood smears. Therefore, the sensitivity of the PCR assay is higher than that of direct microscopic examination. This finding suggests that PCR assays would be a suitable method for screening fowl for the presence of P. juxtanucleare infection.

Plasmodium genes were detected in blood samples by using PCR. A specific PCR fragment of the predicted size (588 bp) was obtained. The partial cox I genes of Plasmodium from the sampled Thai native fowl were sequenced and neighbor-joining analysis placed the partial cox I genes into a cluster with a P. juxtanucleare isolated from Japan [20]. The finding of P. juxtanucleare infection in this study was similar to that in a previous study in Thailand [7]. However, those authors reported molecular characterization of the cyt b gene in infected Burmese red jungle fowls (Gallus gallus spadiceus), whereas, our work characterized them based on the cox I gene in Thai native fowl.

A limitation of this study is the small amount of data available in the DNA database for use in comparing strains of the parasite; regardless, our molecular analysis indicated that the parasite isolated is an Asian Plasmodium strain. More molecular data of P. juxtanucleare and its natural reservoir are required to further describe the evolution and distribution of Plasmodium. Herein, we provide the first nucleotide sequence diversity of the cox I gene of P. juxtanucleare from field isolates in Thailand. The partial cox I gene analysis sequencing revealed that the P. juxtanucleare detected from native fowl in Thailand were very similar to P. juxtanucleare isolated in Japan [20]. This study shows the importance of using molecular assays to screen for parasite presence as the fowl in our study had subclinical signs and would have been misdiagnosed based on the microscopic finding. Currently, nucleotide sequence analysis is the only molecular assay that is useful for differentiating between P. gallinaceum and P. juxtanucleare. The restriction fragment length polymorphism assay was developed for species identification and could be useful for disease diagnosis, but it lacks a DNA sequencing ability. Future studies should investigate samples from commercial poultry that are reared in an area close to backyard birds. Such study will help determine the presence and genetic diversity of Plasmodium parasites in commercial farms of Thailand and will assist in monitoring Plasmodium spp. presence.

In conclusion, our results provide important information on the detection and phylogenetic relationships of P. juxtanucleare present in Thai native fowl in Thailand. The results showed a close relationship among the five isolates and an isolate from Japan. Additionally, the results indicate that the use of PCR-based blood assays is suitable for diagnosis and screening of the P. juxtanucleare status in poultry.

Acknowledgments

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References

5. Fernando MA, Dissanaike AS. Studies on Plasmodium
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