Molecular taxonomy of *Eimeria* sp. from pigeon (*Columba livia domestica*) in Japan

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SUMMARY

The genus *Eimeria* is a group of obligate parasitic protists of the phylum Apicomplexa. They are known to be a major threat to animal production. This genus includes numerous species of which the taxonomic status is unclear. More molecular data are necessary as supplementary data for classification. However, especially in wildlife-host *Eimeria*, collecting such molecular data is difficult because the oocyst population is usually heterogenic. Moreover, the establishment of a clone line is impossible because of their strict host specificity. To overcome such problems, we developed the Single Oocyst Multiplex (SOM) PCR method and analyzed molecular phylogenetic relations on pigeon-host *Eimeria* as a research model. Oocysts were collected from *Columba livia domestica* and classified as *E. columbarum* based on their morphological characteristics. According to phylogenetic analysis of nuclear 18S rRNA gene, pigeon *Eimeria* formed a monophyletic group within an avian coccidian clade. In concatenated analyses with nuclear 18S rRNA gene and ORF470 gene on the apicoplast genome, the pigeon *Eimeria* clade comprised three different sister clades. Similarity of both ITS1 and 18S rRNA gene nucleotide sequences indicated that three lineages might be treated as distinct species. Moreover, nucleotide similarity on ITS1 region suggested the presence of different species within a clade argued above. This work is the first description of molecular data on pigeon-host *Eimeria*.