Plasmodium falciparum in Asymptomatic Immigrants from Sub-Saharan Africa, Spain

To the Editor: A range of infectious diseases have been described in asymptomatic immigrants (*1*), which may justify the implementation of screening after obtaining consent. In particular, asymptomatic malaria caused by *Plasmodium falciparum* parasitemia among recently arrived immigrants may be a major public health problem outside malaria-endemic areas because these patients may be involved in autochthonous transmission cycles and may act as reservoirs capable of reintroducing malaria into areas where it had been previously eradicated.

In 2010, we reviewed the medical records of 314 asymptomatic (defined as patients with no symptoms at the time of consultation) immigrants from sub-Saharan Africa who had settled in Spain, had not traveled to their countries of origin since arrival, and had been examined at the Tropical Medicine Unit (TMU) of the Ramon y Cajal Hospital in Madrid during the previous 5 years. Systematic screening included a blood count; serum biochemistry; basic urine analysis; serologic tests for HIV infection, hepatitis B or C infection, syphilis, and schistosomiasis (if epidemiologic risk factors were present); tuberculin skin test; analysis of fecal samples for parasites; and PCR to identify *Plasmodium* spp. (*2*). Date of arrival in Spain was obtained from the patient and corroborated by the nongovernmental organizations caring for them.

PCR for *Plasmodium* spp. was performed for 216 patients, and 10 (4.6%) had positive test results for *P. falciparum*. Nine were men; median age was 27 years (interquartile range [IQR] 20–31 years). The median period from arrival in Spain to malaria diagnosis was 4.5 months (IQR 1.75–12.5 months). Three men received a diagnosis of *P. falciparum* malaria >1 year after arrival.

Patient 1 was a 32-year-old man from Angola who came to the TMU for screening 13 months after arriving in Spain. He was treated with a standard regimen of artesunate plus sulfadoxine/pyrimethamine; latent tuberculosis (TB) infection and schistosomiasis were also diagnosed. Patient 2 was a 17-year-old man from Senegal, seen at the TMU 14 months after arrival. Malaria treatment was not prescribed because he was lost to follow-up. He was also diagnosed with latent TB infection. Patient 3 was a 28-year-old man from Guinea who visited the TMU 28 months after arrival in Spain. He was treated with a standard regimen of atovaquone/proguanil and also received diagnoses of tuberculosis (TB) infection, schistosomiasis, and strongyloidiasis. No statistically significant association was observed between positive or negative PCR for *P. falciparum* and a diagnosis of tuberculosis (TB) infection, hepatitis B or C virus infection, HIV infection, syphilis, intestinal parasite infection, or schistosomiasis. None of the 3 patients had received a blood transfusion since arriving in Spain.

Reported prevalence of imported malaria among immigrants may be >10%, according to some studies (*1*), with higher rates among persons from sub-Saharan Africa (malaria caused by *P. falciparum* occurring mainly 3 months after arrival). Clinical symptoms of malaria in immigrants are typically mild, with low levels of parasitemia. Many immigrants may be asymptomatic (*1*,*3*), which has been explained by partial immunity acquired gradually after prolonged exposure in areas with stable malaria transmission. Because infected persons may initially have no symptoms, implementation of malaria screening for recently arrived immigrants from disease-endemic areas would seem advisable (*4*).

How long a low level of *P. falciparum* parasitemia may persist once exposure to malaria has been discontinued is not known. Mathematical models have estimated the maximum duration of *P. falciparum* infection after interruption of transmission at ≈4 years (*5*), although delayed clinical presentations of *P. falciparum* malaria have been described as long as 2 (*6*), 4 (*7*), or even 8 years (*8*) after patients have left malaria-endemic areas. These data highlight that low asymptomatic parasitemia may persist long after migration.

Determining in which patients with asymptomatic parasitemia clinical malaria will develop and when, or if, any external factors may act as triggers would also be useful. A study in France found that 2.3% of malaria cases among immigrants developed >1 year after their arrival and that pregnancy and co-infection with HIV were factors associated with late presentation of malaria caused by *P. falciparum* (*9*).

Asymptomatic malaria cases may affect public health in non–disease-endemic areas because persons with low-grade parasitemia are capable of infecting mosquitoes (*10*). These persons could act as unidentified reservoirs and contribute to transmission in areas where malaria has been eliminated. In addition, congenital transmission or transmission by blood transfusion or organ transplantation may occur even when the donor has lived for years outside the malaria-endemic area.

Our cases highlight how malaria parasites may persist in asymptomatic immigrants long after their arrival in the host country (up to 28 months). On the basis of published reports of symptomatic delayed cases, we believe that the prevalence of

persistently low-level parasitemia among asymptomatic immigrants is probably higher than previous estimates. Screening for malaria among immigrants long after arrival would help determine if there are any factors that influence the development of clinical malaria. Delayed screening could also be particularly relevant in certain risk groups, such as pregnant women and persons who are HIV positive. As a public health measure, such delayed screening could play a role in preventing outbreaks or reintroducing malaria in countries where it has been eradicated.

