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Just another white-striped mosquito? A scoping review and group discussion synthesis on *Aedes koreicus* in Europe

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ABSTRACT

Among the several Asian *Aedes* species that have established in Europe over recent decades, *Aedes koreicus* has received comparatively little research attention since its first detection in Belgium in 2008, despite its remarkable ability to colonise montane and peri-alpine localities at elevations beyond the reach of its congener *Aedes albopictus*. Nearly two decades after its European detection, a systematic synthesis of the available evidence and a

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structured assessment of research and operational priorities are overdue. This paper presents the results of a scoping review of the scientific literature on *Ae. koreicus* combined with the outcomes of a multidisciplinary expert workshop held in Trento, Italy, in February 2026, which brought together 41 researchers and practitioners from six European countries with expertise in mosquito surveillance, medical entomology, genomics, ecological modelling and public health practice. Through the literature search we obtained a total of 334 articles, of which 91 were eventually included, all published after 2011. Most of the studies were carried out within Europe, focusing mostly on mosquito surveillance. Building upon the scoping review, the workshop identified key priorities for advancing knowledge and operational responses to *Ae. koreicus*, including strengthened surveillance in montane and lowland areas, improved characterisation of its vector competence and competitive interactions with co-occurring *Aedes* species, and more effective communication strategies for engaging the public and citizen scientists in monitoring efforts.

1. Introduction

Mosquito species belonging to the *Aedes* genus have emerged as significant nuisance and public health concerns due to their remarkable capacity to establish in new geographic areas far beyond their native range. Among these, *Aedes* (*Hulecoeteomyia*) *koreicus* (Edwards, 1917) has attracted growing attention since its first detection outside Asia. Originally described from Korea and widely distributed across East Asia (Seok et al., 2024), *Ae. koreicus* was recorded for the first time outside its native range in Belgium in 2008 (Versteirt et al., 2012a), marking the beginning of nearly two decades of research into its biology, ecology, and distribution in the Western Palearctic.

Since its initial detection in Europe, *Ae. koreicus* has progressively established in several European countries, including Italy, Germany, Switzerland, Hungary, and Russia, often exploiting similar ecological niches to those occupied by its congener *Ae. albopictus* (Capelli et al., 2011; Montarsi et al., 2013; Werner et al., 2016). Like *Ae. albopictus*, it is a container-breeding species capable of surviving cold winters through diapausing eggs, traits that confer a competitive advantage in temperate climates and raise concerns about its further geographic expansion under ongoing climate change (Liu et al., 2023; Marini et al., 2019). Notably, however, *Ae. koreicus* appears to tolerate cooler conditions better than *Ae. albopictus*, enabling it to colonise montane and peri-alpine localities at elevations where its congener struggles to establish (Da Re et al., 2026; Montarsi et al., 2013). This altitudinal reach, combined with its generalistic biting behaviour (Montarsi et al., 2022), makes it a relevant nuisance species in upland communities that have so far remained largely unaffected by invasive *Aedes* mosquitoes.

Despite nearly two decades of records since its European introduction, *Ae. koreicus* remains comparatively understudied, particularly in comparison with the substantial research effort devoted to *Ae. albopictus* (see for instance Reinhold et al., 2018), which is now recognised as one of the world's most invasive species and is the focus of extensive surveillance, experimental, and modelling programmes. A similar observation applies to *Ae. japonicus* (Theobald, 1901), another Asian container-breeding mosquito that has established across much of central Europe and North America and which, unlike *Ae. koreicus*, has been shown to be a comparatively competent vector for several arboviruses and parasites (Abbo et al., 2020; Jansen et al., 2025; Martinet et al., 2019; Veronesi et al., 2018). The contrasting research trajectories of these latter two species, with *Ae. japonicus,* attracting somewhat more attention probably because of its vector competence data, highlights how the epidemiological relevance of a species can shape the depth of scientific investigation it receives, potentially leaving important ecological and public health questions about less-studied invaders unanswered.

To address these gaps, we conducted a scoping review of the scientific literature on *Ae. koreicus*, systematically mapping the evidence base across topics including taxonomy and genetics, distribution and invasion history, bionomics and seasonal ecology, nuisance impact, vector competence, and modelling approaches. Complementing this synthesis, we convened a multidisciplinary expert workshop in Trento, Italy, on 10 February 2026, bringing together researchers and practitioners involved in mosquito surveillance, medical entomology, and ecological modelling to discuss the current status of *Ae. koreicus* in Europe, the challenges associated with its monitoring, and the priorities for future research. Through structured discussions, participants shared field and laboratory experience and modelling perspectives to develop a consolidated view of the species' role in the European invasive mosquito landscape and to formulate actionable recommendations for surveillance programmes.

