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Original Article

Autochthonous chikungunya virus outbreak in Verona province, Italy, 2025

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Abstract

Background: **Chikungunya virus (CHIKV), primarily transmitted by *Aedes* mosquitoes, has increasingly caused autochthonous outbreaks in temperate regions, including Italy. In 2025, a local CHIKV outbreak occurred in Verona province, Veneto Region. We report the findings of integrated epidemiological, virological and entomological investigations.**

Methods: **In 2025, a dedicated surveillance protocol was implemented to assess local transmission of arboviral infections in Verona province, enabling early detection of a local CHIKV circulation. Following notification of the index case, investigations were conducted in accordance with the national and regional arbovirus surveillance plans, including comprehensive epidemiological, virological and entomological analyses.**

Results: **The index case was identified on 6 August 2025, with retrospective detection of the first case with symptom onset on 31 July; the primary case was not identified. As of 15 October, 69 cases were reported (62 confirmed, 7 probable), with a mean age of 55 years; 91.3% had identifiable epidemiological links, mainly clustered in two municipalities of the Verona province. Most cases (76.8%) occurred between mid-August and mid-September. The outbreak lasted approximately 15 weeks, from the end of July to the mid of October. CHIKV-RNA was detectable in whole blood and, less frequently, urine only within the first 5 days after symptom onset, with higher viral loads in blood. CHIKV-specific IgM antibodies were detectable from Days 4–5 and IgG from Days 7–10. A total of 225 *Aedes albopictus* specimens were collected, all testing negative for CHIKV. Phylogenetic analysis revealed a highly homogeneous, monophyletic cluster within the East-Central-South African genotype, closely related to strains from the 2024–2025 Réunion outbreak.**

Conclusions: **This outbreak underscores the value of dedicated surveillance protocols for early detection of febrile/suspected arboviral cases, while also highlighting key vulnerabilities, namely, an undetected primary case and negative entomological findings, pointing to the need for lower testing thresholds and earlier, risk-based vector sampling.**

Keywords chikungunya virus, CHIKV, *Aedes albopictus*, autochthonous, outbreak, Italy, surveillance

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Introduction

Chikungunya is a disease caused by chikungunya virus (CHIKV), first identified in Tanzania in 1952[1] and subsequently detected in several African and Asian countries. The virus is transmitted primarily by *Aedes* mosquitoes, particularly *Aedes aegypti*. However, CHIKV has adapted to multiple mosquito vectors, thereby facilitating its spread into temperate regions, such as Europe.[2]

In recent years, a rising number and a wider geographic distribution of autochthonous transmission events of CHIKV and other arboviruses has occurred in Europe, mainly associated to *Aedes albopictus* species.[3]

In Italy, CHIKV outbreaks with sustained local transmission chains have been documented in 2007, in Emilia Romagna region; in 2017, in the provinces of Rome and Catanzaro (South Italy); in 2025 with 384 cases distributed across seven clusters in four different Italian regions across three separate outbreaks, with the highest number of cases recorded in Emilia Romagna and Veneto.[4]

Surveillance of CHIKV infection in Italy is carried out under the National Plan for Prevention, Surveillance and Response to Arboviral Diseases 2020–2025 (PNA 2020–2025)[5] and is mandatory year-round, with intensified activities during periods of seasonal vector activity. In accordance with the PNA 2020–2025, the Veneto Region has implemented a regional arboviral surveillance system, supported by an intersectoral One Health plan adopted through Regional Government Resolution No. 421 of 22 April 2025 (DGR 421-2025),[6] which includes provisions for the rapid identification and notification of human cases, integrated mosquito control measures in urban areas, and dedicated veterinary surveillance activities.

In addition to the laboratory-based notification system mandated by the PNA 2020–2025, a dedicated surveillance protocol was implemented at IRCCS Sacro Cuore Don Calabria Hospital presenting with fever of unknown origin during the mosquitoes' activity season to assess local transmission of arboviral infections in Verona province, enabling early detection of a local CHIKV circulation.[7]

In this work, we describe the local transmission event occurred in Verona province, Veneto Region. This area is characterized by a predominantly rural landscape, with intense viticultural activity and a high density of outdoor workers during the summer months. The two municipalities most affected are geographically contiguous and administratively part of the same Local Public Health Department (AULSS 9 Scaligera).

Materials and methods

Laboratory investigations

Laboratory diagnosis of suspected CHIKV infections was performed either the Microbiology Laboratory of the IRCCS Sacro Cuore Don Calabria Hospital (ISCDC) or at the Regional Reference Laboratory (LRR) and included molecular and serological tests. A detailed description of the diagnostic methods used is provided in the Supplementary Data.

