For the Barcode of Life Data System see http://www. boldsystems.org

For the Basic Local Alignment Search Tool see https://blast. ncbi.nlm.nih.gov

See Online for appendix

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Aedes aegypti carrying triple knockdown resistance mutations in Beijing, China

Pandemic arthropod-borne viruses have emerged as a global public health concern over the past four decades.¹ Aedes aegypti and Aedes albopictus are vectors of several important arboviral diseases, including yellow fever, dengue, and Zika virus. The detection of A albopictus in southern England, UK,² and the re-emergence of A aegypti in Egypt³ highlighted severe situations of vector introduction. Here, we report for the first time the unexpected presence of A aegypti in Beijing, China, a city with a typical north-temperate climate.

In our efforts to investigate insecticide resistance-associated mutations in A albopictus,4 we discovered three A aegypti in a sample of 56 Aedes spp mosquitoes that were trapped in carbon dioxide in the Grand Canal Forest Park, Beijing, in July, 2017; A aegypti was not observed in samples from 16 other locations in Beijing. The identification of the three mosquitoes as A aegypti was supported by sequence data for four genes: acetylcholinesterase (ace), voltage-gated sodium channel (vgsc), mitochondrial cytochrome oxidase subunit I (coi), and ribosomal DNA

internal transcribed spacer. A search with the *coi* sequence (609 bp) against the Barcode of Life Data System identified the mosquitoes as A *aegypti*. Searches on the US National Institutes of Health's Basic Local Alignment Search Tool revealed entries of A *aegypti* that were identical to our sequences, confirming that the three samples were A *aegypti* (appendix).

Notably, all three A aegypti mosquitoes carried insecticide resistanceconferring mutations in vgsc—namely, Ser989Pro (homozygous), Val1016Gly (homozygous), and Phe1534Cys (heterozygous)—suggesting they had a high level of resistance to pyrethroids. The knockdown resistance mutations of vgsc might facilitate the dispersal of A aegypti because resistant mosquitoes can survive from possible pyrethroid exposure during their journey. The extremely high similarity in gene sequences between the three mosquitoes and those from southeast Asia (appendix) indicates that these A aegypti mosquitoes might originate from southeast Asia.

Because three A aegypti mosquitoes with highly similar gene sequences were detected only in Aedes spp samples collected in the Grand Canal Forest Park, and the presence of A aegypti was not documented in 91 Aedes spp mosquitoes collected in August and September, 2018, and 146 mosquitoes collected in August, 2019, from the same location, we presume that A aegypti has not colonised Beijing. Beijing is a huge city with a population of more than 20 million people, and with busy national and international transport networks, the epidemiological risk of aedes-vectored diseases is high.

The discovery of A aegypti in the Grand Canal Forest Park in 2017 indicates the possibility of the occurrence of this pest in Beijing, at least during warm months. We highly encourage a more vigilant and extensive surveillance programme to monitor the possible occurrence and dissemination of A aegypti in Beijing. To prevent introduction of this potent

disease vector, there should be strict inspections at the various ports of entry.

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Vibrio vulnificus casualties during the American Civil War

An estimated 700 000 soldiers belonging to the Union Army and the Confederate States Army died in the 1861–65 American Civil War.¹ Many camp epidemics attributed to dysentery, typhoid fever, measles, smallpox, cholera, and malaria spread quickly among the troops, affecting the Confederate Army more and surely to some extent shaping the outcome of the war.²

We investigated samples taken from the unmarked graves of nine confirmed Confederate soldiers who died in the first 2 years of the war from camp diseases. The soldiers were in one Confederate state and were to be exhumed and moved to an undisclosed location. Using the dental