2. Methods

2.1. Scoping review

We searched the Web of Science and Scopus databases on June 6, 2025, specifying the string “Aedes koreicus” OR “Ae. koreicus” in the title, abstract and keywords fields. The search was then updated on February 17, 2026, after the workshop. There were no time, language, or location restrictions. Study selection was performed by screening titles and abstracts to ensure the eligibility of studies by two authors (GM and DDR), and when votes disagreed, consensus was reached after discussion. The studies had to meet the following criteria to be selected: i) they had to be published in a peer-reviewed journal, so pre-prints and conference abstracts were all excluded; ii) *Ae. koreicus* had to be among the investigated species (if many). Included studies were labelled according to the following categories: “Biology”, “Europe”, “Genomics”, “Modelling”, “Insecticide effectiveness and resistance”, “Review”, “Surveillance” and “Vector competence” (see Table A.1 for further details).

2.2. Geographical distribution

Distribution data for *Ae. koreicus* extracted from the literature review were fused with institutional datasets (ECDC-VectorNet[3]), and citizen science records from the Mosquito Alert platform (2020–2026) (Južnič-Zonta et al., 2022). Literature records were cleaned and standardised. Geometries from the literature and VectorNet were combined and intersected with the European NUTS-3 administrative network (Nomenclature of Territorial Units for Statistics, level 3, year 2021, 1:10 million resolution) provided by Eurostat via the *giscoR* package (Hernangómez, 2020). NUTS-3 areas with at least one confirmed presence were classified as positive. Validated Mosquito Alert reports (class name: *Aedes koreicus*) were added as point data. Geospatial processing and mapping were conducted in R version 4.5.2 (R Core Team, 2026), using the *sf* package (Pebesma, 2016) for vector operations and *ggplot2* and *ggspatial* (Dunnington, 2017; Wickham, 2016) for map rendering in the WGS 84 projection (EPSG: 4326).

[3] https://www.vectornetdata.org/.

2.3. Workshop and group discussions

2.3.1. Workshop design and participants

The workshop[4] was held in Trento, Italy, on 10 February 2026, and convened 41 participants from six countries (Austria, Belgium, Cyprus, Hungary, Italy, and Switzerland, see Fig. A.1 in the Appendix). Participants were affiliated with a broad range of institutions, including universities, research institutes, and regional or national public health agencies, and represented a balanced disciplinary composition across ecological and epidemiological modelling, medical entomology and public health practice. The group included 22 women and 19 men. A key characteristic of the participant group, relevant for interpreting the workshop outcomes and their geographical focus, is that all attendees were based in the non-native range of *Ae. koreicus*.

The one-day workshop opened with a series of oral presentations covering the current state of knowledge on the biology, surveillance, invasion dynamics, vector competence, and modelling of *Ae. koreicus*. In the afternoon, participants were assigned to five discussion groups of 7–9 people each. Group composition was deliberately designed to ensure disciplinary balance and promote integrative dialogue, with each group including representatives from ecological and epidemiological modelling, medical and field entomology, and public health practice. Efforts were also made to ensure diversity in institutional affiliations, professional seniority and gender representation.

Within each discussion group, a designated rapporteur documented the main arguments, areas of agreement and disagreement, and emerging recommendations. Rapporteurs' summaries were subsequently compiled and reviewed in a plenary session to identify cross-cutting themes and areas of divergence, and constituted the primary qualitative dataset used to inform the structure and content of this paper.

2.3.2. Discussion themes and guiding questions

Discussions in each group were guided by a structured set of thematic prompts designed to elicit perspectives on the current knowledge, operational challenges, and research priorities associated with *Ae. koreicus*, as previously done for a similar workshop focused on *Ae. albopictus* (Romiti et al., 2026). The prompts covered five overarching themes: (i) learning outcomes from field and research experience with the species; (ii) operational priorities, including comparative considerations with *Ae. japonicus*; (iii) biological aspects, including expected responses to climate warming and interspecific competition for breeding sites; (iv) public health relevance and the feasibility of broadening existing *Aedes* surveillance programmes; and (v) communication strategies for engaging the general public and citizen scientists in monitoring and prevention efforts. The full list of guiding questions is provided in Table A.2. The combination of guided prompts and cross-disciplinary participation provides a robust basis for identifying operational priorities and debating the findings of the literature review, providing an expert opinion for the different themes, which are discussed in detail in the following sections.

