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Cross-sectional entomological data reveals an increased risk of arboviral transmission in a year of record-breaking heat in Southern Europe

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Abstract

Background In 2023, an unprecedentedly high number of locally acquired cases of dengue virus occurred in Europe, including the first large outbreak in Rome (Italy). Globally, 2023 was warmer than any previous year on record since 1850, with each month from June to December being warmer than the corresponding month in previous years.

Methods We conducted an extensive analysis of entomological data in Rome to investigate how the unprecedentedly high temperatures seen in 2023 affected the abundance and seasonal dynamics of the local vector *Aedes albopictus* population and the risk of autochthonous transmission of both dengue and chikungunya viruses. We applied a mathematical dynamic temperature-based model to analyse adult mosquito collections in 2023 compared to those available for 2012 and assess the consequent changes in the risk of arboviral transmission. Simulations of potential local transmission triggered by disease importation were used to evaluate the effectiveness of human and entomological surveillance for monitoring transmission risks, providing insights for future action plans

Results Results highlight a higher abundance and longer active season of *Ae. albopictus* as well as a higher risk of local arbovirus transmission in 2023.

Conclusions Our findings raise concern in light of the predictions for more frequent extremely warm years in Europe in the near future.

Plain language summary

The Tiger mosquito can transmit the dengue and chikungunya viruses to humans, which cause disease. In 2023, unusually warm temperatures were seen in Rome. We compared the abundance of the Tiger Mosquito between 2012 and 2023 in Rome. We used a mathematical model to estimate that there was a higher mosquito density in 2023, resulting in a longer duration of potential risk of infection of people with dengue and chikungunya viruses and a greater number of urban sites at which infection could occur. Our findings provide evidence of an increasing risk of transmission of these two viruses in Mediterranean urban areas, underscoring the critical importance of timely case detection and rapid mosquito control responses to prevent potential outbreaks in urbanised settings.

Europe is exposed to the risk of dengue (hereafter DENV) and chikungunya (hereafter CHIKV) virus outbreaks due to the inflow of viremic travellers from endemic areas and the high densities of a competent vector species (i.e. *Aedes albopictus*), particularly in Mediterranean and Balkan countries¹. In 2023 and 2024, an unprecedentedly high number of DENV locally acquired cases (2023: $N = 130$; 2024: $N = 304$) and outbreaks (2023: 8 in France, 4 in Italy and 2 in Spain; 2024: 11 in France, 6 in Italy and 1 in Spain) occurred in

Europe, representing a marked increase compared to the 10-year period 2010–2021, when the overall number of locally acquired cases was 73². This increase is largely due to an increase in the number of travel-related cases of arboviral infections in Europe as a consequence of the growing incidence of cases worldwide³, the increase in the number of endemic countries, and the increase in international travel experienced after the COVID-19 pandemic⁴.

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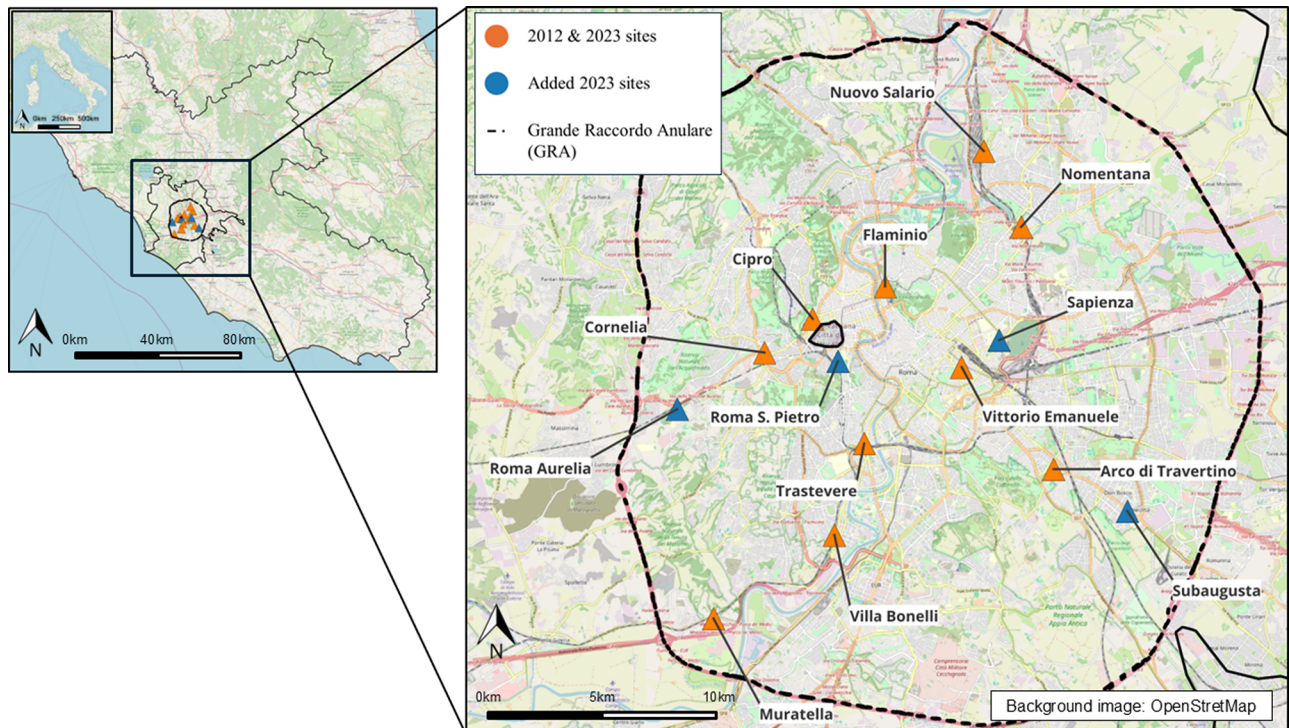


Fig. 1 | Sampling sites within the metropolitan city of Rome monitored in 2012 (N = 10) and 2023 (N = 14). Orange = sites monitored both in 2012 and 2023. Blue = sites monitored only in 2023. Bold dashed line = Grande Raccordo Anulare,

the 68-km long ring-shaped highway encircling the city most urbanised area. This map incorporates data from © OpenStreetMap contributors, which is made available at www.openstreetmap.org/copyright under the Open Database License (ODbL).

