Systemic Isosporosis (Atoxoplasmosis) In British Garden Birds

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Introduction

Systemic infections with *Isospora* protozoa (formerly *Atoxoplasma*) in both wild and captive passerine birds has been documented worldwide. Due to host-parasite co-evolution, infections in passerine birds are commonly subclinical but cross-infection between passerine species can result in severe clinical disease and increased mortality in captive populations (1). This poses a significant risk for conservation and reintroduction programs, particularly captive breeding colonies. The aim of this study is to investigate the occurrence and pathogenicity of systemic isosporosis in British garden birds.

Objectives

1) **Use molecular detection to document systemic isosporosis in multiple species of British garden birds**
2) **Identify *Isospora* genotypes through sequence characterisation**
3) **Perform histopathology to investigate the clinical significance of infection**
4) **Compare *Isospora* detected in wild and captive bird species and assess population structure**

Methods

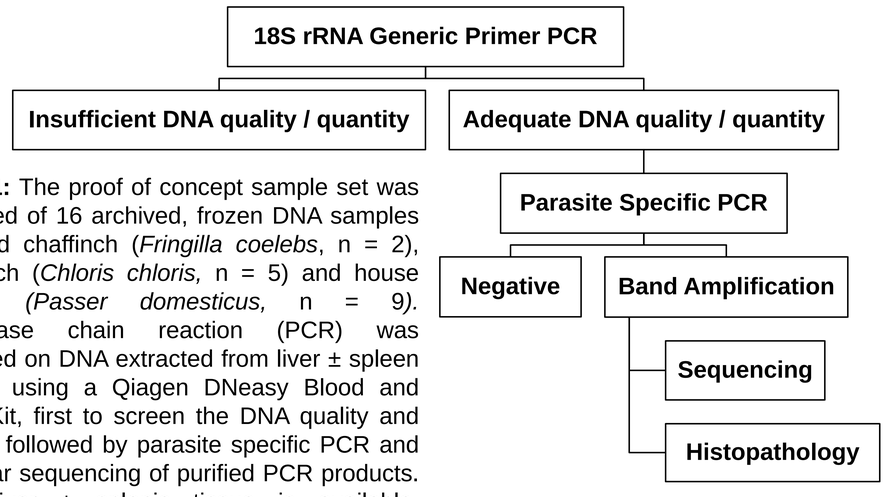

Figure 1: The proof of concept sample set was comprised of 16 archived, frozen DNA samples from wild chaffinch (*Fringilla coelebs*, n = 2), greenfinch (*Chloris chloris,* n = 5) and house sparrow *(Passer domesticus,* n = 9*)*. Polymerase chain reaction (PCR) was performed on DNA extracted from liver ± spleen samples using a Qiagen DNeasy Blood and Tissue Kit, first to screen the DNA quality and quantity, followed by parasite specific PCR and molecular sequencing of purified PCR products. When liver ± splenic tissue is available, histopathological examination will be performed.

Figure 3: Optimal Maximum Likelihood (ML) tree inferred using the partial *Isospora* 23S rRNA locus. Support for each node is presented, indicating outcomes from ML when more than 60% of replicate trees presented the same relationship or the partition probability exceeded 0.6.

Results

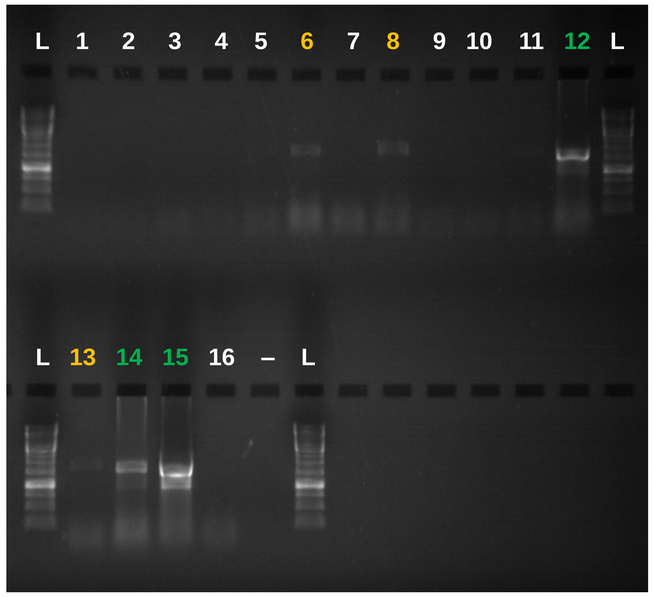

Figure 2: Amplification of *Isospora* genomic DNA by polymerase chain reaction using parasite specific primers targeting the 23S rRNA locus (2). Two greenfinch and four house sparrow (samples 6, 8 & 12, 13, 14, 15 respectively) demonstrated multiple *Isospora* genotypes. Yellow and green samples represent faint and moderate to strong parasite specific PCR band amplification respectively. L = 1kb gene ruler. – = negative control.

Conclusion & Next Steps

- **Successful PCR detection of multiple *Isospora* genotypes in wild greenfinch and house sparrow (Fig 2).**
- **Phylogenetic analysis reveals similarities in the parasite DNA sequences within the same passerine species (Fig 3).**
- **Future work: continuing molecular testing with additional greenfinch and house sparrow, in addition to other British wild bird species, supported by histopathology when feasible, to address the study objectives.**

References:

1. Flach, E., Dodhia, H., Guthrie, A. and Blake, D., 2022. Systemic Isosporiasis (Atoxoplasmosis) In Passerine Birds At The Zoological Society Of London, London Zoo. *Journal of Zoo and Wildlife Medicine*, 53(1), pp.70-82.
2. Schrenzel, M., Maalouf, G., Gaffney, P., Tokarz, D., Keener, L., McClure, D., Griffey, S., McAloose, D. and Rideout, B., 2005. Molecular Characterization Of Isosporid Coccidia (Isospora And Atoxoplasma Spp.) In Passerine Birds. *Journal of Parasitology*, 91(3), pp.635-647.