**Plasmodium knowlesi Reinfection in Human**

To the Editor: In 2004, a large number of patients infected with *Plasmodium knowlesi* (simian malarial species) were reported in Sarawak, Malaysia (1). *P. knowlesi* infection was also reported in Peninsular Malaysia (2).

Here we report a case of human *P. knowlesi* reinfection. Phylogenetic sequence analysis shows that the first and second infections were caused by different strains of *P. knowlesi*.

The patient was a 41-year-old businessman from Peninsular Malaysia. He was first admitted to the hospital in October 2009 with a 4-day history of fever, chills, and headache. His symptoms started ≈2 weeks after a 4-wheel-drive expedition with overnight camping in a jungle in Raub in the state of Pahang. Initial examination showed thrombocytopenia and hepatitis, and *P. knowlesi* malaria was subsequently confirmed with nested PCR by using diagnostic primers for *Plasmodium* small subunit (SSU) rRNA as described (3). He recovered fully after a treatment course of oral quinine plus doxycycline.

The patient was readmitted to the hospital on June 11, 2010, with a 5-day history of fever and chills and rigors, followed by epigastric pain, nausea, and vomiting. His symptoms began 15 days after another 4-wheel-drive expedition with overnight camping in a jungle in Tanjung Malim in the state of Perak. Laboratory investigations showed severe thrombocytopenia. Falciparum malaria was diagnosed initially on the basis of blood film examination with 1% parasitemia. Delay in appropriate treatment, as seen in the second infection of the patient in our study, can cause severe conditions, such as thrombocytopenia, acute renal failure, and hemolysis (4).

To confirm the reinfection, blood samples collected from the patient at the first and second infections were reexamined. Giemsa-stained thin and thick blood films showed 2.0% and 2.5% parasitemia for the first and second infections, respectively. Some parasites showed morphologic features resembling those of *P. falciparum* ring forms and *P. malariae* trophozoite band forms.

We confirmed the *P. knowlesi* in the first and second infections by PCR, sequencing and analysis of the highly variable *csp* gene (5), and SSU rRNA. The nucleotide sequences of the gene were aligned by using ClustalW and analyzed by using MEGA4 software (6). The *csp* gene of the isolate from the first infection (denoted as Pkpah-1) was 1,217 nt, whereas the gene of the isolate from the second infection (denoted as Pkrk-1) contained 1,277 nt. This difference was due to the absence of 2 repetitive sequences.

![Figure. Phylogenetic tree based on nucleotide sequences of small subunit rRNA of *Plasmodium knowlesi* isolates from Peninsular Malaysia (Pkpah-1, Pkrk-1, KAL-1) and surrounding regions (denoted by GenBank accession nos.). The tree was constructed by using the maximum-parsimony method. The percentage of replicate trees in which the associated isolates cluster together in the bootstrap test (10,000 and 1,000 replicates, no differences were observed) is shown next to the branches. Phylogenetic analysis was conducted by using MEGA4 (6). Scale bar indicates nucleotide substitutions per site.](image-url)

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1. Kong PW, et al. Plasmodium knowlesi in Sarawak, Malaysia. Emerg Infect Dis. 2007;13:1552-4.
2. Kong PW, et al. Plasmodium knowlesi in Peninsular Malaysia. Emerg Infect Dis. 2007;13:1551-2.
3. Kong PW, et al. Plasmodium knowlesi in Sarawak, Malaysia. Emerg Infect Dis. 2007;13:1552-4.
4. Kong PW, et al. Plasmodium knowlesi in Peninsular Malaysia. Emerg Infect Dis. 2007;13:1551-2.
5. Kong PW, et al. Plasmodium knowlesi in Sarawak, Malaysia. Emerg Infect Dis. 2007;13:1552-4.
6. Kong PW, et al. Plasmodium knowlesi in Peninsular Malaysia. Emerg Infect Dis. 2007;13:1551-2.
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References

1. Singh B, Lee KS, Matusop A, Radhakrishnan A, Shamsul SSG, Cox-Singh J, et al. A large focus of naturally acquired Plasmodium knowlesi infections in human beings. Lancet. 2004;363:1017–24. doi:10.1016/S0140-6736(04)15864-6

2. Vythilingam I, Norazian YM, Huat TC, Jiram AI, Yusri YM, Azahari AH, et al. Plasmodium knowlesi in humans, macaques and mosquitoes in Peninsular Malaysia. Parasit Vectors. 2008;1:26. doi:10.1186/1756-3305-1-26

3. Singh B, Bobogare A, Cox-Singh J, Snouguou N, Abdulrahman MS, Rahman HA. A genus- and species-specific nested polymerase chain reaction malaria detection assay for epidemiologic studies. Am J Trop Med Hyg. 1999;60:687–92.

4. Daneshvar C, Davis C, Cox-Singh J, Rafa‘ee M, Zakaria S, Divis P, et al. Clinical and laboratory features of human Plasmodium falciiparum infections. Clin Infect Dis. 2009;49:852–60. doi:10.1086/605439

5. Cutchan TF, Kissinger JC, Touray MG, Rogers MJ, Li J, Sullivan M, et al. Comparison of circumsporozoite proteins from avian and mammalian malarias: biological and phylogenetic implications. Proc Natl Acad Sci U S A. 1996;93:11889–94. doi:10.1073/pnas.93.21.11889

6. Tamura K, Dudley J, Nei M, Kumar S. MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. Mol Biol Evol. 2007;24:1596–9. doi:10.1093/molbev/msm092

7. Kantele A, Marti H, Felger I, Muller D, Jokiranta TS. Monkey malaria in a European traveler returning from Malaysia. Emerg Infect Dis. 2008;14:1434–6. doi:10.3201/eid1409.080170

8. Krotoski WA, Collins WE. Failure to detect hypnozoites in hepatic tissue containing exoerythrocytic schizonts of Plasmodium knowlesi. Am J Trop Med Hyg. 1972;31:854–6.

9. Cheesman SO, Mahony E, Pattaradilokrat S, Degnan K, Knott S, Carter R. A single parasite gene determines strain-specific protective immunity against malaria: the role of the merozoite surface protein I. Int J Parasitol. 2010;40:951–61. doi:10.1016/j.ijpara.2010.02.003

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Antibody to Arenaviruses in Rodents, Caribbean Colombia

To the Editor: The ∼20 recognized arenaviruses in the Americas are hosted by rodents of the family Cricetidae; 1 exception may be hosted by a bat (genus Artibeus, family Phyllostomidae) (1). Pichiné virus, hosted by Oryzomys albicularis, was described from animals in the Pichiné Valley near Cali, Colombia (2), and antibody reactive to Pichiné virus was found in 2 of 82 serum samples from humans in the same area. No studies of arenavirus infection in rodents or humans have been conducted in Colombia since 1971. Although Pichiné virus is not associated with human disease, Guanarito virus, which is hosted by Zygometans brevicauda, the short-tailed cane mouse (3,4), causes Venezuelan hemorrhagic fever in the Venezuelan state of Portuguesa (5). This state borders on Colombia, and Z. brevicauda is a common species in Caribbean Colombia. Our aim was to determine the prevalence of antibody to arenaviruses among wild rodents in this region.

During November 1, 2008–June 10, 2009, we trapped 322 rodents in 3 rural localities in the Department of Córdoba, Colombia (Montería, Vereda El Escondido, 8°34.183′N,