TRICHOMONADS IN BIRDS: CLINICAL AND MOLECULAR CHARACTERIZATION OF ISOLATES FROM AVIAN HOSTS

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BACKGROUND: Trichomoniasis caused by Trichomonas gallinae is known as a pathogenetic parasite in Columbiformes and Falconiformes. Tetratrichomonas gallinarum mainly found in the ceca of Galliformes is another avian trichomonal lacking thorough description of the infected species, pathogenicity or host specificity. Trichomonads are increasingly being found in different bird species with unfamiliar clinical manifestations.

OBJECTIVES: In this study the prevalence, clinical signs and genetic diversity of trichomonads in various avian species were investigated.

METHODS: In a one-year period from December 2012 to December 2013, upon admission and based on clinical signs, birds were screened for flagellated protozoa via wet mounts. Data on bird species, clinical signs, and any identifiable concurrent infection in the prepared wet mount were recorded for further analysis. Swabs from flagellate infected birds were cultured in Modified Diamond’s Medium (MDM) and DNA samples from confirmed flagellate positive samples were extracted. Trichomonad-specific primers, were used to amplify the 5.8S rRNA gene and its two flanking areas ITS1 and ITS2.

RESULTS: In this study the occurrence of gastrointestinal trichomonads among 737 birds, containing 28 bird species revealed the overall infection rate of 32.7%. Chi-square statistical analysis proved strong association between bird order/species, diarrhea, yeast infection with the presence of the flagellates (p=.0001). The results demonstrated that in addition to Columbiformes and Falconiformes, Passeriformes and Galliformes are susceptible to clinical trichomoniasis with the involvement of organs other than gastrointestinal. Phylogenetic analysis of complete ITS1-5.8s rRNA-ITS2 sequence from 10 cultured isolates, identified genotypes A and B of T. gallinae and genogroups E and D of Te. gallinarum.

CONCLUSIONS: To further identify the evolutionary origin of current circulating isolates in different avian species, detailed multi-loci molecular analysis of additional samples from wider localities would be recommended. Additionally studies should investigate the clinical and sub-clinical impacts of T. gallinae and Te. gallinarum infection in previously less susceptible avian species.

Key words: Trichomonas gallinae, Tetratrichomonas gallinarum, Avian, Trichomoniasis