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Genotypic study of *Trichomonas gallinae* in Domestic Pigeons in Basrah Province, Iraq

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Abstract

Background: The current study aimed to employ polymerase chain reaction (PCR) for validating the initial clinical diagnosis. Additionally, the research utilized wet microscopic smear sequence analysis and constructed phylogenetic trees to investigate trichomoniasis in domestic pigeons in Basrah province, Iraq.

Methods: After screening dozens of cases attending local clinics, we selected the suspected cases for additional tests and verification. Furthermore, all cases were inspected for postmortem changes and samples were collected from mouth and pharynx for microscopic examination and DNA isolation. We selected fifteen clinically suspected cases that have shown positive microscopic results. DNA samples were PCR amplified for the ITS-rDNA region, followed by sequencing and Phylogenetic analysis.

Results: Our research unveiled consistent manifestations among all positively diagnosed cases. Direct examination through wet mount smears revealed the presence of the parasite. Sequence analysis and phylogenetic investigation identified the B strain of the *T. gallinae* parasite in domestic pigeons within Basrah province, Iraq. This strain exhibited only two haplotypes in the region, haplotype 1 and haplotype 2. Furthermore, our study documented the prevalence of the B genotype of *T. gallinae* in domestic pigeons across various countries, including China, Iraq, Iran, and Saudi Arabia.

Conclusion: The verification of *T. gallinae* infection in domestic pigeons was achieved through a PCR technique that utilized the ITS rDNA region as a genetic marker. Furthermore, the application of haplotype network analysis provided evidence supporting the categorization of the *T. gallinae* parasite in domestic pigeons as belonging to the B strain.