Real-time reverse transcription-polymerase chain reaction (RT-PCR) cycle threshold (Ct) values were reported as mean ± standard deviation (SD). For each patient, the time to CHIKV RNA clearance from whole blood and urine and the time to CHIKV IgM and IgG detection were defined as the number of days from symptom onset (DSO) to, respectively, the first negative RT-PCR result or the first antibody detection by IFA. The dataset analysed in this study included all laboratory results of confirmed and probable autochthonous CHIKV cases.

NGS sequencing

All clinical specimens from a total of 25 patients who tested positive by real-time RT-PCR, with cycle threshold (Ct) values ≤ 28 were selected for full-genome sequencing, as lower viral loads did not consistently yield sequence data of sufficient quality for phylogenetic comparison (Supplementary Table S1). Of the 51 real time RT-PCR-positive cases, 25 (49%) were analysed by next generation sequencing (NGS) sequencing representing a convenience sample based on viral load rather than a stratified selection across hotspots or transmission periods. Full details of the NGS sequencing methods used are provided in the Supplementary Data.

Epidemiological investigation, public health interventions and data collection

Upon confirmation of autochthonous CHIKV transmission, the AULSS 9 Scaligera initiated a field epidemiological investigation in accordance with the PNA 2020–2025 and DGR 421-2025.[5,6] A summary of Italian national and regional regulatory framework for arboviral disease surveillance is provided in the Supplementary Data.

Case finding was conducted through active surveillance, combining passive notification from clinical facilities—including hospital emergency departments, general practitioners and the IRCCS Sacro Cuore Don Calabria Hospital—with proactive contact tracing in the affected areas. All patients included in this study were symptomatic at presentation; no seroprevalence surveys were conducted, and therefore no additional asymptomatic or subclinical cases were captured beyond those identified through clinical presentation. For each identified case, a structured epidemiological questionnaire was administered by public health personnel, collecting information on: date of symptom onset, date of first medical contact, date of laboratory diagnosis, municipality and specific address of residence, travel history in the 14 days preceding symptom onset, history of mosquito bites, georeferenced probable exposure and potential epidemiological links with other confirmed or probable cases or with areas where transmission had been documented (Supplementary Table S2). Questionnaires were administered by telephone or in person, within a standardized door-to-door survey conducted among residents and individuals spending significant time within a 300-m radius of each confirmed case's household.

Epidemiological data were entered and managed through the regional infectious disease notification system SIRMI (*Sistema Informativo Regionale Malattie Infettive*), which operates in applicative cooperation with the national notification platform PREMAL (*Sorveglianza delle malattie Infettive*). A geolocation system was activated to map case distribution and support the vector control interventions.[8]

An epidemiological link was considered established if a case reported residing in, regularly spending time in, or having visited such an area during the plausible exposure window. Exposure was

assessed through patient-reported recurrent leisure-time attendance at specific locations, rather than through standardized, quantifiable time thresholds. In particular, exposure to Parona, a popular green riverside area frequently visited for walking and recreational purposes, was defined based on patients reporting recurrent recreational visits to this location during the outbreak period.

Cases without an identifiable geographical or person-to-person link were classified as having no established epidemiological connection and investigated separately.

The outbreak period was defined from the date of symptom onset of the first case (31 July 2025) to the date of symptom onset of the last reported case (14 October 2025). The interval between symptom onset and laboratory diagnosis was calculated for all cases with a documented onset date and used as a proxy indicator of surveillance timeliness.

Local larvicide and adulticide disinfestation protocols, were activated within 24 h of case notification in all instances. The area targeted for vector control interventions was determined based on the diagnostic delays of the cases and the spatial distribution of cases, with additional measures implemented in high-risk areas or locations hosting public events. Consequently, in some instances the radius of vector control interventions was extended beyond 300 m from the cases and from locations where exposure to potentially infected mosquitoes may have occurred.

Entomological investigation

Entomological surveillance and vector control activities were carried out as described in PNA 2020–2025, and in the DGR 421-2025.[5,6] Entomological investigation was started within 24 h from the notification of the index case. Sampling was not uniformly distributed across all 10 sites but was specifically prioritized[9] in the two transmission hotspots of Sant'Ambrogio di Valpolicella/Domegliara and San Pietro in Cariano. Questionnaires were administered by phone or in person as part of a standardized door-to-door survey to assess the presence of adult *A. albopictus* and larvae within a 300 m radius of each confirmed case's household. Full details of the entomological investigations' methods adopted are provided in the Supplementary Data.

Ethical statement

Ethical approval was not required. The data and human blood samples were collected and analysed as part of public health surveillance activities.

Results

Epidemiological and clinical findings

All cases were identified in the province of Verona. The index case was a 64-year-old resident of the municipality of Negrar (Arbizzano district), who presented to the Emergency Unit of ISCDC on 6 August 2025, with a 4-day history of acute fever, rash and arthralgia.

