

## Parallel Decline of Malaria and *Rickettsia felis* Infections in Senegal

Oleg Mediannikov,<sup>1,3</sup> Cédric Abat,<sup>1</sup> Cheikh Sokhna,<sup>2,3</sup> and Didier Raoult<sup>1\*</sup>

<sup>1</sup>Aix-Marseille Univ, IRD, APHM, MEPHI, IHU-Méditerranée Infection, Marseille, France; <sup>2</sup>Aix-Marseille Univ, IRD, APHM, VITROME, IHU-Méditerranée Infection, Marseille, France; <sup>3</sup>Campus International IRD-UCAD Hann Maristes, Dakar, Senegal

**Abstract.** *Rickettsia felis* is a common emerging pathogen in sub-Saharan Africa. Comparing dynamics of morbidities due to malaria and *R. felis* infections in two Senegalese villages, we found a strong and significant correlation between them. Malaria morbidity is strongly decreasing because of the implementation of long-lasting insecticidal nets, so we hypothesize that the same measure may decrease the *R. felis* infections.

*Rickettsia felis* is a worldwide emerging arthropod-borne pathogen. It was described as a human pathogen in 1991.<sup>1</sup> Then, the detection of *R. felis* in laboratory-reared colonies of cat fleas, *Ctenocephalides felis*, drove scientists to the conclusion that this bacterium is hosted and transmitted by fleas.<sup>1</sup> Numerous detections of *R. felis* in fleas collected from wild and domestic animals all around the world confirmed this hypothesis. The disease associated with *R. felis* has been named as “flea-borne spotted fever.”<sup>2</sup> Multiple laboratory experiments confirmed that *R. felis* may be transmitted by cat fleas.<sup>3</sup> However, until 2010, *R. felis* cases were very rarely reported. The disease has become

increasingly more recognized in the tropical countries of Africa<sup>4</sup> and Asia<sup>1</sup> after simultaneous reports of high prevalence of *R. felis* infection in Kenya<sup>4</sup> and in Senegal<sup>5</sup> had been published. It was reported that fleas collected in an *R. felis*-endemic region in Senegal did not contain this bacterium<sup>6</sup>; this may suggest that another transmission mechanism exists. Moreover, it appears that the epidemiologies of malaria and *R. felis* infection in Senegal are very similar.<sup>5</sup>

These observations led us to the hypothesis that *R. felis* may be transmitted by mosquitoes in tropical countries.<sup>7–9</sup> We have reported the correlation between mosquito-transmitted malaria and *R. felis* infection regarding geographic distribution,

