

# Liver parasite lacks key genes for fatty acid synthesis: Genome sequencing of *Clonorchis sinensis*

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The human liver fluke *Clonorchis sinensis* affects more than 35 million people in South East Asia and 15 million in China. Infection by this parasite causes clonorchiasis. Repeated or chronic infection can lead to serious disease of the liver, gall bladder or bile ducts, including the frequently fatal bile duct cancer - cholangiocarcinoma (CCA). The complete genome sequence the genome of *C. sinensis*, published in BioMed Central's open access journal *Genome Biology*, has provided insight into the biochemical pathways available to the fluke and shows that they are lacking enzymes required for fatty acid biosynthesis.

*C. sinensis* has a complex lifestyle. The eggs float in fresh water until eaten by snail. Once inside the snail they develop and grow into a free swimming stage. These burrow out of the snail and into a fish where the coat themselves in an acid resistant covering. Humans and other mammals are infected by the parasite by eating uncooked fish. Once in the small intestine the flukes migrate to the [bile ducts](#) in the liver where they live out their adult lives.

Over 16,250 genes were found within the 516Mb genome (the human genome has about 23,000 genes over 3Gb of DNA). Genes were found corresponding to genes for energy metabolism, both aerobic (used by the juveniles) and anaerobic (used by the adults). While the genes coding for proteins needed for [fatty acid metabolism](#) were all present, key enzymes were missing from [fatty acid synthesis](#).

Prof Xinbing Yu, who led the team which performed this work, explained that, "Two other liver flukes *S. Japonicum* and *S. Mansoni* are also missing these enzymes. This means that liver flukes evolved to use their host's fatty acids before the species separated." Prof Xinbing concludes, "Genomic information is not only able to help us understand evolution but the sequence of *C. sinensis* is helping us understand liver fluke biology. This in turn will help find new ways of controlling diseases caused by this parasite or provide new targets for making a vaccine."

**More information:** The draft genome of the carcinogenic human liver fluke *Clonorchis sinensis*, Xiaoyun Wang, Wenjun Chen, Yan Huang, Jiufeng Sun, Jingtao Men, Hailiang Liu, Fang Luo, Lei Guo, Xiaoli Lv, Chuanhuan Deng, Chenhui Zhou, Yongxiu Fan, Xuerong Li, Lisi Huang, Yue Hu, Chi Liang, Xuchu Hu, Jin Xu, Xinbing Yu, *Genome Biology* (in press)

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