So far, the first and the largest European *Ae. albopictus*-transmitted arbovirus outbreaks occurred in Italy: 330 CHIKV cases in Emilia Romagna Region in 2007⁵ and 199 DENV cases in Marche Region in 2024⁶. In particular, Rome is the only European metropolis to have experienced autochthonous transmission of both CHIKV (2017)⁵ and DENV (in 2023)⁷.

Table 1 | The estimated mean density of *Aedes albopictus* females and human population density per hectare for each sampling site within the most urbanised area of the city of Rome (Italy) between June 1st and December 1st 2012 (10 sites) and 2023 (14 sites)

Sites	Mean adult <i>Ae. albopictus</i> females/ha (95% CI)		Human population density (N° inhabitants/ha)	
	2012	2023	2012	2023
Muratella	560 (481–648)	1214 (1120–1312)	2.19	8.45
Villa Bonelli	717 (619–811)	1313 (1197–1421)	359.57	382.16
Trastevere	679 (586–775)	2004 (1868–2126)	308.58	225.88
Cornelia	899 (825–982)	946 (853–1046)	209.44	234.65
Cipro	974 (870–1072)	1932 (1793–2070)	290.75	279.20
Flaminio	303 (260–362)	629 (545–719)	51.55	50.89
Vittorio Emanuele	2241 (2101–2405)	2540 (2400–2674)	302.14	271.69
Arco di Travertino	1157 (1073–1260)	1694 (1574–1832)	240.43	121.42
Nomentano	2884 (2726–3027)	1886 (1749–2035)	292.27	294.11
Nuovo Salario	905 (825–1011)	2049 (1904–2218)	82.20	96.85
Roma Aurelia	-	1151 (1055–1278)	-	21.10
Roma S. Pietro	-	1501 (1379–1626)	-	141.91
Subaugusta	-	2448 (2264–2629)	-	376.84
Sapienza	-	1195 (1105–1296)	-	92.28

In 2012, we conducted extensive entomological field collections over a 70 km transect from the Tyrrhenian Sea coast of the Lazio region in Italy to the foot of the Apennine mountains, encompassing the Rome metropolitan area and estimated the effect of climatic and socio-environmental variables on *Ae. albopictus* abundance and seasonal dynamics along the transect⁸. The data proved instrumental in calibrating mathematical models for characterising the transmission dynamics of 2017 CHIKV outbreak⁹ and to provide a quantitative assessment of the risk of Yellow Fever virus in Lazio region¹⁰ and of CHIKV, DENV, and Zika virus transmission in Europe¹¹.

In 2023, we replicated and extended the entomological collections in the central part of the 2012 transect, corresponding to the most urbanised part of the Rome metropolitan area. *Ae. albopictus* abundance data from 2023 and 2012 samplings are here exploited to feed a mathematical dynamic temperature-based model to quantify mosquito abundance and to assess the risk of DENV and CHIKV secondary transmission. Notably, at the global level, 2023 showed the warmer temperature data records than any preceding year since 1850, 0.6 °C warmer than the 1991–2020 average and 1.5 °C warmer than the 1850–1900 pre-industrial level. In particular, each month from June to December was warmer than the corresponding month in any previous year¹². The same trend was observed in Europe¹³.

Results highlight a higher abundance and a more prolonged active season of *Ae. albopictus*, as well as a higher risk of secondary transmission in 2023, raising concern in view of the predictions of increasing frequencies of warmer years in the near future in Europe and other temperate regions. In addition, model simulations of the risk of secondary cases arising from an infected case importation are also exploited to compare the effectiveness of human and entomological surveillance for monitoring transmission risks, providing indications for future action plans.

Materials and methods

Entomological collections in 2012–2023

A total of 14 sampling sites within the “Grande Raccordo Anulare” —i.e. a 68-km long ring-shaped highway encircling Rome’s most urbanised area— were monitored from April 13th to December 15th 2023 (35 weeks), 10 of

Table 2 | Epidemiological parameters used for dengue and chikungunya R_0 estimations in Rome (Italy)

Pathogens	Parameters	Description	Distribution	Min; Max	Refs
CHIKV	μ_V	Adult mortality (day ⁻¹)	NA	0.031–95820 * e ^{-(T-50.4)}	16
	β	Biting rate (bite/mosquito/day)	Uniform	0.08:0.10	9
	ϕ	Vector preference (%)	NA	0.6°	22,37,38
	χ_H	Probability of vector-to-human transmission per bite (%)	Uniform	75;80	39
	χ_V	Probability of human-to-vector transmission per bite (%)	Uniform	50;55	39
	ω_V	Extrinsic incubation period (day ⁻¹)	Uniform	2;3	40
	γ	Human infectious period (days)	Uniform	2;7	41
DENV	μ_V	Adult mortality (day-1)	NA	0.031–95820 * e ^{-(T-50.4)}	16
	β	Biting rate (bite/mosquito/day)	Uniform	0.08:0.10	9
	ϕ	Vector preference (%)	NA	0.6°	22,37,38
	χ_H	Probability of vector-to-human transmission per bite (%)	NA	7.35 * 10 ^{(-4)*T*(T-15.84)*√36.40 - T}	28
	χ_V	Probability of human-to-vector transmission per bite (%)	NA	4.39 * 10 ^{(-4)*T*(T-3.62)*√36.82 - T}	28
	ω_V	Extrinsic incubation period (day ⁻¹)	NA	1.09 * 10 ^{(-4)*T*(T-10.39)*√43.05 - T}	28
	γ	Human infectious period (days)	Uniform	2;5	42

T = temperature in degree Celsius.
 ° The value of Vector preference is the mean.

which were also monitored in 2012 (22 weeks from July 10th to December 4th) (Fig. 1 and Table 1). The full site’s description is provided in Supplementary Note 1. Briefly, *Ae. albopictus* adult collections in each sampling site were conducted by four/five sticky traps (STs¹⁴), dispersed within a 300 m radius area. Every week, sticky panels were replaced with freshly glued ones and trapped mosquitoes were morphologically identified and counted on-site. Due to the specificity of the ST for *Ae. albopictus* and the absence of other morphologically similar species in the study area, the identification was feasible also when glued specimens were partially damaged.

