rural southwestern United States (10) and a strain of pathogenic B. elizabethae, a bacteria that can cause human endocarditis, in the Huayllacallán Valley in Peru (3).

Because most identified *Bartonella* spp. have been reported as infectious agents for humans, our results should prompt public health concern. However, our findings require further investigation about the pathogenicity of these *Bartonella* genotypes. The detection of both pathogens in intradomestic and peridomestic areas where humans are in close contact with rodents could indicate that the incidence of both diseases in humans from Echarate District might be underestimated.

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Buruli Ulcer Disease in Republic of the Congo

To the Editor: Buruli ulcer, which is caused by the Mycobacterium ulcerans bacterium, is a severe disabling necrotic disease of the skin, occurring mainly in swampy rural areas of western and central Africa. This tropical disease is neglected, despite being the third most common mycobacterial disease of humans, after tuberculosis and leprosy. The disease has become substantially more frequent over the past decade, particularly around the Gulf of Guinea, and has been detected or suspected in at least 31 countries (1). Clinical diagnosis of Buruli ulcer disease should be confirmed by PCR, as recommended by the World Health Organization (WHO); and case-patients should be treated with rifampin/ streptomycin daily for 8 weeks (therapy available since 2004), combined, if necessary, with surgery.

Although confirmed cases of Buruli ulcer disease have been reported in all countries neighboring the Republic of the Congo (hereafter called Congo) (2–4), only 1 report of a confirmed case in Congo has been published (5) (Figure, panel A). During 2007–2012, a total of 573 clinical cases of Buruli ulcer disease were reported to WHO by the National Leprosy, Buruli Ulcer and Yaws Control Program in Congo. We report 108 cases (19% of all cases reported) that

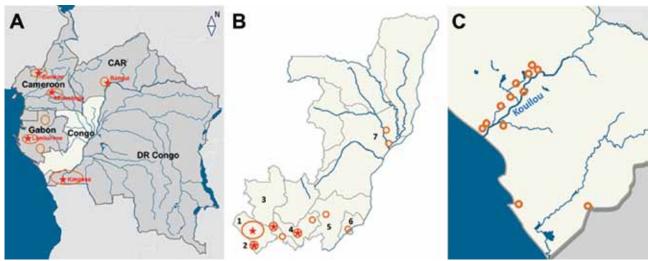


Figure. Buruli ulcer—endemic areas in the Republic of the Congo (RC) and neighboring countries. A) Buruli ulcer cases have been reported in all countries neighboring RC. CAR, Central African Republic; DR Congo, Democratic Republic of the Congo. B) RC (representing the white area in panel A). The numbers indicate the 7 departments or communes (of 12 total) where PCR-positive cases of Buruli ulcer disease were diagnosed. 1, Kouilou Department; 2 Pointe Noire Commune; 3, Niari Department; 4, Bouenza Department; 5, Pool Department; 6, Brazzaville Commune; 7, Cuvette Department. C) Kouilou Department (department 1 in panel B). Most Buruli ulcer case-patients from Kouilou Department were living close to the Kouilou River. Stars indicate locations of health centers that treat Buruli ulcer disease; circles indicate areas where persons with Buruli ulcer disease were identified. A color version of this figure is available online (wwwnc.cdc.gov/eid/article/20/6/13-1498-F1.htm)

were confirmed, in accordance with WHO recommendations, by quantitative PCR, the most sensitive and specific testing method available (6).

The National Leprosy, Buruli Ulcer, and Yaws Control Program, with the support of the Raoul Follereau Foundation (Paris, France), performed passive and active surveillance of Buruli ulcer in Congo during 2007–2012. Fine-needle aspirate or swab samples were obtained from patients with suspected Buruli ulcer and sent to Angers University Hospital (Angers, France) for confirmation by quantitative PCR as described (6,7). Of the 283 samples analyzed, 114 (40%) from 108 different patients were PCR positive. Of the 114 PCR-positive samples, 20 (18%) were fine-needle aspirate samples and 94 (82%) were swab samples (at least 2 swabs/lesion). The 108 case-patients included 60 (56%) female and 48 (44%) male patients; 56% of the casepatients were <15 years of age. The most common clinical form of the disease (86% of cases) was the ulcerative stage with edema or plaque. All confirmed Buruli ulcer case-patients

were treated in accordance with WHO recommendations (8): antibiotic treatment (rifampin/streptomycin) plus surgery if necessary. All patients with nonconfirmed cases were treated according to the alternative diagnosis reached by the clinician.

