

SFU Press Releases Collection

These archival copies have been generated from web press releases maintained and originally written by SFU Communications and Marketing. Where possible, an effort has been made to preserve the public comments left on the website as well as any included photos or other images. All textual content should be faithful to the original press releases; contact numbers have been removed but they have not otherwise been altered in any way. However, this collection of documents spans multiple generations of web authoring software and not all formatting will be exact.

MEDIA RELEASE

Unravelling malaria's genetic mysteries

December 22, 2011

[Tweet](#) [Facebook](#) [Pinterest](#) [Email](#) [Print](#)**Contact:**Jack Chen (UniverCity resident), 778.782.4823, chenn@sfu.caChristian Frech (Burnaby resident), 778.782.7649, cfa24@sfu.caCarol Thorbes, PAMR, 778.782.3035, cthорbes@sfu.ca[Photos on Flickr](#)Link to paper: <http://at.sfu.ca/UxfKiD>

Simon Fraser University researchers in biology and computing sciences are starting to piece together a picture that may help scientists and doctors save more than a million lives annually.

These lives — mostly children in developing countries — are claimed by two of 200 known species of malaria parasites carried by mosquitoes.

SFU molecular biologist [Jack Chen](#) and his doctoral student [Christian Frech](#) are unravelling genetic clues about why these two species cause all malaria deaths and 90 per cent of human infections.

The pair analysed the genomes of the two most deadly malaria parasites infecting humans (*Plasmodium falciparum* and *Plasmodium vivax*). They also analysed the genomes of a parasite infecting monkeys and humans (*P. knowlesi*) and three infecting rodents (*P. berghei*, *P. yoelii* and *P. chabaudi*).

Building on five years of collaborative work with other SFU researchers, Chen and Frech used an array of powerful bioinformatics programs to sift through thousands of genes that define six malaria parasites. Chen's lab and computing sciences researchers co-developed two of the programs.

Chen and Frech have isolated 44 genes as unique because they aren't shared between the species.

Sixteen of the 44 isolated genes were found only in malaria parasites infecting primates (humans and monkeys) and not rodents. Three of these genes help to produce vitamin B1, which is essential to all living organisms' survival.

"Why particularly human malaria parasites produce their own vitamin B1 and do not rely on vitamin B1 uptake from their host is now an intriguing question for future research," says Frech.

Another 13 isolated genes were found only in the two virulent human-infecting parasites.

"Some of these genes are specifically active in the developmental stages of the parasite within the mosquito," says Chen. "This suggests these genes could play an important role in the mosquito's transmission of malaria to humans."

“Gene loss and gain in a species often dictate their comparative strengths and weaknesses,” says Chen. “That leads us to believe that the genes unique only to the human-infecting parasites, which happen to be the most deadly, are linked to disease development, transmission and virulence in humans.”

The [Public Library of Science \(PLOS\) Computational Biology journal](#), a high-impact, non-profit open-access scientific publishing project, has just published their findings.

— 30 —

Backgrounder on gene analysis programs

As part of his doctoral thesis, Frech used OrthoCluster and genBlastG, two bioinformatics analysis software programs, to compare the genomes of the six malaria parasites he was studying with Chen.

“The most unique strength of our research is the building of a high resolution platform for comparative genomics analysis — a genomics sifter,” says Chen. “It allows us to identify with confidence differences between the genomes of harmful and benign malarial parasites.

“Until now, researchers didn’t have the level of resolution needed to look at genomes of related species. If it turns out the genes we’ve isolated govern malaria transmission to and between humans, they’ll be useful in many ways. For example, they could become drug targets to prevent parasites from switching from one host to another — for example from monkeys to humans — in the future.”

Chen’s former master student Matthew Nesbitt and his former doctoral student Ismael Vergara in collaboration with SFU computing science professor Jian Pei’s group developed OrthoCluster to compare genomes.

Jeffrey Chu, another former doctoral student of Chen’s worked with SFU computing science professor Ke Wang’s group to develop genBlastG to distinguish truly unique genes from incorrectly annotated ones.

In 2006, SFU recruited Chen from Cold Spring Harbour Laboratory in New York State. He has been involved in comparative genomic analysis of many important research organisms, including nematodes and sea urchins, simple spiny marine animals, since coming to SFU. Chen helped discover many of the [sea urchin’s genes](#) are the same as those in humans and other complex vertebrates.

— 30 —

No comments yet

[Comment Guidelines](#) 

[Admission](#)

[Programs](#)

[Learning](#)

[Research](#)

[Community](#)

[About](#)

[Maps + directions](#)

[Library](#)

[Academic Calendar](#)

[Road Report](#)

[Give to SFU](#)

[Emergency Information](#)

CONNECT WITH US

[Facebook](#)

[Instagram](#)

[Twitter](#)

[YouTube](#)

CONTACT US

Simon Fraser University

8888 University Drive

Burnaby, B.C.

Canada V5A 1S6

[Terms and conditions](#)

© Simon Fraser University