Mosquito population model

We calibrated the mosquito population mathematical model already applied for estimating *Ae. albopictus* populations^{9,10,15,16} with data from *Ae. albopictus* adult female ST’s captures carried out in 2023 and 2012⁸ (further details in Supplementary Method 1). The model considers four developmental stages (eggs, larvae, pupae and adults) and mimics the mosquito life cycle based on temperature-dependent parameters regulating the stage-specific mortality and development rates (Supplementary Table 1). The model takes as input average daily temperature records obtained from the closest weather station to each sampling site in the year of sampling¹⁷. For each year, the model is initialised on 1st March with 1000 mosquito eggs and runs until 31st December. We considered 100 and 10,000 initial eggs for sensitivity analysis. The free parameters of the model (i.e. site and year-specific larval carrying capacities) were estimated using a Markov Chain Monte Carlo (MCMC) approach based on a Poisson likelihood on the observed entomological collection¹⁵. Model simulations were used to compare the population dynamic in each site and between years. The full model description is provided in Supplementary Method 1. The results of model calibration and the sensitivity analysis are provided in Supplementary Methods 2, 3 and 4 (Supplementary Figs. 1–6; and Supplementary Tables 2–3). The mosquito population dynamics model was then coupled to an epidemiological transmission model describing the spread of the epidemic in both humans and mosquitoes (Supplementary Fig. 7).

Epidemiological risk in urbanised areas

To assess the risk of secondary transmission of DENV and CHIKV, human population size within a spatial polygon of 300 m radius buffer centred in each sampling site was derived from single census units (source: <https://esploradati.istat.it/databrowser/#/en>), using a focal filtering approach¹⁸. Briefly, human inhabitants within a circular buffer of radius 150 m, drawn around each cell of size 10 × 10 m, falling within the site polygons, were

calculated using a weighted spatial overlapping method from census units. For each site, the cell with the highest value was considered as the human population size, aiming to capture high levels of exposure to mosquito bites occurring within walking distance from individuals’ residences. We focused our analysis only on sites with an estimated human population density above 30 humans/hectare. The simulated *Ae. albopictus* females population was used to compute the basic reproduction number R_0 , which represents the number of human secondary cases caused by a primary human infector, according to the equation:

$$R_0 = (\beta\phi)^2 \frac{V \chi_V \chi_H}{N_H \gamma \mu_V} \frac{\omega_V}{\omega_V + \mu_V} \tag{1}$$

where β is the biting rate, ϕ shapes the host preference, γ is the human infectious period, χ_V is the probability of human-to-vector transmission per bite, χ_H is the probability of vector-to-human infection per bite, μ_V is temperature dependent mortality of *Ae. albopictus* adult females, V is the number of females adult mosquitoes, N_H is the number of susceptible humans, ω_V is the extrinsic arbovirus incubation period (Table 2).

Following the same approach used by Guzzetta et al.¹⁹ and Manica et al.^{9,10}, we simulated the transmission dynamics associated with DENV and CHIKV using a standard SEI-SEIR approach. In the model, mosquitoes can develop a lifelong infection after an (extrinsic) incubation period following the bite to an infectious human (SEI sub-model), whereas humans can develop a temporary infection after an (intrinsic) incubation period following the bite of an infectious mosquito. After recovery, humans develop persisting immunity against infection (SEIR sub-model). For both CHIKV and DENV, we assumed that each symptomatic case is notified to local health authorities according to reporting rates²⁰ and delays²¹ estimated from the CHIKV outbreaks that occurred in Italy in 2007 and 2017⁵. We analysed the expected epidemic trajectories in mosquitoes and humans resulting for each sampling site, considering independent epidemics across sites and exploring alternative timings for the first human case introduction. Specifically, for each site, we sampled 100 carrying capacities from their posterior distribution and run 100 stochastic simulations for each carrying capacity, leading to a total of 10.000 simulation runs per site. In each simulation, we uniformly sampled the date of introduction between 1st May and 16th November 2023 and 2012.

For each site, simulation results were combined to compute the probability of observing at least more than 10 autochthonous cases (corresponding to the lowest number of cases detected in an arboviral outbreak

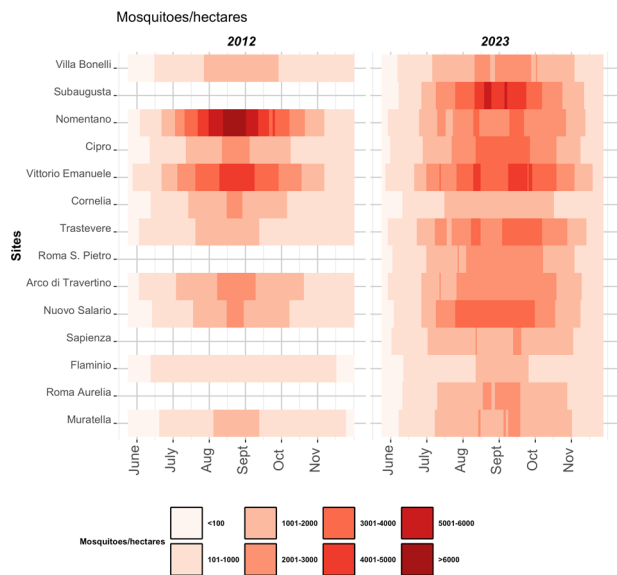


Fig. 2 | Average posterior distribution of *Ae. albopictus* females' density (females/hectare) in 10 (2012) and 14 (2023) sampling sites within the most urbanised area of the city of Rome (Italy).

in Italy so far, i.e. DENV outbreak in Veneto region in 2020, 18). The full model description is available in the Supplementary Method 5.

Entomological and human surveillance

We explored the potential effectiveness of entomological surveillance (infected *Ae. albopictus* females in the traps) in detecting possible arboviral transmission at the local scale and compared its performance with the one of human surveillance (notification of human cases to local health authorities). To this aim, we considered the previously simulated epidemic trajectories in mosquitoes and humans coupled with the modelling of entomological and human surveillance efforts. Entomological surveillance was modelled in each site by assuming active daily surveillance based on two capture rates, either 1 mosquito collected out 1000 mosquitoes present (hereafter, lower capture rate, estimated for a BG-Sentinel trap daily operating in the site¹⁹) or 1 out 100 (hereafter, higher capture rate, roughly corresponding to the efficacy of 10 BG-Sentinel traps). The likelihood of capturing at least one infected mosquito was estimated assuming a Binomial distribution, with the probability of success set at the considered capture rate. We sampled daily captures from the simulated population of infected mosquitoes for each one of the stochastic simulations, without removing the captured mosquitoes from the simulated population. The time required to detect an infected mosquito was computed as the days elapsed between the day of index case importation and the first day when we simulated at least one captured infected mosquito. Human surveillance was modelled in each site by assuming estimates of case ascertainment ratio and reporting delays available in the literature (Supplementary Table 5). The time required to detect an infected case was computed as the days elapsed between the day of index case importation and the first day when we simulated at least one notified autochthonous human case. IRB approval was not required for this study, as it did not involve human subjects or individual human data. The human surveillance referenced is synthetic and based on simulations.