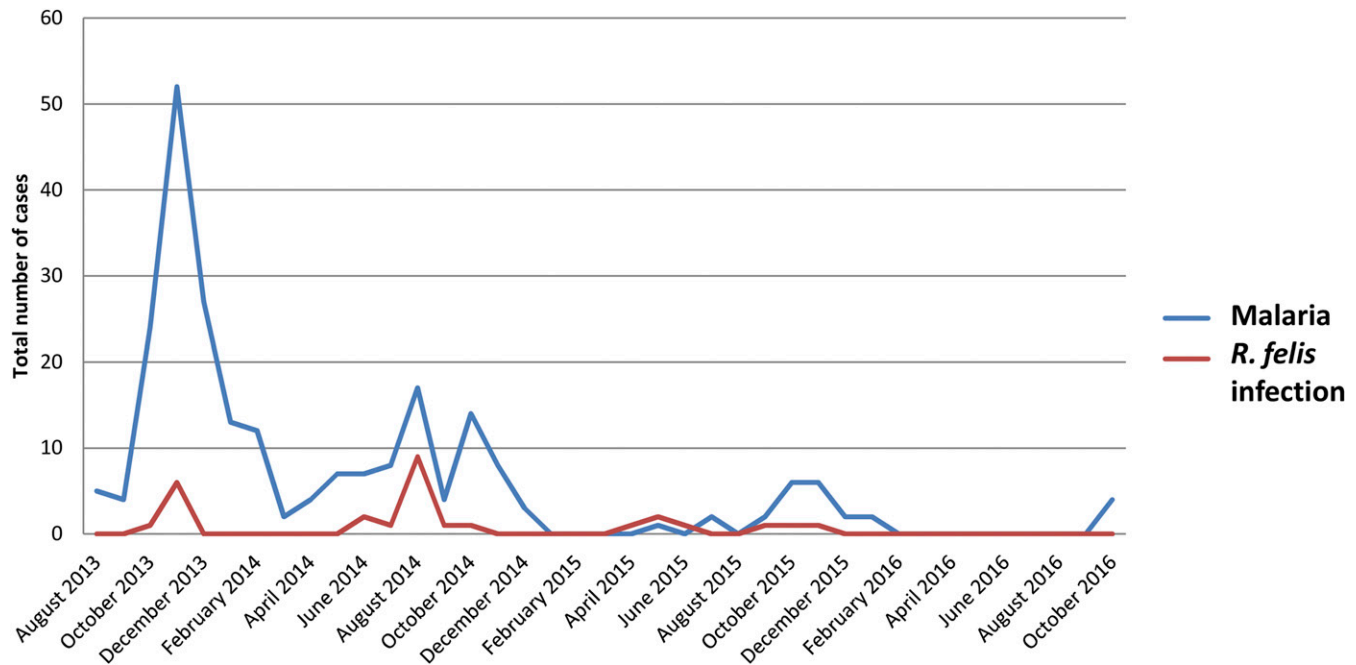


FIGURE 1. Evolution of malaria and *Rickettsia felis* infection morbidity in Dielmo and Ndiop villages, Senegal, in 2013–2016. This figure appears in color at [www.ajtmh.org](http://www.ajtmh.org).

\* Address correspondence to Didier Raoult, URMITE, Aix Marseille University, UM63, CNRS 7278, IRD 198, INSERM 1095, Institut Hospitalo-Universitaire (IHU) Méditerranée Infection, 19-21 Boulevard Jean Moulin, Marseille 13385, France. E-mail: [didier.raoult@gmail.com](mailto:didier.raoult@gmail.com)

seasonality, asymptomatic infections, and a potential vector.<sup>5</sup> *Rickettsia felis* has been also detected in wild *Anopheles* and in *Aedes*.<sup>8</sup> Later, the ability of *Anopheles* mosquitoes to acquire and transmit *R. felis* to susceptible hosts was proven in an experimental model.<sup>7–9</sup> Here, we report additional evidence of the connecting epidemiologies of both diseases. Dielmo and Ndiop are two villages in the Sine-Saloum region of Senegal situated 5 km from each other, with a total population about 800 persons and where the point-of-care laboratory was installed in 2011<sup>10</sup> to perform rapid detection of both pathogens. This laboratory serves two village dispensaries where all cases of acute febrile diseases are reported. The diagnosis is performed by using quantitative polymerase chain reaction and rapid diagnostic immunochromatographic tests. We analyzed the total monthly number of cases of malaria and *R. felis* infection in both villages for the period from August 2013 to October 2016, including the episode of malaria rebound in 2013.<sup>11</sup> Over the study period, 236 and 28 human cases of malaria and *R. felis*, respectively, were identified. Figure 1 illustrates the dynamics of monthly number of cases of these infections. Both curves show the same peaks and declines. Using the R software (R Project, Auckland, New Zealand), we performed a Pearson correlation test to determine if there was a correlation between the cases of malaria and that of *R. felis* throughout the study period. Intriguingly, we identified a strong and significant correlation between the appearance and disappearance of the two diseases (correlation coefficient equal to 0.6,  $P$  value  $< 10^{-3}$ ).

