Cutaneous Leishmaniasis Caused by *Leishmania killicki*, Algeria

To the Editor: Cutaneous leishmaniasis (CL) is a widespread and resurging vector-borne disease caused by a protozoan parasite belonging to genus *Leishmania* (1). After Afghanistan, Algeria is the second largest focus of CL in the world. Although CL is a serious public health problem in Algeria, few data are available from this country.

During 2004–2008, an average of ≈44,050 CL cases were reported per year, and the estimated annual incidence ranged from 123,300 to 202,600 cases. Two main forms of CL have been described for more than a century in Algeria, the zoonotic, caused by *L. major* and the sporadic, caused by *L. infantum*. Since 2004, 11 strains belonging to the *L. tropica* complex, including *L. killicki* (2), were identified in 1 focus in the northern part of the Sahara (3) and in 2 foci in the northeastern Algeria (4,5). We report here a recent outbreak of CL, including infection with *L. killicki* strains, in the Tipaza area of northern Algeria.


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in Mediterranean countries, in the Near East and Middle East (2), possibly in relation to changes in environmental conditions. Urbanization and/or climatic changes that have occurred in recent years could have played a role in the spread of the disease. The cases reported here were observed in urban areas, which suggests transmission according to an anthroponotic mode.

Each species responsible for CL has its own epidemiologic pattern. Clinicians must be aware of the specificity of leishmaniasis that may be encountered in North African countries. *L. tropica* complex lesions heal spontaneously over a period of 12 months or more, a duration longer than for *L. major* infections (8). *L. tropica* infections are also less responsive to treatment compared to infections with other Old World *Leishmania* species. In addition, *L. tropica* may cause leishmaniasis recidivans. This type of CL, appearing often years after the initial infection showed signs of complete resolution, manifests as papules that transform slowly into a spreading granuloma resembling lupus vulgaris (6). *L. tropica* can also produce visceral infections on rare occasions, resulting in unexplained systemic illness, including classic symptoms of visceral leishmaniasis, in persons returning from areas where this *Leishmania* complex is endemic (9).

Other epidemiologic studies are required to detect additional foci, including those of the *L. tropica* complex, that may coexist with those of *L. infantum* and *L. major* in Algeria. Travelers to North Africa should also be informed about the existence of this spreading disease (10).

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**LETTERS**

**Rift Valley Fever in Kedougou, Southeastern Senegal, 2012**

To the Editor: Rift Valley fever (RVF) is an acute, febrile, viral disease caused by Rift Valley fever virus (RVFV), a phlebovirus of the family Bunyaviridae that is endemic to sub-Saharan Africa. RVF mortality and abortion rates among young domesticated ruminants and pregnant females are high.

In humans, clinical manifestations range from mild to severe syndromes, which can include neurologic, hemorrhagic, and hepatic features and retinitis, and which sometimes result in death (1). Diagnosis of RVF is challenging for clinicians because clinical manifestations are not specific (2). Heavy rainfall and flooding create conditions for emergence of RVF vectors (Aedes and Culex spp. mosquitoes), and dispersion of this disease into new areas is linked to migration of infected livestock, wildlife, or mosquitoes.

Since 1987, when the Diama dam was built, RVF outbreaks in Mauritania have been reported regularly (3). In Kedougou, southeastern Senegal, RVFV was isolated 4 times from Ae. dalmatii mosquitoes and once from a person with a mild case of RVF (4). We report results of a field investigation and laboratory findings for a human case of RVF detected by surveillance of acute febrile illnesses in Kedougou.

On October 16, 2012, a 27-year-old man (school teacher) who lived and worked in Baya village in the Kedougou region of Senegal (12°27’50”N, 12°28’6”W) visited the Kedougou military health post because of high fever, chills, headache, back pain, myalgia, and arthralgia that started on October 14. He reported regular contact with domesticated animals (cows, sheep, and goats) during farming.

A thick blood smear for the patient showed a positive result for malaria, and specific treatment was given. As part of surveillance for acute febrile illnesses, blood samples from the patient were tested for IgM against RVF, chikungunya, dengue, West Nile, yellow fever, Zika, and Crimean-Congo hemorrhagic fever viruses; and for viral RNA and virus (5,6). All test results for IgM against the 7 viruses were negative.

RVFV was isolated from newborn mice that were intracerebrally inoculated with a blood sample from the patient. Viral RNA was detected by reverse transcription PCR in serum from the patient. Phylogenetic analysis of the partial nonstructural protein gene on the small RNA segment showed that the RVFV isolate was closely related to a strain that had circulated in Mauritania in 2012 (Figure).

An epidemiologic field investigation was conducted to assess the extent of RVFV circulation. During this investigation, the case-patient provided an additional blood sample. In addition, 115 contacts of the case-patient, including primary school students, friends, family members and neighbors (median age 12 years, range 6–75 years; female:Male sex ratio 1.6) were also sampled and questioned to identify asymptomatic and benign cases. A total of 218 samples from patients attending the nearest health posts in Ibel and Thiokoye villages during October 2012 were also tested during surveillance of acute febrile illnesses.

All 334 samples were negative for RVFV RNA and IgM and IgG against RVFV except for samples from 3 patients, including the case-patient, which were positive for RVFV-specific IgG and malaria parasites. The 2 other patients were a 32-year-old tradesman and a 20-year-old housewife sampled during surveillance of acute febrile illnesses in Kedougou and Bandafassi, which is 30 km from Baya (online Technical Appendix Figure, wwwnc.cdc.gov/EID/article/20/3/13-1174-Techapp1.pdf). No RVFV RNA was detected.