Reporting summary

Further information on research design is available in the Nature Portfolio Reporting Summary linked to this article.

Results

Entomological collection

A total of 10573 *Ae. albopictus* females were collected weekly by sticky traps from April 18th to December 15th, 2023, in 14 sampling sites within the 68-

km long ring-shaped highway encircling Rome's most densely populated and historically relevant area (Fig. 1). The first female was captured in the second collection week (19–26 April). From the 9th of June to the 29th of November the species was observed in all sites. The collection week characterised by the highest number of captured *Ae. albopictus* females were heterogeneous among sites, spanning from the collection week 19–26 July to 22–29 August. The highest number of captured *Ae. albopictus* females were heterogeneous among sites, too, ranging from 42 to 149 females collected. Sporadic captures were also reported until the collection week 5–12 December.

In the case of 10 sampling sites, the results of 2023 collections were compared with those from collections carried out following the same experimental scheme in the same sites in the previous field trial (from 10th July to 4th December 2012)⁸. The overall average number of *Ae. albopictus* females/trap/week was always higher in 2023 (2023: 10th–31st July = 41.2, August = 45.8; September = 36.3, October = 37.3; November = 5.5; 2012: 10th–31st July = 14.4, August = 34.7; September = 33.3, October = 28.2; November = 3.3).

Aedes albopictus female/hectare

Results of the mathematical model applied to collections of *Ae. albopictus* in 2023 and 2012 provide estimates of their seasonal patterns, mimicking the mosquito life cycle based on temperature-dependent parameters regulating the stage-specific developmental and mortality rates. The model results closely reflect the observed temporal dynamics of captured *Ae. albopictus* females along the season (Supplementary Figs. 1–2, Supplementary Table 3) and the high heterogeneities in abundance among sites (Table 1 and Fig. 2). Between 1st June and 1st December, the model estimates suggest a higher mosquito abundance in 2023 compared to 2012 (Table 1) in most sampling sites (9/10), as well as an average increase in female abundance of 64% (95% CI: 59%–68%), 54% (95% CI: 48%–60%) and 142% (95% CI: 133%–151%) in June–July, August–September, and October–November, respectively. The daily estimated mean *Ae. albopictus* females' density for each site was reported in Supplementary Figs. 3–4.

Risk of DENV and CHIKV secondary transmission in urban Rome

Following the approach by Guzzetta et al.¹⁹ and Manica et al.^{9,10}, we simulated DENV and CHIKV transmission dynamics in 2012 and 2023 in the sites with a human population density above 30 humans/hectare (Fig. 3). Results highlight high variability in R_0 estimates among sites in both years (Supplementary Table 4). All sites at risk for CHIKV transmission are also at risk for DENV transmission, albeit to a much lower extent. Moreover, the number of sites where potential arbovirus transmission ($R_0 > 1$) may occur increases from 33% to 66% from 2012 to 2023.

For DENV, the median R_0 values from June to September ranged between 0.14 and 2.71 in 2023 and between 0.05 and 0.98 in 2012. The median DENV R_0 over June–September 2023 is estimated to be above 1 in only 3 out of 12 sites, and never during the same period in 2012 (Supplementary Table 4). For sites sampled in both years, the epidemic period (i.e. the number of weeks for which the estimated R_0 was above 1) is estimated to be on average 5 weeks in 2012 (30th July–2nd September, min = 4 weeks; max = 5 weeks) and 7 weeks in 2023 (24th July–17th September, min = 1 week; max = 11 weeks); 40% of the sites samples in 2023 (5 out of 12) are estimated to be at risk of onward transmission ($R_0 > 1$) for DENV also in September (Fig. 3).

The proportion of simulations resulting in an outbreak with more than 10 DENV-cases was heterogeneous among sites, ranging from 0 to 25%, and substantially higher in 2023 than in 2012, extending the risk from July up to August (Fig. 4a). Overall, in 2023, the mean probability that an imported DENV case would trigger an outbreak with at least one secondary case is <5% until the 25th week (June), increasing up to 30% in August, and becoming negligible at the end of September. However, the probability of observing 10 DENV-human secondary cases or more peaks between the end of July and early August (6%) becomes negligible at the end of August (Fig. 5a).

