Giardia lamblia poly(A) polymerase. Structural and functional characteristics.

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Giardia lamblia is a pathogenic unicellular microorganism . It is one of the most frequently identified causes of water-borne diarrhoea epidemics worldwide. It is a major cause of epidemic childhood diarrhea in developing countries. In the United States *G. lamblia* is one of the most commonly identified intestinal parasites. It is the most common gut parasite in the United Kingdom, and infection rates are especially high in Eastern Europe.

Most infected subjects do not have symptoms, and most infections are self-limited. However, chronic infections, marked by chronic diarrhea can occur and can last from weeks to months. Death is rare and usually occurs in malnourished children.

Recent medical treatments show that *G.lamblia* is sensitive to combined antibiotic medications. But, like most microorganisms, *G. lamblia* could acquire drug resistance. Thus, other treatment methods should be identified, in order to fight the infection more efficiently

The aim of my project was to investigate the structural and functional characteristics of one giardial enzyme. It is called poly(A) polymerase and is involved in the so called polyadenylation reaction, which is part of a series of events involved in the cell protein synthesis system. Previously, the gene for the giardial poly(A) polymerase had been identified and isolated. To investigate the protein product of the gene I used computer analysis to predict how soluble it is in water, how stable it is, and which other proteins it resembles. The results showed that this was a short-lived protein, which was water soluble except for for its terminal parts. This data was used for deciding on appropriate purification techniques in order to acquire pure giardial poly(A) polymerase to be further studied. During the purification, improvements were made on giardial poly(A) polymerase solubility. A lot of the protein was lost during the procedures and polyadenylation activity could not be detected. The final conclusions drawn from the laboratory experiments combined with the computational data suggested that the giardial poly (A) polymerase interacts with another protein in order to function properly.

In the future the poly(A) polymerase binding partner should be identified, and then their interaction could be analysed. This could be a suitable new drug target. Another application of this research could be the development of a more sophisticated *in vitro* system for performing the polyadenylation reaction.

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