This finding prompted retrospective testing and diagnosis of an earlier, retrospectively identified case in a patient who had presented to the same hospital a few days before (31 July). This patient was a 39-year-old resident of the municipality of Affi, approximately 18 km from Negrar, with a 1-day acute high fever and rash without arthralgia.

Following laboratory confirmation, the public health authorities initiated an epidemiological investigation, including contacting tracing among residents living within a 300-m radius from the patients' households. A total of 320 questionnaires were administered as described.

All patients included in this study were symptomatic at presentation; no seroprevalence surveys were conducted, and therefore no additional asymptomatic or subclinical cases were captured beyond those identified through clinical presentation. As of 15 October 2025, a total of 69 cases had been reported, of which 62 were classified as confirmed and 7 as probable. Of the 69 cases, 35 were males and 34 females; mean age was 55 years (SD $\pm$21). An epidemiological link was identified for 63 (91.3%) of the 69 cases. Specifically, 52 individuals reported living or spending most of their time in two hotspots of the CHIKV epidemic (the municipalities of Sant'Ambrogio di Valpolicella/Domegliara and San Pietro in Cariano); other 11 individuals had visited areas where cases had been reported during the same period. For the remaining six cases, it was not possible to identify epidemiological or geographical links with other cases (Fig. 1).

The number of confirmed and probable cases per day by date of symptom onset is shown in Fig. 2. Most cases (76.8%) had a date of diagnosis between 15 August and 15 September, while the last case was diagnosed 14 October. The median time from symptom onset to diagnosis was 3.0 days [interquartile range (IQR) (2–9)]. Despite extensive public health epidemiological investigations, the primary case could not be identified.

Seven cases remained classified as probable, as they were identified solely based on the detection of CHIKV-specific IgM and IgG antibodies, without confirmation by neutralisation test. Regarding clinical findings at admission, 87.0% of patients presented with fever [median duration 3 days, IQR (2–4)] and 61.1% showed rash [median duration 5 days, IQR (3–7)]. All patients reported conjunctivitis, retro-orbital pain and asthenia. Arthralgia was present in 98.1% of patients.

Virological findings

All suspected cases were tested using both molecular and serological assays. Both CHIKV RNA load and antibody dynamics were stratified by DSO.

Figure 3 shows the kinetics and load of CHIKV RNA in whole blood and urine, along with IgM and IgG dynamics. CHIKV RNA detection was limited to the first 5 days from symptom onset and was observed in all whole blood samples except for one patient who was IgM positive and CHIKV RNA negative at 4 DSO. At 5 DSO, only three patients were positive for both CHIKV RNA and IgM, whereas five patients were IgM-positive and CHIKV RNA-negative, indicating the transition from acute to convalescent phase.

A smaller proportion of patients had detectable CHIKV RNA in urine, which showed lower viral loads compared with whole blood (urine 36.6 $\pm$ 1.4 vs whole blood 25.2 $\pm$ 3.4). No case showed detectable CHIKV RNA in whole blood or urine beyond 5 DSO. The mean CHIKV RNA real time RT-PCR cycle threshold (Ct) values for whole blood and urine at different DSO were summarized in Table 1.

All patients developed specific antibodies within the first 10 days after symptom onset. IgM antibodies appeared at 4–5 DSO,