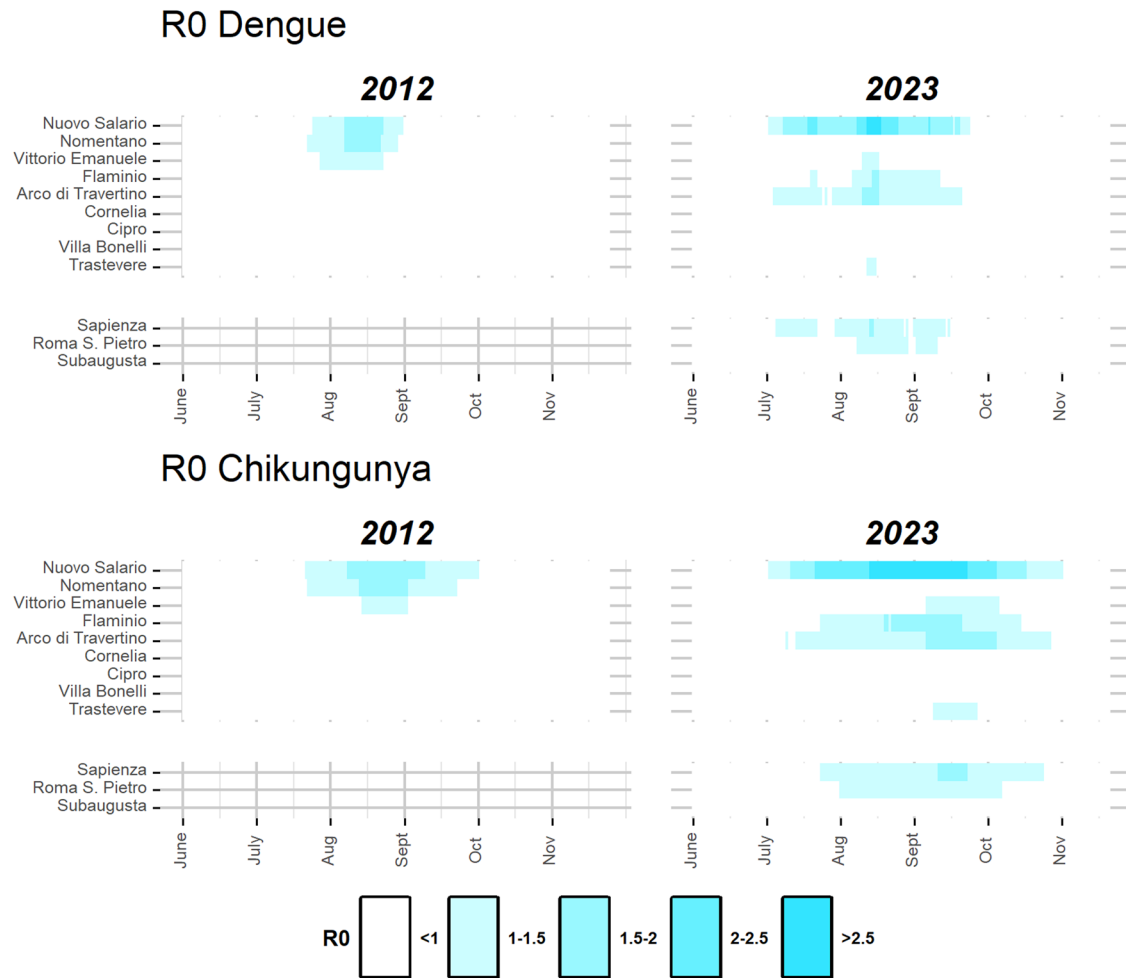


Fig. 3 | Estimated basic reproduction number (R0) of Dengue and Chikungunya in 9 (2012) and 12 (2023) sites within the most urbanised area of the city of Rome (Italy). R0 represents the basic reproduction number, i.e. the number of human

secondary cases caused by a primary human infector. White = days in which R0 is not above epidemic threshold ($R_0 < 1$). Gradient of Blue = days in which R0 is above epidemic threshold ($R_0 > 1$).

For CHIKV, the median R0 values from June to September ranged between 0.14 and 3.82 in 2023 and 0.08 and 1.96 in 2012. The median CHIKV R0 over the period June–September 2023 is estimated to be above 1 in 4 out of 12 sites, and in 2 out of 9 sites during the same period in 2012 (Supplementary Table 4). For sites sampled in both years, the epidemic period is estimated to be on average 8 weeks in 2012 (30th July–23rd September, min = 2 weeks; max = 10 weeks) and 11 weeks in 2023 (7th August–22nd October, min = 3 weeks; max = 17 weeks). Remarkably, in 2023, 60% of sampling sites (7 out of 12) are estimated to be at risk of onward transmission in October (Fig. 3).

The proportion of simulations resulting in an outbreak with more than 10 CHIKV-cases was heterogeneous among sites, ranging from 0 to 40%, and substantially higher in 2023 than in 2012, extending the risk from August up to October. (Fig. 4b). Overall, in 2023, the mean probability that an imported CHIKV case would trigger an outbreak with at least one secondary case is <5% until the 24th week (June), increasing up to 40% in August, and becoming negligible at the end of October. The probability of observing 10 CHIKV-human secondary cases or more peaks between the end of July and early August (14%) becomes negligible at the end of September (Fig. 5b).

Entomological and human surveillance

Focusing on model simulations that resulted in at least one secondary case, we assessed both the probability of (i) detecting a secondary arbovirus case by the surveillance of human symptomatic cases and (ii) detecting an

infected mosquito by entomological surveillance. We assumed two different capture rates: low (1 captured out of 1.000 mosquitoes) and high (1 out of 100 mosquitoes). The two levels considered roughly represent the trapping efficacy of one and ten BG traps, respectively, in an area experiencing ongoing transmission.

In the case of DENV, we estimated the secondary case detection probability of human surveillance to range from 31% to 66% between June and October. During the same period, our results suggest that the detection probability of entomological surveillance (i.e. percentage of simulations when at least one infected mosquito is captured) ranges from 1% to 22% assuming a low capture rate and from 17% to 66% with a high capture rate (Fig. 5c).

In the case of CHIKV, we estimated the secondary case detection probability of human surveillance (i.e. the percentage of simulations when at least one secondary case is detected) to range from 62 to 87% between June and October. During the same period, the detection probability of entomological surveillance (i.e. the percentage of simulations when at least one infected mosquito is captured) ranges from 3% to 31% assuming a low capture rate and from 28% to 69% with a high capture rate (Fig. 5d).

The estimated average delay from the index case importation and the detection of a secondary case through human surveillance is 49 and 42 days for DENV and CHIKV, respectively, assuming the introduction of an infected case between the end of June and the end of October (Fig. 5e, f). A longer delay is estimated for DENV at the

Fig. 4 | Probability (%) of observing an outbreak with >10 cases of dengue or chikungunya in 2012 and 2023. Probability (%) of observing an outbreak with >10 cases of dengue **a** or chikungunya **b** in 2012 (red) and 2023 (yellow) following the introduction of a single imported human case at different weeks from May 1st to November 1st across different study sites located in the metropolitan city of Rome. Estimates were derived for sites associated with more than 30 residents per hectare. Boxplots show the probability (%) of observing an outbreak with >10 cases. The box represents the upper and lower quartiles, the centre line the median and the whiskers the 95% prediction interval. $N = 9$ independent samples for both years. The horizontal dashed line indicates the 5% probability used as a reference in the text. Dots = probability (%) of observing an outbreak with >10 cases of dengue or chikungunya in each site in 2012 and 2023.

