

# Researchers unlock the genetic code of cancer-causing liver fluke parasite

September 10 2014

---



The liver fluke parasite *Opisthorchis viverrini*. Credit: A\*STAR

An international team of scientists from Singapore, Thailand, China and Australia has cracked the genetic code of the liver fluke parasite, *Opisthorchis viverrini*, using a unique DNA analysis technique developed at A\*STAR's Genome Institute of Singapore (GIS).

GIS's DNA analysis technique has allowed the researchers to further study the biology of *Opisthorchis viverrini* to understand the cause and the eventual development of treatments for bile duct cancer, a condition caused by the parasite. The breakthrough was published in the scientific journal *Nature Communications*.

*Opisthorchis viverrini* is a trematode that infects millions in Asia, and it is classified as a Group 1 carcinogen by the International Agency for Research on Cancer (IARC). It is also a significant risk factor for Cholangiocarcinoma (CCA) or [bile duct cancer](#). This parasite is endemic to some countries in Southeast Asia including Northeastern Thailand, Laos and Cambodia, with only 96 per 100,000 cases being reported in these countries. Despite its prevalence, there is no vaccine and only one drug (praziquantel) available to counter the parasitic worm.

The fluke enters the human body through the ingestion of raw or undercooked contaminated fish. Once in the small intestines, the worm migrates to the liver's bile ducts, where it lodges, feeds and matures. It is not known for certain how the fluke causes cancer. One widely accepted hypothesis is that the fluke secretes a protein mimicking the [human growth hormone](#), granulin, which is extremely potent at stimulating cell growth and proliferation and is therefore highly regulated in the body.

Infected individuals however, are constantly exposed to granulin-like proteins secreted by flukes, which subsequently cause host cells to proliferate uncontrollably, leading to tumour growth.

By mapping out the genes of this parasite, researchers aim to better understand its molecular pathways. This will help them identify new biological markers which could potentially be developed into powerful diagnostic tools and effective treatments for parasite-specific diseases.

This research was part of an international collaboration involving team leads, Dr Niranjana Nagarajan and Professor Patrick Tan from Singapore's GIS, and Dr Neil Young and Professor Robin B. Gasser from Australia's University of Melbourne, and others from Thailand and China.

"This study gives deep new insights into the life of a parasitic fluke in the human [bile duct](#), and was enabled by the development of an exciting new genome assembly tool called OPERA-LG in our lab. It has allowed us to assemble and characterise the largest parasitic worm genome studied to date," said Dr Niranjana Nagarajan.

Professor Tan added, "This work builds on our earlier work to complete the picture of host and pathogen genetics of cholangiocarcinoma. These new genomic resources provide a foundation for systems biology investigations of host-pathogen interactions, with a view to uncovering new treatment strategies."

"GIS is constantly developing new genome analytic techniques to realise the huge potential of genomics in finding future cures. The success in sequencing the genome of the [liver fluke](#) is a testament of our capabilities to help scientists take their research a level up towards medical discovery," said Professor Ng Huck Hui, Executive Director of GIS.

**More information:** "The *Opisthorchis viverrini* genome provides insights into life in the bile duct" by Neil D. Young "The *Opisthorchis viverrini* genome provides insights into life in the bile duct" by Neil D. Young et al. *Nature Communications*, 2014.

Provided by Biomedical Sciences Institutes (BMSI)

Citation: Researchers unlock the genetic code of cancer-causing liver fluke parasite (2014, September 10) retrieved 26 April 2024 from <https://phys.org/news/2014-09-genetic-code-cancer-causing-liver-fluke.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.