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The genome of the liver Fluke *Fasciola gigantic* present novel protein kinases as drug targets

Timir Tripathi

Assistant Professor, Molecular and Structural Biophysics Laboratory, Department of Biochemistry, North-Eastern Hill University, Shillong -793022
E-mail: timir.tripathi@gmail.com

Fascioliasis is a neglected food-borne disease caused by liver flukes (genus *Fasciola*) and affects more than 200 million people worldwide. Despite technological advances, little is known about the molecular biology and biochemistry of the fluke. We present the draft genome of *Fasciola gigantica* for the first time. The assembled draft genome has a size of ~1.04 Gb with an N50 of 129 kb. A total of 20,858 genes were predicted. The *de novo* repeats identified in the draft genome were 46.85%. In pathway analysis, all the genes of glycolysis, Kreb's cycle and fatty acid metabolism were found to be present, but the key genes for fatty acid production in fatty acid biosynthesis were missing. This indicates that the fatty acid required for the survival of the fluke may be acquired from the host bile. The genomic information will provide a comprehensive resource to facilitate the development of novel interventions for fascioliasis control. Eukaryotic protein kinases (ePKs) are regulators of several cellular processes, the most important being phosphorylation. We used various computational and bioinformatics tools to extensively analyze the ePKs in *F. gigantic* (FgePKs) genome. A total of 455 ePKs were identified that represent ~2% of the parasite genome. Out of these, 214 ePKs are typical kinases (Ser/Thr- and Tyr-specific ePKs), and 241 were other kinases. Several FgePKs were found to possess unusual domain architectures. This study provides a platform that may open new avenues into our understanding of helminth biochemistry and drug discovery.

Keywords: Genome sequence; liver fluke; trematode; *de novo* repeats; protein kinases, domain organization, drug targets.

Reference:

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