Metabolic differences between *Giardia intestinalis* and *Giardia muris*: Minor differences with a major evolutionary impact?

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Giardia muris has been used as a model for understanding the pathogenesis and response of the host during a *G. intestinalis* infection. Several major findings of *Giardia* biology and immunity have been pioneered in *G. muris*, and later been shown to be transferable to *G. intestinalis*. Unlike *G. intestinalis*, *G. muris* only infects rodents. One important reason for this specificity could be the different conditions that both species undergo inside the hosts. Using the published genomes from *G. intestinalis* and a new draft genome from *G. muris*, we compare the metabolism of these two species. Even though there are specific differences, both species share the main metabolic pathways. Our results show that *G. muris* lacks the enzyme purine nucleoside phosphorylase, which is a potential drug target in *G. intestinalis*. On the other hand, *G. muris* seems more versatile in the use of carbon sources for glycolysis. The presence of a fructokinase and mannose-6-phosphate isomerase enable the use of fructose and mannose-6-phosphate. Other significant unique features in *G. muris* are the presence of genes for arginase, trytophanase, the synthesis of acetyl-CoA from pantothenate and ferritin-like protein. This last protein may cause differences in the storage of Fe within the cell. *G. muris* encodes three proteins putatively related with the interaction with the gut microbiota of the host: Tae4, a protein with peptidoglycan degrading amidases activity, a bactericidal/permeability-increasing (BPI) protein, and a quorum-quenching N-acyl-homoserine lactonase. The identification of these metabolic differences and the improvement in the understanding of their evolution can shed light on parasite adaptation to different hosts.