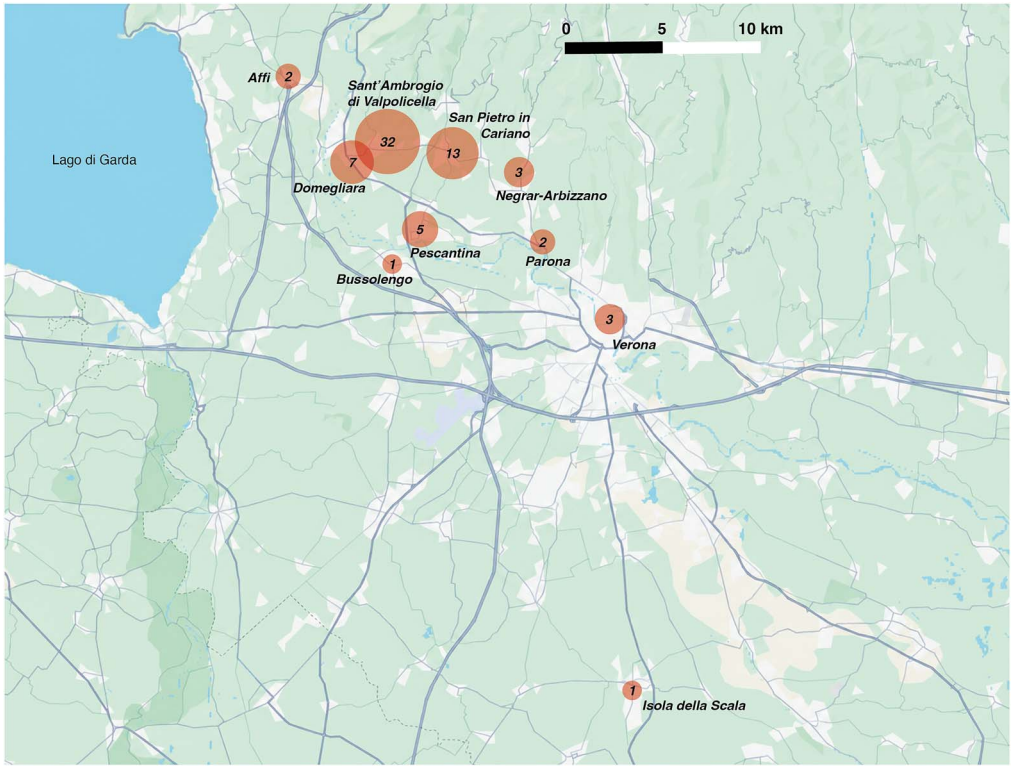


Figure 1 Map with geographical distribution of chikungunya cases along the duration of outbreak.

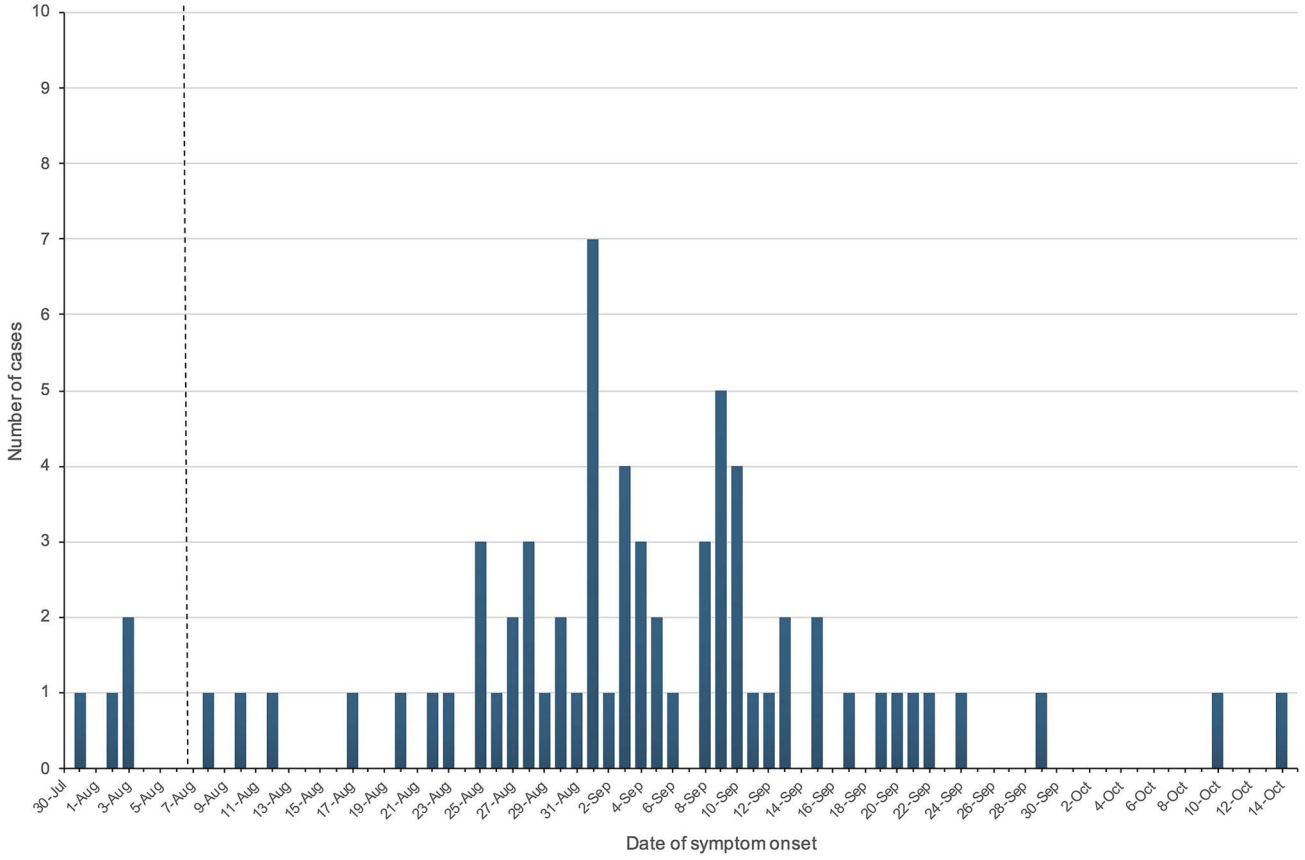


Figure 2 Epidemic curve per day by date of symptom onset of probable and confirmed autochthonous CHIKV cases, Verona, Italy, August–October 2026 ($n = 69$). The dotted line indicates the date of diagnosis of the index case.