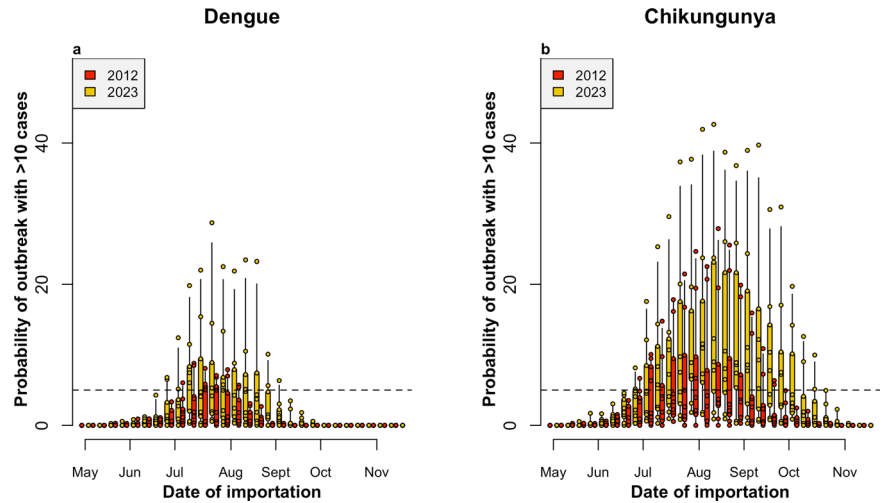
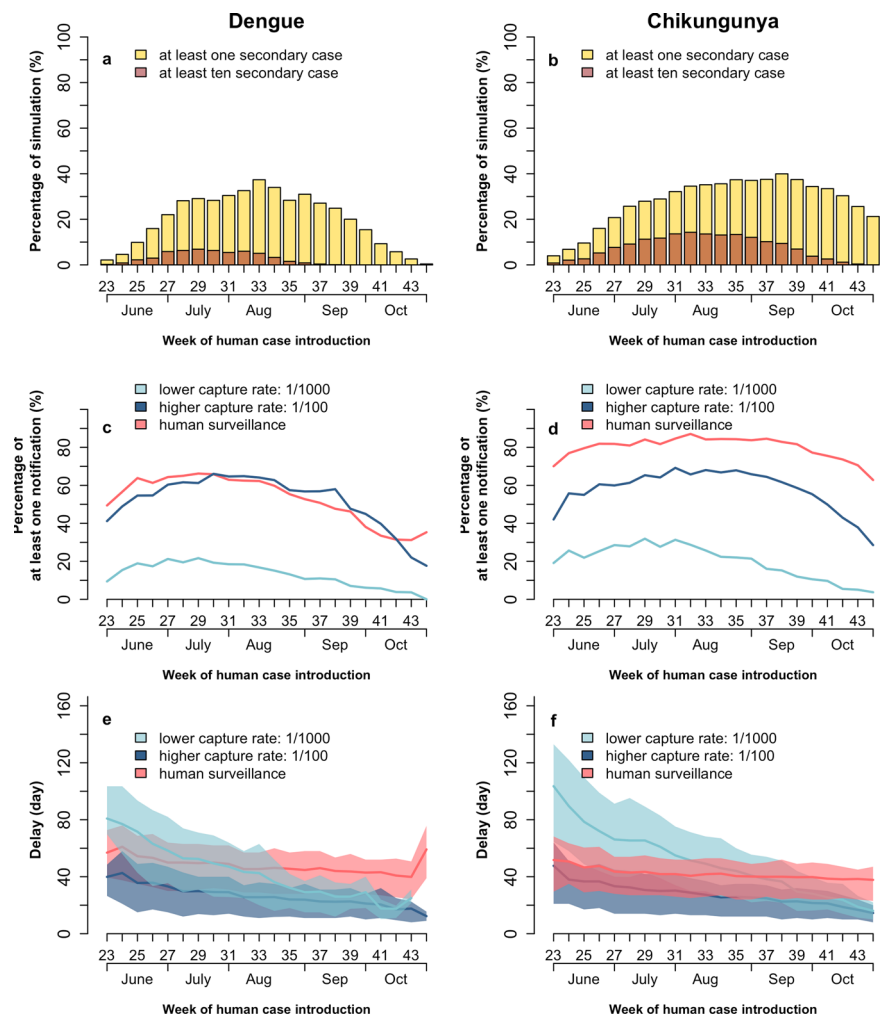


Fig. 5 | Probability of observing an outbreak with at least one secondary human case, probability of detecting at least one mosquito infected and human infected, and the mean reporting (solid lines) delays. Probability of observing an outbreak with at least one secondary human case (yellow) and at least ten human cases (brown) for DENV (a) and CHIKV (b). The probability of detecting at least one mosquito infected and human-infected calculated during outbreaks with at least one autochthonous human case for DENV (c) and CHIKV (d) calculated as the percentage of simulations producing secondary transmission detected by the surveillance system. Red = human surveillance; light blue = mosquito lower capture rate (1/1000); dark blue = mosquito higher capture rate (1/100). The mean reporting (solid lines) delays (day) and 95% CI (dashed lines) from a case importation and the first detection of autochthonous transmission either by the collection of an infected mosquito under different capture rates (light and dark blue) or by notification of a symptomatic case (red) for DENV (e) and CHIKV (f), based on simulations producing at least one secondary transmission events. $N = 12$ independent samples.



end of the season (i.e. 44th week), but this is likely to be attributed to stochasticity arising in the presence of a few transmission events. Irrespective of the disease, the estimated average delay from the index case importation and the detection of an infected mosquito through entomological surveillance is 50 and 26 days under the assumption of either low or high capture rates (Fig. 5e, f).

Discussion

When an arbovirus viremic case is imported in a non-endemic region, the risk of secondary transmission largely depends on the epidemiological interconnections between susceptible hosts and vectors, suitable environment and pathogen characteristics. For instance, mosquito abundance as well as the availability of breeding sites are strongly dependent on eco-

climatic conditions and, thus, they may vary greatly both geographically and temporarily. In Europe, the relatively small size and limited geographical distribution of past dengue and chikungunya outbreaks do not allow for a comprehensive assessment of transmission risks across different regions and time periods. This highlights the need to integrate available epidemiological evidence with detailed entomological data to monitoring spatio-temporal trends in the risk of local transmission of arboviral infections in non-endemic regions. Recent modelling efforts used correlative approaches that relate *Ae. albopictus* abundance or habitat suitability with eco-climatic covariates to estimate the mosquito population size and the subsequent risk of arbovirus transmission in temperate areas^{11,22,23}. In the present study, we used fine-scale daily temperature and entomological weekly data collected in different sites within Rome in 2012 and 2023 to directly infer *Ae. albopictus* female population dynamics and simulate potential risks of local arbovirus transmission in the 2 years. The fact that the species has been well established in Rome metropolitan areas since 2000, allows us to attribute the unprecedentedly high temperatures in 2023 to the overall higher species abundance and risk of autochthonous arbovirus transmission predicted throughout the mosquito reproductive season compared to 2012.

