

Notes from the Field

An Outbreak of Chikungunya Fever in China — Foshan City, Guangdong Province, China, July 2025

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Chikungunya fever (CF) is caused by chikungunya virus (CHIKV), which is transmitted to humans through the bites of infected female *Aedes* mosquitoes. CHIKV has been documented in over 110 countries across Asia, Africa, Europe, and the Americas (1). China reported its first imported case of CF in 2008. Between 2010 and 2019, local outbreaks resulting from imported cases were documented in Guangdong (2), Zhejiang (3), and Yunnan provinces (4).

On July 9, 2025, Foshan City, Guangdong Province reported a cluster of CF cases. As of July 26, a total of 4,824 confirmed cases had been reported (5) across 12 prefecture-level cities in Guangdong, with 4,754 cases (98.5%) occurring in Foshan and 70 cases (1.5%) distributed among the other 11 prefectures. The majority of cases were concentrated in Shunde District of Foshan, which accounted for 4,208 cases (87.2% of all provincial cases).

Among the confirmed cases, the earliest symptom onset date was June 16. Daily case reports reached their peak on July 19, with 681 cases recorded. The male-to-female ratio was 1:0.97, and the median age was 44 years (range: 0–95 years). Adults aged 15–64 years comprised the largest proportion of cases (3,229 cases; 66.9%), followed by older adults aged ≥65 years (940 cases; 19.5%), school-aged children aged 5–14 years (546 cases; 11.3%), and young children under 5 years (109 cases; 2.3%).

All cases reported to date were mild, with no severe illness or death documented. A preliminary analysis of the early 1,634 cases in Shunde District revealed that 1,418 cases (86.8%) presented with fever, 1,330 (81.4%) experienced joint pain, 1,070 (65.5%) developed rashes, and 838 cases (51.3%) manifested all three cardinal symptoms.

All cases were confirmed by reverse transcription polymerase chain reaction (RT-PCR) (6). Whole genome sequencing (7) was performed for 190 cases. Genomic sequence analysis demonstrated high homology among these viral strains, which all belonged to the Central African Clade of the East-Central-South

African (ECSA) genotype.

Following the outbreak, authorities implemented comprehensive surveillance and case management protocols. Active case detection was combined with differential screening to distinguish dengue from CF among patients presenting with fever, rash, or joint pain. Healthcare facilities in Foshan began conducting nucleic acid testing for CHIKV as part of routine diagnostic procedures.

Confirmed cases received targeted vector control interventions within seven days of symptom onset. These measures included installing insecticide-treated window screens and bed nets at patients' rooms, along with applying residual repellents to living spaces. This patient-focused strategy provided continuous mosquito protection during the infectious period, effectively interrupting virus transmission from humans to vectors.

Simultaneously, comprehensive vector control measures were implemented across affected communities. Targeted adulticide spraying and systematic elimination of mosquito breeding sites were conducted within a minimum 100-meter radius of confirmed case residences, workplaces, and frequently visited locations. Real-time vector surveillance using the Breteau Index and Area Density Index provided critical metrics to assess and optimize transmission control effectiveness.

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