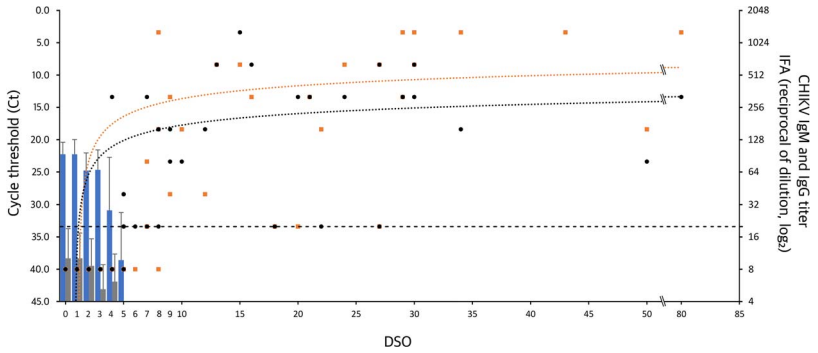


Figure 3 Laboratory findings in cases of chikungunya infection according to days from symptom onset (DSO). Histograms show mean Ct ± SD values of CHIKV RNA viral load in whole blood (blue) and urine (gray), left y-axis. Specific CHIKV IgM (black circles) and IgG (orange squares) antibody titers (IFA, reciprocal dilution values) are also shown, right y-axis (cut off <1:20, dashed line). The two dotted curves represent logarithmic regression used to describe the non-linear trend of the data over the observation period (IgM: black dotted curve; IgG orange dotted curve). Black dotted line represents IFA screening dilution threshold.

Table 1 CHIKV RNA cycle threshold (Ct) mean values for whole blood and urine at different days from symptoms onset.

	DSO											
	0		**1**		**2**		**3**		**4**		**5**	
	Whole blood (*n* = 5)	**Urine (*n* = 2)**	**Whole blood (*n* = 14)**	**Urine (*n* = 4)**	**Whole blood (*n* = 18)**	**Urine (*n* = 10)**	**Whole blood (*n* = 5)**	**Urine *(n = 1)***	**Whole blood (*n* = 5)**	**Urine (*n* = 2)**	**Whole blood (*n* = 3)**	**Urine *(n = 1)***
Ct (SD)	22.0 (±2.3)	35.7 (±1.9)	24.3 (±2.3)	36.6 (±1.1)	24.5 (±2.8)	36.6 (±1.6)	24.2 (±3.1)	37.3	27.2 (±2.5)	37.3 (±1.8)	30.2 (±4.7)	37.1

n = number of samples tested positive

whereas IgG antibodies were detected between 7 and 10 DSO. In all cases confirmed by microneutralization assay, neutralising antibody titres were ≥40 within 20–40 days from symptom onset, corresponding to the reciprocal of the highest serum dilution showing 100% neutralisation of cytopathic effect.

Entomological findings

A total of 17 samplings were conducted across 10 sites where human cases were identified. Overall, 225 *A. albopictus* specimens (152 females and 73 males) were collected during 33 sampling sessions using BG-Sentinel traps (*n* = 158) and 8 HLC collections (*n* = 67). All mosquitoes were collected in public and private areas. Larvae were also observed in standing water containers found in private gardens. A total of 71 pools were analysed, and all tested negative for CHIKV.

Phylogenetic analysis and variant calling

Phylogenetic analysis was conducted by comparing the consensus sequences generated in this study with publicly available genomes downloaded from NBCI and GISAID repositories (Fig. 4). All Verona outbreak-associated sequences grouped closely within the phylogenetic tree exhibiting minimal genetic divergence. Genetic distances among the outbreak samples ranged from approximately 2×10^{-6} to 2×10^{-3} substitutions per site, indicating a high degree of genetic similarity. Phylogenetic analysis showed that all Verona outbreak-associated sequences clustered within a single, well-supported clade belonging to the East-Central-South African (ECSA) genotype of CHIKV, ECSA-II lineage. The topology of the tree indicates a monophyletic grouping of the study sequences, which cluster together with genomes generated during the recent Réunion Island outbreak, consistent with previously reported genomic surveillance data for the 2024–2025 epidemic.[10]

Variant analysis further supported the close genetic relatedness among Verona outbreak associated sequences, as evidenced by limited number of single nucleotide variants (SNVs) and insertions/deletions (indels) identified (Supplementary Fig. S1). The phylogenetic tree highlights the high genetic similarity among samples, with minimal branch lengths, consistent with a recent common ancestor and limited intra-outbreak diversification.