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References

1. Monge-Maillo B, Jimenez BC, Perez-Molina JA, Norman F, Navarro M, Perez-Ayala A, et al. Imported infectious diseases in mobile populations, Spain. Emerg Infect Dis. 2009;15:1745–52.
2. Rubio JM, Post RJ, van Leeuwen WM, Henry MC, Lindergard G, Hommel M. Alternative polymerase chain reaction method to identify *Plasmodium* species in human blood samples: the semi-nested multiplex malaria PCR (SnM-PCR). Trans R Soc Trop Med Hyg. 2002;96:S199–204. http://dx.doi.org/10.1016/S0035-9203(02)90077-5
3. Mascarello M, Gobbi F, Angheben A, Concia E, Marocco S, Anselmi M, et al. Imported malaria in immigrants to Italy: a changing pattern observed in north-eastern Italy. J Travel Med. 2009;16:317–21. http://dx.doi.org/10.1111/j.1708-8305.2009.00321.x
4. Monge-Maillo B, Lopez-Velez R. Is screening for malaria necessary among asymptomatic refugees and immigrants coming from endemic countries? Expert Rev Anti Infect Ther. 2011;9:521–4. http://dx.doi.org/10.1586/eri.11.37
5. Sama W, Killeen GF, Smith T. Estimating the duration of *Plasmodium falciparum* infection from trials of indoor residual spraying. Am J Trop Med Hyg. 2004;70:625–34.
6. Krajden S, Panisko DM, Tobe B, Yang J, Keystone JS. Prolonged infection with *Plasmodium falciparum* in a semi-immune patient. Trans R Soc Trop Med Hyg. 1991;85:731–2. http://dx.doi.org/10.1016/0035-9203(91)90434-Z
7. Greenwood T, Vikerfors T, Sjoberg M, Skeppner G, Farnert A. Febrile *Plasmodium falciparum* malaria 4 years after exposure in a man with sickle cell disease. Clin Infect Dis. 2008;47:e39–41. http://dx.doi.org/10.1086/590250
8. Szmitko PE, Kohn ML, Simor AE. *Plasmodium falciparum* malaria occurring 8 years after leaving an endemic area. Diagn Microbiol Infect Dis. 2009;63:105–7. http://dx.doi.org/10.1016/j.diagmicrobio.2008.08.017
9. D'Ortenzio E, Godineau N, Fontanet A, Houze S, Bouchaud O, Matheron S, et al. Prolonged *Plasmodium falciparum* infection in immigrants, Paris. Emerg Infect Dis. 2008;14:323–6. http://dx.doi.org/10.3201/eid1402.061475
10. Schneider P, Bousema JT, Gouagna LC, Otieno S, van de Vegte-Bolmer M, Omar SA, et al. Submicroscopic *Plasmodium falciparum* gametocyte densities frequently result in mosquito infection. Am J Trop Med Hyg. 2007;76:470–4.

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Pandemic (H1N1) 2009 Virus Circulating in Pigs, Guangxi, China

To the Editor: A novel swine-originated influenza A virus known as pandemic (H1N1) 2009 was first isolated from humans in Mexico in April 2009 (*1*), and a worldwide pandemic followed, which affected >214 countries and resulted in >18,000 deaths (*2*). In August 2010, the World Health Organization stated that the pandemic caused by this virus had ended. As this virus emerged, animals, including swine, turkeys, ferrets, cats, and cheetahs, were found to have been infected (*3*). In addition, transmission from humans to pigs in porcine herds has been reported (*4*).

Swine influenza A virus (SIV) belongs to the family *Orthomyxoviridae* and is a causative agent of respiratory disease in pigs (*5*). Currently, 3 subtypes of influenza viruses are circulating in the swine population globally: H1N1, H3N2, and H1N2 (*6*,*7*). Pigs can be simultaneously infected with avian influenza viruses and human influenza viruses, and the viruses can exchange genes and produce new variants, which suggests that pigs have become mixing vessels for influenza viruses (*8*). Pandemic (H1N1) 2009, caused by a virus usually circulating in pigs in Europe and Asia, is a triple hybrid that contains swine, human, and avian virus gene segments, which further emphasizes that SIVs pose a serious threat to public health. We describe an outbreak of pandemic (H1N1) 2009 virus, which was isolated from a pig farm in Guangxi Province, People's Republic of China, and report the consequences of subsequent epidemiologic studies.

In January 2011, an outbreak of severe respiratory problems occurred in pigs on a pig farm. Nine hundred growing and fattening pigs exhibited