As expected, in both years, modelling results showed high geographical heterogeneities in estimates of *Ae. albopictus* female abundance among sampling sites (i.e. estimated females/hectare in June–November = 876–2540 in 2023, and 129–2884 in 2012). Despite the high spatial variability, the general trend showed markedly higher female abundance in 2023 than in 2012, with a 130% increase at the end of the breeding season (October–November). This suggests that the exceptionally high temperatures in 2023 (Supplementary Fig. 8), favourable to the rapid completion of both the aquatic developmental stages and the gonotrophic cycle, allowed for a prolonged season. Consequently, this led to an earlier onset and rapid expansion of the mosquito population at the beginning of the breeding season, as well as prolonged vector activity into late autumn, thereby amplifying the overall risk of sustained local transmission.

Estimates of the spatio-temporal distribution of *Ae. albopictus* females were used to assess the associated risks of DENV and CHIKV transmission across sites where mosquito collections were performed. Results highlighted a potential risk of secondary transmission for both arboviruses in both years, but a higher, more widespread and more prolonged risk in 2023.

Estimated median values of DENV R0 during the season ranged among sites from 0.1 to 2.7 in 2023 and from 0.05 to 1.0 in 2012. The estimated R0 values for 2023 are in line with the value estimated for the DENV outbreak in Lodi²⁴ (i.e. 0.76–1.98) and Marche Region⁶ (i.e. 2.08–3.31); Median R0 values > 1 were estimated in almost two-thirds of the sites sampled in 2023, a double rate compared to 2012. Moreover, in 2012 the risk was restricted to August, while in 2023 it extended from July to September. Since both dengue and chikungunya are not endemic in Europe, small clusters of transmission are more often observed compared to large epidemics. The occurrence of at least one autochthonous case triggers epidemiological investigations and responses to arboviral outbreaks, without discrimination based on the number of cases. To better differentiate single transmission events from longer transmission chains, we used an illustrative threshold of 10 cases, corresponding to the lowest number of cases detected in an arboviral outbreak in Italy so far (i.e., the DENV outbreak in the Veneto region in 2020²⁵). The proportion of simulations resulting in >10 secondary cases when assuming a disease case importation was substantially higher and more prolonged in 2023. Notably, three different transmission events of DENV occurred in metropolitan Rome in 2023, leading to a total of 38 confirmed human cases scattered across the city²⁶. The first cases were detected in August and the last in November, highlighting the difficulties in controlling local transmission in highly urbanised areas.

Estimated median values of CHIKV R0 during the season among sites were higher (0.1–3.8 in 2023 and 0.1–2.0 in 2012) than for DENV and in line with values estimated for the two CHIKV outbreaks occurred in Italy (i.e. 1.8–6 in 2007 and 1.5–2.6 in 2017)⁵ and with risk estimates obtained for

other Italian regions¹¹. Median R0 values > 1 were estimated in 4 out of 12 sites sampled in 2023, and in 2 out of 9 sampled in 2012. A key difference between the 2 years that emerged from our analysis is a 3-week extension in the average risk period from 2012 to 2023 compared to DENV. In addition, as for DENV, the proportion of simulations resulting in >10 secondary CHIKV cases is substantially higher and more prolonged in 2023.

So far, it remains unclear whether the increased number of local dengue outbreaks in 2023 is part of a consistent worsening trend driven by changes in eco-climatic conditions combined with increased global incidence and human mobility, or if it is simply due to the stochastic nature of transmission events observed in non-endemic regions. Maintaining continuous entomological surveillance in the coming years would allow understanding the relative contribution of climate change and extreme weather events to epidemiological risks associated with vector-borne diseases.

The following limitations should be taken into consideration when interpreting the model's epidemiological predictions. First—differently from correlative approaches estimating mosquito population sizes and the related risk of arbovirus transmission based on mosquito abundance or habitat suitability with eco-climatic covariates—the present mathematical model only allowed estimating the risk of local secondary transmission by considering an area of 300-m buffer zones centred in each sampling site and did not allow spatialization of the estimates obtained. This means that the potential spatial spread of CHIKV and DENV epidemics was not assessed. Second, the model parametrization of mosquito, host and pathogen transition rates was based on literature data. Yet, while for DENV there are studies estimating temperature-dependent transition rates^{27,28}, none were available for CHIKV despite some studies investigating the effect of temperature^{29,30}. Therefore, in our model, temperature-dependent transition rates were implemented only for DENV, making the comparison of results between the two viruses disputable. Further studies to better characterise these relationships could help provide more accurate estimates, also for CHIKV. Third, human density data correspond to resident data, which does not fully reflect the actual potential availability of human hosts in a tourism-dense area such as Rome, although tourists are likely to play a major role in disease importation, increasing the occurrence of initial source of infection that could trigger local outbreaks, rather than increasing the risk of secondary transmission. Fourth, the model estimates do not account for other ecological factors that may influence mosquito population dynamics (e.g. rainfall patterns, habitat availability), which may synergise with temperature to further boost mosquito abundance. This may partially explain the model underestimation observed in August at some sites, despite the presence of high temperatures. Another limitation is that the data used to inform the model with respect to the human host is limited to the resident population. Therefore, our estimate might not reflect the actual epidemiological risk in highly frequented areas with few resident inhabitants. Moreover, the model is not considering nor for heterogeneities in the proportion of human population exposed to mosquito bites, due to differences in awareness of pathogen circulation, personal protection and reactive control measures (which may vary according to socio-economic conditions³¹). Preventive mosquito control interventions have been sparsely implemented by public health authorities and private citizens in Rome since >20 years in order to reduce mosquito nuisance. Therefore, we do not expect large differences in the impact of these interventions on the mosquito population between the two study years. However, in 2023, pyrethroid spraying was implemented in a 200 m radius area around each of the 38 autochthonous dengue human cases reported in the city²⁶. The lack of detailed records on the geographical location of human cases during the outbreak prevented us from evaluating the impact of interventions in response to case emergence. Thus, we cannot exclude the possibility that higher mosquito abundance would have been observed in 2023 in the absence of this outbreak. This further reinforces our conclusion that temperatures in 2023 contributed to increasing abundance and prolonging the active season of *Ae. albopictus*, as well as to increase risk of local arbovirus transmission. In order to provide an illustrative example of the potential impact of vector control measures, we evaluated the effort needed to

interrupt the transmission (i.e. to reduce R_0 to <1) in the sampling site where the transmission risk was predicted to be highest. Results showed that in August 2023, when the risk of transmission peaked, control efforts would have been needed to reduce the adult mosquito population by 30% (CI 16%–60%) and 52% (CI 41%–75) and to drive DENV and CHIKV R_0 below the epidemic threshold, respectively. In the same site, in 2012, a reduction of 27% (CI 14%–58%) for DENV and 23% (CI 10%–61%) and CHIKV would have been required.

