



## Baseline study of the morphological and genetic characteristics of *Haemoproteus* parasites in wild pigeons (*Columba livia*) from paddy fields in Thailand

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### ABSTRACT

*Haemoproteus columbae* is a common haemosporidian parasite of wild pigeons (*Columba livia*) reported worldwide. In Thailand, the wild pigeon population is increasing due to paddy field monoculture. However, there are limited reports on the presence of *H. columbae* in these pigeon populations. The aim of the study was to characterize *H. columbae* in wild pigeons. A total of 87 wild pigeons were examined using microscopic and molecular methods. *Haemoproteus columbae* was detected in approximately 27.6% of pigeons and their morphological characteristics were described. The partial cytochrome *b* (*cyt b*) gene sequence of *H. columbae* was then characterized into three common lineages (HAECOL1, COLIV03, and COQUI05). By highlighting the morphologic and genetic characteristics of *H. columbae* commonly found in this population of pigeons, this study provides essential regional knowledge about haemosporidian parasites that could benefit future taxonomic and phylogeographic studies.

### 1. Introduction

*Haemoproteus columbae* is a haemosporidian parasite found in wild pigeons (*Columba livia*) (Valkiunas et al., 2010). Pigeons infected with *H. columbae* exhibit gametocyte stages: exo-erythrocytic (tissue) meronts, which are found in liver, spleen, and other organs (Earle et al., 1993; Ferrell et al., 2007), can have severe pathological effects (Valkiunas and Iezhova, 2017). The louse fly *Microlychnia pusilla*, *Pseudolychnia canariensis*, and *P. brunnea* are vectors of *H. columbae* (Cepeda et al., 2019; Klei and DeGiusti, 1975; Valkiunas, 2004). Because *H. columbae* together with wild pigeons (*Columba livia*) have been introduced worldwide, they have a wide geographic distribution (Boano et al., 2018; Chagas et al., 2016; Fecchio et al., 2017; Gil-Vargas and Sedano-Cruz, 2019; Nebel et al., 2020; Tang et al., 2018; Yumoto et al., 2021).

In Thailand, wild pigeons are an invasive species (Round, 2019) distributed throughout the country — especially in lowland regions with

large areas of paddy fields, such as Nakhon Sawan and Phitsanulok provinces. Wild pigeons are granivorous and frequently invade Thailand's paddy fields, which are increasing to meet rising rice export demands (Batool et al., 2020; Thai Rice Exporters Association, 2000). As a result, the wild pigeon population in Thailand is rapidly growing and widely dispersed in paddy fields (Tang et al., 2018). Wild pigeons are known to harbor various zoonotic pathogens, such as *Chlamydia* bacteria, *Cryptosporidium* protozoa, and *Alphainfluenzavirus influenzae* (Koompapong et al., 2014; Prompiram et al., 2022; Sariya et al., 2015). However, the common epizootic pathogens, such as *H. columbae*, in wild pigeons in Thailand have rarely been studied, with only an unidentified *Haemoproteus* parasite reported in urban areas of the Chiang Mai province (Buranapim et al., 2019). Therefore, it is necessary to better understand Haemosporidia found in the wild pigeon population in Thailand.

This study aimed to identify *H. columbae* species using traditional morphological and molecular methods and to delineate haplotype

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