

DIFFERENTIAL PROTEIN EXPRESSION ANALYSIS TO STUDY THE PATHOGENICITY OF THE PROTOZOAN PARASITE *TRICHOMONAS GALLINAE*

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Avian trichomonosis is a parasitic disease caused by *Trichomonas gallinae*, a protozoa which can cause lethal caseous lesions on the mouth and the oesophagus of birds. Parasite main hosts are Columbiformes, especially rock pigeon (*Columba livia*), which is blamed to be the responsible of the worldwide distribution of the parasite. Although many avian families can be parasitized by the protozoa, birds of prey are the most affected group, overall ornithophagous species which feed regularly on pigeons. Strain differences in pathogenicity have been reported, but no studies have been done considering the proteins implicated in the virulence of the parasite.

To investigate potentially virulent proteins, we have developed a quantitative proteomic study using two strains, one obtained from a bird with granulomatous lesions (genotype B) and the other obtained from a pigeon without signs of disease (genotype A).

Soluble proteins from trophozoites were extracted by sonication, and analyzed by 2D difference gel electrophoresis (2D-DIGE). Protein regulation data were obtained using DeCyder software. A total of 1090 proteins were equally expressed by both strains. Two hundred and eighty proteins were upregulated in genotype B (virulent strain) compared to genotype A, while 240 proteins were downregulated in the same strain. Spots of interest were analyzed by MALDI-TOF and/or MALDI-TOF/TOF mass spectrometry. Proteins were identified using MASCOT and by searching for matching peptide mass fingerprinting in a protein database of the related parasite *Trichomonas vaginalis*, which has been recently sequenced. Metabolic proteins are the largest group of modulated proteins in this analysis, but more studies are necessary in order to elucidate the relevance of these changes.