In the presence of a non-negligible risk of exotic arbovirus transmission in temperate regions and of a higher risk with increasing temperature, an effective proactive surveillance system is instrumental to prevent viral circulation. In Europe, the key points in the prevention of exotic arbovirus outbreaks are the timely notification of both imported and secondary cases and the control of the mosquito population around the infected cases to interrupt the ongoing transmission chains³². Evidence from previous studies highlighted marked delays in disease identification during past outbreaks that occurred in Europe (7–36 days from the onset of symptoms in the first symptomatic case to the identification of the outbreak)²¹. However, many factors limit the effectiveness of human case surveillance, among which are the presence of asymptomatic infections and the limited knowledge about these exotic pathogens and their clinical outcomes by general practitioners³³, travellers, and citizens in general³⁴. We leveraged the mathematical model used to estimate the risk of DENV and CHIKV secondary transmission to assess the likelihood of detecting a secondary case by surveillance of human symptomatic cases or by entomological surveillance. Arbitrarily low and high capture rates considered in our analyses reflect the capture rate associated with either 1 or 10 BG traps monitored daily in a 300 m buffer, respectively. Results confirmed that despite its challenges, human surveillance is the most effective approach in detecting secondary transmission in the tested scenario. Only in the case of DENV and with the higher capture rate, the two systems proved similarly effective, but this would imply an entomological sampling scheme (i.e. 10 BG-traps operating 24 h/day in a 300 m buffer zone) which is unrealistic to implement at a large scale. However, results also suggest that the latter sampling scheme may effectively complement human surveillance during an outbreak by strategically positioning traps in areas of highest risk of disease spread. These may include areas neighbouring the residence of the identified cases (where mosquito spraying is performed following their laboratory confirmation) and locations of likely exposure identified during epidemiological investigations. In Italy, consistent with our findings, observed CHIKV outbreaks were generally associated with higher transmissibility compared to DENV outbreaks^{9,24}. This results in a shorter time to detect CHIKV outbreaks compared to DENV, but also in a higher number of silent transmission events occurring before the outbreak is detected. However, our results regarding the higher likelihood of detecting CHIKV compared to DENV should be interpreted in light of the uncertainty surrounding the symptomatic ratio for dengue in non-endemic areas. While data from endemic regions typically report a symptomatic ratio around 20%³⁵, recent observations from outbreaks in Italy suggest that this ratio may exceed 80%^{6,20,24}. This considerable uncertainty is reflected in our model estimates. Additionally, it is important to note that both the detection rate of human-infected cases and the reporting delays used in the model are based on estimates from CHIKV Italian outbreaks^{20,21}. However, these parameters are likely varying in different geographical areas, as well as in relation an increased awareness and knowledge following the increasing global rise of DENV and other arbovirus cases. Nevertheless, these results represent the first attempt to compare the effectiveness of human and entomological surveillance in detecting viral circulation in non-endemic settings.

Our results suggest that, in light of the potential increase and lengthening of mosquito activity due to increasing temperatures, more efforts should be placed in preventing high mosquito abundance. Controlling mosquitoes in a complex landscape such as that one of a Mediterranean metropolis is a challenging task that can be achieved only by coordinated

and integrated vector management strategies. These strategies must involve actors and actions at all levels, from the private citizen to the public health authority. Additionally, to prevent further arboviral outbreaks, it is crucial not only to control the vector but also to enhance the detection capabilities of the public health systems by raising awareness about arboviral infection among both the general public and medical personnel. More studies are needed to provide stronger evidence to guide decision-makers in charge of arbovirus prevention in Europe and other temperate regions, taking into account the possible benefits (but also operational costs) associated with human and entomological large-scale surveillance, as well as their challenges.

Conclusions

Two main factors raise concerns about a possible worsening of exotic arbovirus transmission in Mediterranean metropolitan areas. First, the increase of DENV circulation at the global level, which may escalate the risk of importation of viremic cases from endemic regions, as occurred in 2023 and is occurring in 2024². Second, the possible effect of present and forthcoming climate changes, which may affect the abundance and the breeding season duration of mosquito vectors. This latter factor, and its consequences on arbovirus transmission, are difficult to assess due to the scarcity of longitudinal entomological data. Results from the entomological collections carried out in 2012 and 2023 in Rome (the first European city so far to have experienced large outbreaks of both DENV and CHIKV) and from mathematical modelling suggest that the exceptionally warm conditions in 2023 have favoured both the abundance and longer persistence of *Ae. albopictus* active season, as well as the risk of DENV and CHIKV secondary transmission and outbreaks. Thus, our findings are paradigmatic of the future risks to which Mediterranean urban areas are going to be increasingly exposed in the near future, when higher temperatures are expected to become more and more frequent, as it was the case in 2024, which was even warmer than 2023. In fact, although too high temperatures may have a detrimental effect on mosquito survival, results suggest that the major impact of the record-breaking hot temperature in 2023, compared to 2012, was to extend both the mosquito season and the risk of arbovirus transmission to autumn months.

Data availability

The entomological and the human population data used for the analysis is available in Zenodo with the identifier <https://doi.org/10.5281/zenodo.15241441>³⁶. The source data for Figs. 4, 5e, f can be found in Zenodo with the identifier <https://doi.org/10.5281/zenodo.15241441>³⁶. Census data are available for individual population census sections, released by ISTAT under open access policy available at https://esploradati.istat.it/databrowser/#/it/censpop/categories/SUB_MUN_DATA/PCENS2021.

Code availability

The C script used for the analysis is available in Zenodo with the identifier <https://doi.org/10.5281/zenodo.15241441>³⁶.

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Author contributions

C.V., M.M., P.P., and B.C. conceived the study; E.L., C.G., M.M., C.T., and L.V. collected entomological data; E.L., C.M.D., and F.F. collected temperatures and human population data; C.V., M.M., and P.P. developed the model; C.V. performed the simulations; C.V. and M.M. analysed the data; C.V., M.M., P.P., S.M., and B.C. interpreted data and results; C.V. and Ad.T. wrote the paper. M.M., P.P., S.M., and B.C. critically revised the manuscript. All authors approved the final version of the manuscript.

Competing interests

The authors declare no competing interests.

Additional information

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