Sequencing yielded an average of 4 million reads per sample. Sequencing metrics, quality control parameters and genome coverage against the RefSeq NC_004162.2 are reported in Supplementary Table S1. All Verona outbreak-associated sequences displayed identical amino acid substitution profiles, with 87 non-synonymous substitutions shared across all samples, involving both structural (C, E1, E2, 6K) and non-structural viral proteins (nsP1–nsP4) (Supplementary Table S2). No sample-specific amino acid substitutions or insertions were detected. All samples were characterized by the presence of a 96 bp deletion (11380–11 476 bp). A limited number of sample-specific nucleotide changes were observed, consisting of four private SNVs and

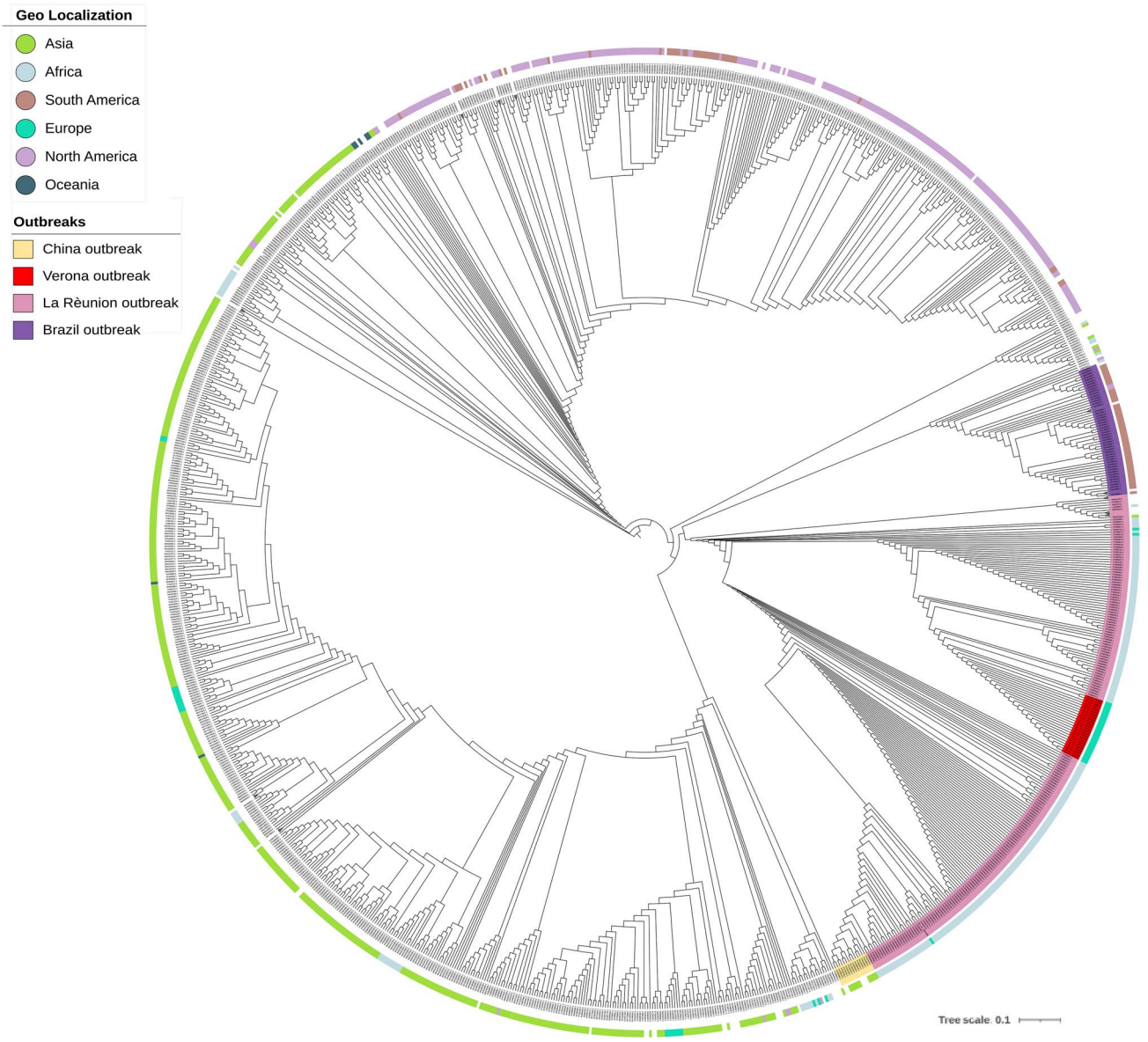


Figure 4 Phylogenetic tree. Maximum likelihood phylogenetic tree of CHIKV complete genomes. The tree includes consensus sequences generated in this study ($n = 25$) together with publicly available CHIKV genomes downloaded from the NCBI virus repository ($n = 1242$), Verona outbreak-associated sequences cluster within a single, well-supported clade belonging to the ECSA genotype and group closely with genomes from the 2024–2025 Réunion Island outbreak. The outer strip colors indicate the geographic origin of sample collection; labels color represent the samples belonging to the three main 2025 outbreaks (i.e. Rèunion outbreak in pink, China in yellow, Brazil in purple and Verona sequences in red). Triangles indicate collapsed sequences.

three private nucleotide deletions, each detected in individual samples. In addition, a single insertion (11421:G) was identified in a subset of samples (15/28, Supplementary Table S2) and was not associated with any annotated amino acid insertion or frameshift.

Discussion

This report describes the epidemiological, virological, entomological investigations, as well as the public health control measures implemented during an autochthonous chikungunya outbreak in Verona province from August to October 2025, which resulted in 69 cases (62 confirmed and 7 probable). The primary case was not identified despite extensive public health epidemiological investigations, including door-to-door interviews, reinforced surveillance among general practitioners and paediatricians, and enhanced syndromic surveillance in emergency departments. Mainland France itself reported an unprecedented number of approximately 800 autochthonous chikungunya cases in 79 distinct transmission episodes during the 2025 season,[11] the vast majority attributed to the 2024–2025 La Réunion epidemic. Large-scale importation from Réunion to continental Europe appears to be the most plausible explanation for the introduction into the Verona area.

The clinical presentation observed in our cohort at the admission is consistent with the classic chikungunya symptom triad of fever, rash and arthralgia, although with some differences