Long-lasting insecticide-treated nets (LLIN) marked a real breakthrough in malaria prevention, resulting in a significant decline in morbidity and mortality. It seems that the renewal of LLIN in 2013 helped to stop malaria<sup>10</sup> and *R. felis* infection rebound in Dielmo. As the growing number of cases of *R. felis* infection dropped to zero at the same time, it seems that this effective tool to reduce malaria burden may also decrease the number of acute *R. felis* infection cases. The strong significant correlation between the number of cases of *R. felis* infection and that of malaria further reinforces the hypothesis that most cases of *R. felis* infection in tropical areas may be transmitted by mosquitoes, in particular *Anopheles* spp.

Received March 13, 2017. Accepted for publication April 1, 2018.

Published online June 4, 2018.

Authors' addresses: Oleg Mediannikov, URMITE, Aix Marseille University, UM63, CNRS 7278, IRD 198, INSERM 1095, Institut Hospitalo-Universitaire (IHU) Méditerranée Infection, Marseille, France, and IRD, URMITE UMR198, Campus Communs IRD/UCAD Hann Maristes, Dakar, Senegal, E-mail: olegusss1@gmail.com. Cédric Abat and Didier Raoult, URMITE, Aix Marseille University, UM63, CNRS 7278, IRD 198, INSERM 1095, Institut Hospitalo-Universitaire (IHU) Méditerranée Infection, Marseille, France, E-mails: cedric.abat@gmail.com and didier.raoult@gmail.com. Cheikh Sokhna, URMITE, Campus IRD d' Hann Maristes, Dakar, Senegal, E-mail: cheikh.sokhna@ird.fr.

## REFERENCES

1. Angelakis E, Mediannikov O, Parola P, Raoult D, 2016. *Rickettsia felis*: the complex journey of an emergent human pathogen. *Trends Parasitol* 32: 554–564.
2. Raoult D, La Scola B, Enea M, Fournier PE, Roux V, Fenollar F, Galvao MA, de Lamballerie X, 2001. A flea-associated *Rickettsia* pathogenic for humans. *Emerg Infect Dis* 7: 73–81.
3. Brown LD, Macaluso KR, 2016. *Rickettsia felis*, an emerging flea-borne rickettsiosis. *Curr Trop Med Rep* 3: 27–39.
4. Richards AL, Jiang J, Omulo S, Dare R, Abdirahman K, Ali A, Sharif SK, Feikin DR, Breiman RF, Njenga MK, 2010. Human infection with *Rickettsia felis*, Kenya. *Emerg Infect Dis* 16: 1081–1086.
5. Mediannikov O et al., 2013. Common epidemiology of *Rickettsia felis* infection and malaria, Africa. *Emerg Infect Dis* 19: 1775–1783.
6. Roucher C, Mediannikov O, Diatta G, Trape JF, Raoult D, 2012. A new *Rickettsia* species found in fleas collected from human dwellings and from domestic cats and dogs in Senegal. *Vector Borne Zoonotic Dis* 12: 360–365.
7. Parola P, Mediannikov O, Dieme C, Raoult D, 2015. Reply to Slesak et al.: so much about *Rickettsia felis* infection to be discovered. *Proc Natl Acad Sci USA* 112: E6595–E6596.
8. Socolovschi C, Pages F, Ndiath MO, Ratmanov P, Raoult D, 2012. *Rickettsia* species in African *Anopheles* mosquitoes. *PLoS One* 7: e48254.
9. Dieme C, Bechah Y, Socolovschi C, Audoly G, Berenger JM, Faye O, Raoult D, Parola P, 2015. Transmission potential of *Rickettsia felis* infection by *Anopheles gambiae* mosquitoes. *Proc Natl Acad Sci USA* 112: 8088–8093.
10. Sokhna C, Mediannikov O, Fenollar F, Bassene H, Diatta G, Tall A, Trape JF, Drancourt M, Raoult D, 2013. Point-of-care laboratory of pathogen diagnosis in rural Senegal. *PLoS Negl Trop Dis* 7: e1999.
11. Wotodjo AN et al., 2015. The implication of long-lasting insecticide-treated net use in the resurgence of malaria morbidity in a Senegal malaria endemic village in 2010–2011. *Parasit Vectors* 8: 267.