cytochrome (*cox1*) gene amplification. (*1*). PCR products were inserted into pCR 2.1 TOPO (https://www.thermofisher.com), cloned, and sequenced (at Macrogen USA, Rockville, MD, USA; https://www.macrogenusa.com). Our search for a 128-bp consensus sequence by using BLAST (https://blast.ncbi.nlm.nih.gov/Blast.cgi) found a 98% match to the *Versteria* species *cox1* gene (GenBank accession no. KT223034). After disease recurrence and soon after extraction of the ocular cyst, we subsequently subjected DNA from the preserved ocular cyst to Nanopore sequencing (Oxford Nanopore Technologies, https://nanoporetech.com) and assembled the complete mitochondrial genome, which we deposited at GenBank (accession no. MK681866) (Figure).

The definitive hosts of the new *Versteria* (*Taenia mustelae*) cestodes are usually mustelids (*2*), a family of carnivorous mammals including weasels, ermine, mink, and others, which are found throughout the northern United States (*3*). This patient reported exposure to fishers in her residence in western Pennsylvania, where a resurgence in the population of these members of the family Mustelidae has been observed. Her husband was screened for signs of a parasitic infection and results were negative. The only other reported human infection with *Versteria* sp. involved a kidney transplant patient, who also had lung and liver lesions. Histopathologic examination of that patient's liver lesions revealed focal necrotizing granulomas with hooklets and a protoscolex (*4*).

The diagnosis of a cestode infection is usually suggested by the presence of specific cestode structures (e.g., a protoscolex, tegument, or calcareous corpuscles). However, unlike the previous report of human infection, histopathologic examination of the liver lesion and ocular cyst from this patient did not detect hooklets or protoscoleces, mimicking the histopathologic appearance of racemose disease sometimes seen in patients with subarachnoid neurocysticercosis. Because histopathologic examination is insufficient for species-level identification (specific cestode structures), molecular testing is necessary for definitive diagnosis of *Versteria* sp. cestode infection.

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Increased Threat of Urban Malaria from *Anopheles stephensi* Mosquitoes, Africa

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Malaria continues to be a major health threat in Africa, mainly in rural areas. Recently, the urban malaria vector *Anopheles stephensi* invaded Djibouti and Ethiopia, potentially spreading to other areas of Africa. Urgent action is needed to prevent urban malaria epidemics from emerging and causing a public health disaster.

The pernicious life-threatening disease malaria continues to place a heavy burden on communities in Africa, where >92% of malaria cases occur today (*1*). Mosquitoes of the genus *Anopheles* transmit malaria parasites to humans. Africa has ≥128 indigenous *Anopheles* species (*2*), several of which, *An. gambiae sensu stricto*, *An. coluzzii*,

and *An. funestus sensu stricto*, are among the world's most efficient malaria vectors. These species are found predominantly in rural areas, where they thrive in a variety of natural and manmade aquatic sites. Because mosquito densities fluctuate with rainfall, malaria is prevalent in rural areas in Africa with strong seasonal variations (*3*).

Malaria also occurs in urban centers in Africa, but at much lower levels, mostly in the peripheries, where small-scale commercial gardens collect surface water (*4*). Malaria is not the only mosquito-borne disease threat in urban Africa. The *Aedes aegypti* mosquito is a vector for dengue, yellow fever, chikungunya, and Zika viruses in urban settings.

Many countries in Africa are experiencing rapid urban development because people from the countryside, attracted by opportunities for work and education, are moving into urban centers. According to the United Nations, cities like Nairobi, Kenya; Dar es Salaam, Tanzania; Kinshasa, Democratic Republic of the Congo; Lagos, Nigeria; Abidjan, Côte d'Ivoire; and Dakar, Senegal, have doubled in population during the last decade and are predicted to expand further (https://population.un.org/wup).

The global malaria eradication campaign, launched in 2005, has led to major reductions in malaria prevalence (*5*), but recent data on malaria in Africa suggest that further reductions are less clear. In many parts of sub-Saharan Africa, progress in malaria control has stalled, and malaria is still widespread (*1*). In addition, the campaign does not focus on urban areas, where malaria prevalence is low or absent.