in relative frequency: fever was present in 87.0%, rash in 61.1% and arthralgia in 98.1% of patients. This is broadly comparable to travellers returning to mainland Europe from the concurrent La Réunion outbreak,[12] among whom fever and arthralgia were near-universal and rash was observed in 85.7% of cases, supporting a clinical spectrum consistent with the source epidemic and reinforcing the epidemiological and genomic evidence of a direct importation event.

Our virological data confirm that urine is not a useful diagnostic matrix beyond the first 2–3 days after symptom onset. Moreover, no patient showed detectable CHIKV RNA in blood or urine beyond 5 days from symptoms onset (DSO); among those tested at 5 DSO, only 3/8 remained RNA-positive, while 5/8 were already IgM-positive/RNA-negative, indicating transition to the convalescent phase. Furthermore, when arbovirus infection is suspected, both molecular assays for direct virus detection and serological tests for indirect diagnosis should be performed, regardless of the reported time since symptom onset.

The genomic characterization of the Verona outbreak-associated CHIKV sequences revealed a highly conserved amino acid profile across all samples, indicating limited viral diversification during the outbreak, despite the sequencing coverage was uneven and non-stratified across the two main transmission hotspots of Sant'Ambrogio di Valpolicella/Domegliara and San Pietro in Cariano limiting our ability to detect potential within-hotspot viral evolution. The observed genomic homogeneity should therefore be interpreted as reflecting the sequenced subset, rather than confirming the complete absence of within-outbreak viral diversity. Several non-synonymous substitutions identified in this study have been previously reported in other CHIKV genomes,[2,13] including the well-established E1-A226V substitution associated with viral adaptation to transmission by *A. albopictus*.[14,15] The phylogenetic placement of the sequences within a monophyletic clade of the ECSA genotype is consistent with recent reports describing the CHIKV lineage responsible for the ongoing epidemic on Réunion Island. In addition, the close clustering of the Verona outbreak sequences with this lineage supports their attribution to the same epidemic wave and suggests a recent common ancestor (Fig. 4).[10,16,17] Moreover, a small number of sample-specific nucleotide substitutions and deletions were identified. These unique SNVs indicates a limited but detectable micro-evolution within the viral population (Supplementary Table S3 and Figure S1). Interestingly, we observed a ~96 nt deletion in the 3′ untranslated region (3′UTR), larger than previously described[11] deletions in CHIKV. Given the known role of the 3′UTR in regulating viral replication and host–vector interactions, this structural variation may reflect adaptive processes, although its biological significance requires further investigation.

The three municipalities (Sant'Ambrogio di Valpolicella, Domegliara and San Pietro in Cariano) most affected are geographically contiguous and administratively part of the same local health unit (AULSS 9 Scaligera). Their proximity, combined with the high density of *A. albopictus* vectors documented in the area during the summer season, created favourable conditions for sustained local transmission.

