

## **INVITED SPEAKER PRESENTATION**

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## Origin of the human malaria parasite *Plasmodium* falciparum in gorillas

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Plasmodium falciparum is the most prevalent and lethal of the malaria parasites infecting humans, yet the origin and evolutionary history of this important pathogen remain controversial. Here, we used single genome amplification (SGA) strategies to show that wild-living African apes are naturally infected with at least nine Plasmodium species, including one that is the direct precursor of P.falciparum. Among nearly 3,000 ape fecal specimens collected from 57 field sites throughout central Africa, we found *Plasmodium spp.* infection in chimpanzees (Pan troglodytes) and western gorillas (Gorilla gorilla), but not in eastern gorillas (Gorilla beringei) or bonobos (Panpaniscus). Ape plasmodial infections were highly prevalent, widely distributed, and almost always made up of mixed parasite species. To obtain Plasmodium sequences not confounded by in vitro recombination, we used SGA to amplify fragments of the mitochondrial (956bp of the *cytochrome b* gene; 3.4kb and 3.3kb half-genome fragments), apicoplast (390bp of the caseinolytic protease C gene) and nuclear (772bp of the *lactate dehydrogenase* gene) genomes. Among more than 1,100 such sequences from 80 chimpanzee and 55 gorilla samples, we found nine that were related to P. malariae, P. ovale or P. vivax. All others grouped within one of six chimpanzee- or gorilla-specific lineages representing distinct Plasmodium species within the Laverania subgenus. One of these from western gorillas was comprised of parasites that were nearly identical to P. falciparum. In phylogenetic trees of full-length mitochondrial sequences, human P. falciparum formed a

monophyletic lineage within the gorilla parasite radiation. These findings indicate that *P. falciparum* is of gorilla origin and not of chimpanzee, bonobo or ancient human origin, and that all known human strains appear to have resulted from a single cross-species transmission event.

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