

New findings shed light on complexities of emerging zoonotic malaria

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Zoonotic malaria has been shown to be caused by two genetically distinct *Plasmodium knowlesi* parasite subpopulations associated with different monkey host species in Malaysia, according to new research published in *PLOS Pathogens*. The authors believe this could have important implications for how the parasite adapts and spreads in humans.

Plasmodium knowlesi is a zoonotic [malaria parasite](#) which is common in forest-dwelling macaques. In recent years, increasing numbers of cases of *knowlesi* malaria have been reported in humans. The disease is now the most common form of human malaria in many areas of Malaysia, and has been reported across south-east Asia.

The new study, led by researchers at the London School of Hygiene & Tropical Medicine and University of Malaysia Sarawak (UNIMAS), used sensitive genotyping methods to analyse samples of 599 *P. knowlesi* infections (552 in humans and 47 in wild macaques) at 10 sites in Malaysia. They identified two genetically divergent subpopulations of *P. knowlesi* in [human](#) cases, each associated predominantly with a different species of reservoir host - long-tailed macaques and pig-tailed macaques respectively.

Senior author, David Conway, Professor of Biology at the London School of Hygiene & Tropical Medicine, said: "We were very surprised to find that *knowlesi* malaria is really two separate zoonoses going on at the same time. There is a lot of genetic diversity within each of the parasite types, but the high level of divergence between them indicates

they are probably different sub-species being transmitted separately, within the same areas.

"In most places we surveyed, both parasite types coexist and infect people. If zoonotic transmission continues to be common, it becomes more likely that the two types may hybridise genetically, leading to new possibilities for parasite adaptation to humans or additional mosquito vectors. However, as parasite mating occurs within the mosquito, hybridisation would depend on whether the same vector species is sometimes infected by both types, which needs investigation."

Study lead author, Paul Divis, from the London School of Hygiene & Tropical Medicine and UNIMAS, said: "Hybridisation between species or sub-species has been seen in other [parasites](#) that are associated with the emergence of novel pathogenicity. Therefore, the transmission of two types of *P. knowlesi* in humans might increase the opportunity for evolution of virulence or enhanced transmission."

Although the conclusions from the data were highly significant, the authors note that further work is needed to understand the divergence between the parasite subpopulations more precisely by analysis of whole genome sequences, and by studying parasites from more locations in different parts of south-east Asia.

More information: Paul C.S. Divis, Balbir Singh, Fread Anderios, Shamilah Hisam, Asmad Matusop, Clemens H. Kocken, Samuel A. Assefa, Craig W. Duffy, David J. Conway (2015) Admixture in humans of two divergent *Plasmodium knowlesi* populations associated with different macaque host species. *PLOS Pathogens* DOI: ppat.1004888

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