The geographical and environmental characteristics of the sub-district played a significant role in shaping the outbreak dynamics. The mosaic landscape—alternating agricultural land with densely vegetated residential areas, private gardens, irrigation ditches and rural settlements—created favourable ecological conditions for *A. albopictus* proliferation and hampered the implementation of widespread vector control interventions.[18] The heavy rainfall recorded at the end of August likely reduced the effectiveness of larvicidal treatments and may have contributed to the subsequent peak in cases observed in early September, highlighting the sensitivity of vector-borne disease dynamics to meteorological events.

However, despite the high number of sampling sessions ($n = 33$), relatively few mosquitoes were collected because most collections took place after vector control interventions, when mosquito abundance was expected to be markedly reduced. This strategy reflected the priority given to the immediate implementation of vector control measures, ensuring that entomological investigations did not delay public health interventions.

This finding is consistent with the well-documented low sensitivity of entomological virus detection relative to the intensity of human transmission and should not be interpreted as evidence against active local vector-borne transmission, which is otherwise strongly supported by the epidemiological and genomic data.[19]

Moreover, despite extensive epidemiological investigation, not all elements of the transmission chain could be fully reconstructed with certainty. In particular, while whole-genome sequencing confirmed that the index case, the two retrospectively identified cases in Affi and the cases occurring outside the two main hotspots belonged to the same transmission lineage, no epidemiological link could be established connecting these cases to one another or to the two main hotspots. As a result, the precise route and timing of transmission linking these cases to the core outbreak could not be determined, and the primary case responsible for introducing CHIKV into the area was never identified. This limitation likely reflects a combination of factors, including the frequently mild or non-specific clinical presentation of early chikungunya infection, which may delay or prevent clinical suspicion and testing, as well as the inherent difficulty of retrospectively reconstructing individual movement patterns and social contacts over an extended, multi-week transmission period.

From a public health perspective, this outbreak highlighted both the strengths and the residual vulnerabilities of the regional response system. The rapid activation of the regional arbovirus standard operating procedure, the prompt coordination between public health regional and local authorities, clinical facilities, virological and entomological reference laboratories and Local Health Authority of Verona, allowed for timely case ascertainment, vector control and communication.

Although this local transmission event resulted in fewer cases compared to those in Italy in 2007, 2017 and other regions in 2025,[3] transmission persisted for approximately 15 weeks after the index case was notified. This persistence may have been influenced by factors such as misdiagnosis or delayed screening for arboviruses. Notably, the primary source of introduction was not identified in this outbreak, which is not unusual in autochthonous arboviral clusters detected in non-endemic areas and mirrors similar reports in the literature.[20] This underscores a critical challenge for travel medicine: enhancing clinical suspicion and diagnostic capacity for arboviral infections among returning travellers remains central to preventing undetected introductions and subsequent local transmission, for example by promoting a lower threshold for arboviral testing in patients presenting with fever of unknown origin during the Aedes activity season, irrespective of an explicitly reported travel history.

In fact, public awareness requires systematic investment. A key message that must be clearly communicated to the public is that vector control is not solely a municipal responsibility: while local authorities are mandated to implement larvicidal and adulticide treatments in public areas, *A. albopictus* breeding sites are predominantly found in private settings, gardens, courtyards, terraces and any outdoor space where standing water can accumulate.

Conclusion

Looking ahead, the progressive establishment of competent vectors and the increasing frequency of importation events call for a structural strengthening of intersectoral preparedness, grounded in a One Health framework that integrates human, animal and environmental health surveillance. This includes the consolidation of entomological monitoring networks, the enhancement of epidemiological intelligence tools for contact tracing and geospatial analysis, closer integration with international travel and epidemiological intelligence systems (e.g. European Centre for Disease Prevention and Control (ECDC) threat reports) to support earlier recognition of importation risk from active outbreaks abroad, and the development of pre-agreed response protocols that can be activated rapidly and at scale. Rapid case identification, laboratory confirmation and immediate vector control measures were likely decisive in limiting the extent of this outbreak; sustaining and reinforcing these capabilities—at regional, national and international levels—remains essential to prevent, detect and contain future arboviral events.

These findings highlight the need for greater attention to autochthonous arboviral transmission within Europe, including a reassessment of the current epidemiological case definition to better account for locally acquired infections in areas where competent vectors are established.

Supplementary data

Supplementary data are available at *JTM* online.

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Author contributions

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Conflicts of interest

The authors have declared no conflicts of interest.

Data availability

Data supporting the findings of this study are available upon reasonable request in compliance with data protection regulations. All genome sequences were deposited in GISAID (https://gisaid.org/).

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