

Unraveling malaria's genetic mysteries

December 22 2011



SFU molecular biologists Jack Chen and Christian Frech review a graphic representation of genomic similarities and differences they've isolated between two major human malaria parasites.

(PhysOrg.com) -- 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 like Africa — 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 unraveling 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.”

More information: Genome comparison of human and non-human malaria parasites reveals species subset-specific genes potentially linked to human disease, *PLoS Computational Biology*:

www.sfu.ca/content/dam/sfu/pam...os_compbio_final.pdf

Provided by Simon Fraser University

Citation: Unraveling malaria's genetic mysteries (2011, December 22) retrieved 13 March 2024 from <https://phys.org/news/2011-12-unraveling-malaria-genetic-mysteries.html>

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