Our findings show that Buruli ulcer disease affects persons in several of Congo's administrative divisions (Figure, panel B); of the 108 patients, 77 (71%) were from Kouilou Department (Figure, panel C). The village of residence was recorded for 55of these 77 patients, 46 (84%) of whom lived in 9 villages along the Kouilou River, encompassing an area of \approx 50 km \times 20 km: Madingo-Kayes, Kanga, Loukouala, Mfilou, Koubotchi, Mboukoumassi, Tchisseka, Magne, and Loaka villages. This disease-endemic area includes 2 lakes, Dinga and Nanga, both of which are fed by the Kouilou River. The remaining 31 (29%) confirmed patients (i.e., those not living in Kouilou Department) lived in Niari Department (9%), Bouenza Department (6.5%), Pool Department (3%), or Cuvette Department (5.5%) or in Pointe

Noire Commune (2%) or Brazzaville Commune (3%) (Figure, panel B).

The distribution of Buruli ulcer cases in Congo is unusual. The Kouilou River region was most affected, but several other areas, all in southern Congo, have confirmed Buruli ulcer patients. Cuvette Department is the 1 exception; although it is in northeastern Congo, this department did have a cluster of cases. The cases in Cuvette were identified (and the infections were diagnosed and treated) during active research into Buruli ulcer during 2009–2010. (Note that there has been no survey in this region since 2010.)

Buruli ulcer is also endemic in some areas of the countries neighboring Congo. In the Democratic Republic of the Congo, the disease is highly endemic in the Bas Congo region, which shares a border with departments in southern Congo where the disease is endemic (9). By contrast, the small cluster of cases diagnosed in Cuvette Department in northeastern Congo seems to be isolated from other areas where the disease is known to be endemic.

M. ulcerans is known to be associated with wetlands, and the Kouilou River environment is certainly suitable for its spread (10). Identification of this zone as a high-risk area for Buruli ulcer disease will help the Ministry of Health improve early detection, biological confirmation, and treatment programs. In the other regions, active and continuous surveillance is necessary to establish a detailed map of the villages and areas where Buruli ulcer disease is endemic; such information would enable the implementation of targeted control activities. However, active surveillance in Congo has substantially declined since 2011. Our findings support the reactivation of such surveillance campaigns to ensure the early identification and confirmation of Buruli ulcer cases and to improve patient management.

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Rapid Metagenomic Diagnostics for Suspected Outbreak of Severe Pneumonia

To the Editor: Recent outbreaks of severe pneumonia or acute respiratory distress syndrome (ARDS) have attracted much public interest. Given current awareness levels, clinical personnel and health officials must rapidly and adequately respond to suspected outbreaks to prevent public disturbances. We report a case that highlights the potential of next-generation sequencing (NGS) to complement conventional diagnostics in such scenarios.

On March 29, 2013, a police officer (patient 1) was admitted to the emergency department of the University Medical Centre Hamburg–Eppendorf in Hamburg, Germany, because of ARDS. The patient was given mechanical ventilation; all diagnostic test results for pathogens commonly known to cause pneumonia were negative (www.virus-genomics.org/supplementaries/EID1406.pdf). Although treatment with antimicrobial drugs was immediately initiated, the patient died 6 days later of multiple organ failure.

On April 5, a second police officer (patient 2) from the same county was admitted to the same emergency department because of ARDS. He was transferred to the intensive care unit and given mechanical ventilation. Similar to the situation for patient 1, diagnostic test results were negative, prompting the news media to suspect an outbreak of a novel or mutated virus (1,2). Especially because of simultaneous outbreaks of avian influenza and infections with Middle East respiratory syndrome coronavirus in other parts of the world, these reports caused serious concern among the public and health officials.

After the death of patient 1 and hospitalization of patient 2, we subjected