

Resurgence of Yellow Fever in Angola, 2015–2016

[Announcer] This program is presented by the Centers for Disease Control and Prevention.

Yellow fever virus is endemic in tropical and subtropical Africa and South America, and it's transmitted to humans and nonhuman primates through the bites of infected mosquitoes. The virus causes yellow fever which, in severe cases, manifests as fulminant hemorrhagic fever. Outbreaks of yellow fever in humans occur mostly in the urban cycle of the virus, which involves its transmission through the bites of the day-feeding infected *Aedes aegypti* mosquitoes. As many as 130,000 cases with fever and jaundice or hemorrhage may occur annually with a concomitant 78,000 deaths. A low capacity for yellow fever diagnosis and lack of surveillance in disease-endemic countries likely contribute to case underreporting.

During 2005–2016, Sudan was the most affected country. Three outbreaks were reported, resulting in 1,508 cases and 368 deaths.

Yellow fever was first recognized in Angola in the 1930s, but not until 1971 and 1988 were sizeable outbreaks reported. As of July 1, 2016, a total of 3,552 suspected cases, including 875 laboratory-confirmed cases and 355 deaths, had been reported from all 18 provinces of Angola, with most cases occurring in Luanda Province. In this account, the authors provide laboratory confirmation that the first suspected viral hemorrhagic fever cases in Angola were yellow fever virus infections and reported preliminary sequencing data.

On January 14, 2016, the authors received whole blood samples from 3 patients who resided in Luanda, Angola, and were suspected of having viral hemorrhagic fever. All were men, two 22 and one 30 years of age. Clinical manifestations in all patients were fever, headache, nausea, and vomiting. Myalgia, malaise, reduced consciousness, and jaundice occurred in 2 patients; abdominal pain, back pain, ecchymosis, conjunctivitis, and bleeding gums occurred in 1 patient. Two of the patients died 7 days after disease onset. Laboratory diagnosis consisted of testing for filoviruses, arenaviruses, and bunyaviruses, as well as for chikungunya and dengue viruses by using reverse transcription PCR. All results of RT-PCRs were negative. A real time RT-PCR for yellow fever virus produced positive results for samples from all 3 patients. PCR and sequencing results were reported to Angolan Public Health Institute on January 19, 2016.

The identification of the outbreak prompted cordon vaccination in Luanda in February 2016, followed by mass vaccination in other areas. The initially localized outbreak in Angola developed into the biggest and most widespread yellow fever epidemic recorded in Africa for decades. Sequencing and phylogenetic analysis indicate that the outbreak virus is highly similar to that identified during the epidemic in Angola in 1971. This finding reiterates the endemicity of yellow fever in Angola and emphasizes the need for consistent routine mass vaccination of the at-risk population to prevent future outbreaks.

I've been reading an abridged version of the October 2016 article, "Resurgence of Yellow Fever in Angola, 2015–2016." You can read the entire article, online now, at cdc.gov/eid.

I'm Sarah Gregory for Emerging Infectious Diseases.

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