DIFFERENTIAL PROTEIN EXPRESSION ANALYSIS OF SEVERAL ASSEMBLAGES OF GIARDIA INTESTINALIS

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Giardia spp., one of the most common protozoa that infect humans, a wide range of domestic and wild animals, and birds, is a significant cause of diarrhoea and nutritional disorders. The parasite is ingested as the inactive cyst form. After passage through the acid environment of the stomach, the active trophozoite form is released from the cyst in the duodenum where it initiates infection.

The application of molecular tools has revealed that *Giardia* is a phenotypically and genotypically heterogeneous assemblage of genotypes that are largely morphologically identical, but host-adapted in nature, having a narrow spectrum of natural hosts.

Assemblages A and B have been found in humans and many other animals, whereas assemblages C, D, F and G seem to be host specific for nonhuman species. Assemblage E has been reported as an artiodactyl specific assemblage affecting pigs, sheep and cattle.

To investigate potentially virulent proteins-host specific, we have developed a quantitative proteomic study using two assemblages**,** A and E.

Both assemblages were purchased from ATCC®. Trophozoites were grown in a normal TYI-S-33 medium. Soluble proteins from trophozoites obtained were extracted by sonication, and analyzed by 2D difference gel electrophoresis (2D-DIGE). Protein regulation data were obtained using DeCyder software. A total of 951 proteins were equally expressed by both assemblages. Ninety seven spots were considered to be significantly deregulated, thirty-three spots were found solely in assemblage E and fifty-five spots presented exclusively in the assemblage A.

These spots were excised from preparative 2D gels and 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 generated by automatic annotation of the *Giardia* genome site (*http://gmod.mbl.edu/perl/site/giardia)*. Among them we identified a NADH oxidase and a phosphoglycerate kinase.

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