In 2016, *An. stephensi* mosquitoes were found for the first time in Ethiopia, where this species has since become established (*6*). This discovery followed earlier reports of the species in neighboring Djibouti (*7*). *An. stephensi* mosquitoes are native to southern and western Asia, where the species serves as an efficient malaria vector (*8*). Unlike other malaria vectors in Africa, *An. stephensi* mosquitoes are found not only in rural areas but also in cities, where they breed in manmade water containers, such as household water storage containers and garden reservoirs. The *An. stephensi* mosquito is considered to be the main malaria vector in urban centers in India and Pakistan (*8*). Recently, the species was recorded for the first time in Sri Lanka, demonstrating its ability to disperse across large bodies of water and establish successfully in new geographic regions (*9*).

Because Africa currently does not have a malaria vector adapted to urban centers, establishment of *An. stephensi* mosquitoes on the continent poses considerable health risks. If the species disperses beyond its current distribution in eastern Ethiopia and successfully invades large cities, such as Khartoum, Sudan; Mombasa, Kenya; and Dar es Salaam, the region could face malaria outbreaks of unprecedented size. Because of relatively high levels of malaria prevalence in persons of all ages in rural areas, high mobility between rural and urban areas, and inadequate healthcare, countries in Africa are unprepared to deal with rapid spread of malaria in their cities and towns by a vector species well adapted to urban infrastructures.

To halt the potential risk and prevent further spread of this vector requires urgent action. Historic examples demonstrate that a well-coordinated eradication of a species is possible, such as elimination of invasive *An. gambiae* mosquitoes from Brazil, as well as their eradication from Egypt. However, once a species disperses and covers larger geographic areas, eradication becomes nearly impossible. For example, the *Ae. albopictus* mosquito, a vector of chikungunya and dengue, has spread globally from its original location in Southeast Asia and has become a threat in many countries.

The World Health Organization's Global Vector Control Response 2017–2030 (GVCR; https://www.who.int/vector-control/publications/global-control-response/en) calls for multisectoral approaches to vector control. Urban mosquito control programs in Africa can use GVCR strategies to closely examine mosquito vectors thriving in cities and develop programs to reduce the threat to public health. In our view, surveillance for mosquito vectors in urban centers is essential for preventing outbreaks of infectious vectorborne diseases by eliminating newly established foci of vectors while they are still small (*10*). The invasion of *An. stephensi* mosquitoes on the African continent is a threat to health in tropical Africa but also provides an opportunity to build out vector control strategies as outlined in the GVCR.

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Outbreak of African Swine Fever, Vietnam, 2019

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African swine fever is one of the most dangerous diseases of swine. We confirmed the 2019 outbreak in Vietnam by real-time reverse transcription PCR. The causative strain belonged to p72 genotype II and was 100% identical with viruses isolated in China (2018) and Georgia (2007). International prevention and control collaboration is needed.

Since its first identification in East Africa in the early 1900s, African swine fever (ASF) spread to Kenya in the 1920s; transcontinental outbreaks in Europe and South America in the 1960s and in Georgia (Caucasus) in 2007 led to subsequent transmission to neighboring countries east of Georgia. Along with the outbreaks in the eastern territory of the Russian Federation, acute ASF outbreaks were reported in China in 2018 (*1*).

During January 15–31, 2019, a disease outbreak at a family-owned backyard pig farm in Hung Yen Province, Vietnam, was reported. The farm, ≈50 km from Hanoi and 250 km from the China border, housed 20 sows. In the early stage of the outbreak, 1 piglet and 1 sow exhibited marked redness all over the body, conjunctivitis, and hemorrhagic diarrhea. Breeding gilts demonstrated anorexia, cyanosis, and fever (>40.5°C).

On February 1, 2019, after confirming that the mortality rate at this farm had surpassed 50%, we collected organ samples (e.g., spleen, liver, kidney, tonsil, and lymph nodes) from dying pigs and submitted them to the diagnostic laboratory at the Vietnam National University of Agriculture for ASF diagnosis. All specimens underwent homogenization, followed by extraction of viral DNA (*2*). ASF virus DNA was identified by routine PCR, as recommended by the Office International des Epizooties (Paris, France), and by commercialized real-time PCR (Median Diagnostics Inc., http://www.mediandiagnostics.com). We named the detected ASF virus VNUA/HY-ASF1 and deposited the following complete genome sequences into GenBank: p10 (accession no. MK795932), p11.5 (MK795933), p12 (MK795934), p14.5 (MK795935), p17 (MK795936), p22 (MK795937), pE248R (MK795938), p30 (MK757460), p54

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