3. Results and discussion

3.1. Review results

We obtained a total of 334 articles from Web of Science and Scopus, of which 222 were duplicates. After discarding 21 studies not meeting eligibility criteria, 91 articles, all published after 2011 (see Fig. 1A), were included and labelled according to at least one of the above-mentioned categories. Most of the studies were carried out within Europe (n = 81, see Fig. 1B, first bar of the horizontal barplot). The large majority of the included articles focus mostly on mosquito surveillance (n = 55) (Andreeva et al., 2021; Anicic et al., 2023; Arnoldi et al., 2022; Baldacchino et al., 2017c; Ballardini et al., 2019; Bezzhonova et al., 2014; Boukraa et al., 2015; Capelli et al., 2011; Cherix, 2019; Cull, 2025; Deblauwe et al., 2014, 2022; Desiato et al., 2021; Fuehrer et al., 2020; Ganushkina et al., 2020, 2016; Garamszegi et al., 2023b, 2023a; Gradoni et al., 2021; Hohmeister et al., 2021; Kalan et al., 2017; Kampen et al., 2017; Kurucz et al., 2016, 2018, 2020, 2022; Lee et al., 2024; Miranda et al., 2022; Montarsi et al., 2013, 2015b; Mosca et al., 2022; Müller et al., 2020; Negri et al., 2021; Penazziová et al., 2026; Pfitzner et al., 2018; Romi et al., 2018; Sauer et al., 2023; Schenkel et al., 2019; Schneider et al., 2016; Seok et al., 2024; Soresinetti et al., 2025; Steinbrink et al., 2019; Suter et al., 2015; Sycheva et al., 2025; Szentivanyi et al., 2025; Varga et al., 2025; Versteirt et al., 2012a, 2012b, 2015; Vojtíšek et al., 2022; Walther and Kampen, 2017; Werner et al., 2016, 2020; Wittwer et al., 2024; Zamburlini et al., 2019), thus providing, for instance, evidence of new invaded areas or observed seasonal dynamics, and biology (n = 18) (Alfano et al., 2019; Anicic et al., 2023; Baldacchino et al., 2017b, 2017a; Cebrián-Camisón et al., 2020; Ciocchetta et al., 2023, 2017; Da Re et al., 2025; Damiani et al., 2022; Marcondes et al., 2018; Marini et al., 2022, 2019; Montarsi et al., 2022, 2013; Negri et al., 2024; Rosso et al., 2018; Sauer et al., 2023; Shin and Jung, 2020). We identified 10 studies providing some kind of phylogenetic analysis (Catapano et al., 2023; Kurucz et al., 2022; Nagy et al., 2024; Penazziová et al., 2026; Reichl et al., 2024; Schaffner et al., 2014; Shin and Jung, 2020; Soresinetti et al., 2025, 2023; Zadra et al., 2023), nine studies modelling *Ae. koreicus* population dynamics or establishment probability (Arnoldi et al., 2022; Da Re et al., 2022; Garamszegi et al., 2025, 2023b; Kurucz et al., 2020; Liu et al., 2023; Marcantonio et al., 2016; Marini et al., 2019; Seok et al., 2023) and eight studies assessing *Ae. koreicus* competence for some kind of pathogen transmission (Ciocchetta et al., 2018; Höller et al., 2025; Jansen et al., 2022, 2021; Kurucz et al., 2018; Montarsi et al., 2015a; Szentivanyi et al., 2025; Varga et al., 2025). Finally, we also found five reviews focusing also on this species (Cebrián-Camisón et al., 2020; Da Re et al., 2025; Ganassi et al., 2022; Giunti et al., 2023; Romi et al., 2018) and four studies evaluating insecticide effectiveness and resistance (Negri et al., 2024; Ryu et al., 2019; Stoops et al., 2025, 2023). As shown in Fig. 1B, some studies fall in more than one category: for instance, 36 articles are labelled as "Surveillance" and “Europe” (first column of the histogram).

3.2. Geographical distribution

The native distribution of *Ae. koreicus* includes China, Korea, and eastern Russia, where it was repeatedly reported throughout the 20th century (Seok et al., 2024). The first documented finding outside its native range occurred in continental Europe (Belgium) in 2008 (Versteirt et al., 2012a), although the first evidence (based on our research in the available scientific literature and the workshop consensus) was published in 2011, describing the finding of *Ae. koreicus* in Northern Italy in 2011 (Capelli et al., 2011). The importation of the species into Belgium, most likely from Jeju-do, an island south of the Republic of Korea, and from there possibly to Italy, has probably occurred via international trade (Kurucz et al., 2022; Versteirt et al., 2012a). These first detections raised awareness of this new species, triggering subsequent findings across several countries in the Eurasian continent (see Table 1 and Fig. 2).

3.3. Identification challenges and implications for surveillance

Many of the workshop participants who are involved in mosquito surveillance highlighted that a fundamental challenge underlying the surveillance of *Ae. koreicus* is the difficulty of distinguishing it from other invasive species such as *Ae. japonicus,* both belonging to the Japonicus group (Wilkerson et al., 2022). In particular, they remarked the similarities of these two species at adult stage (Cull, 2025; European

[4] https://www.vectormodelling.com/Trento2026/.

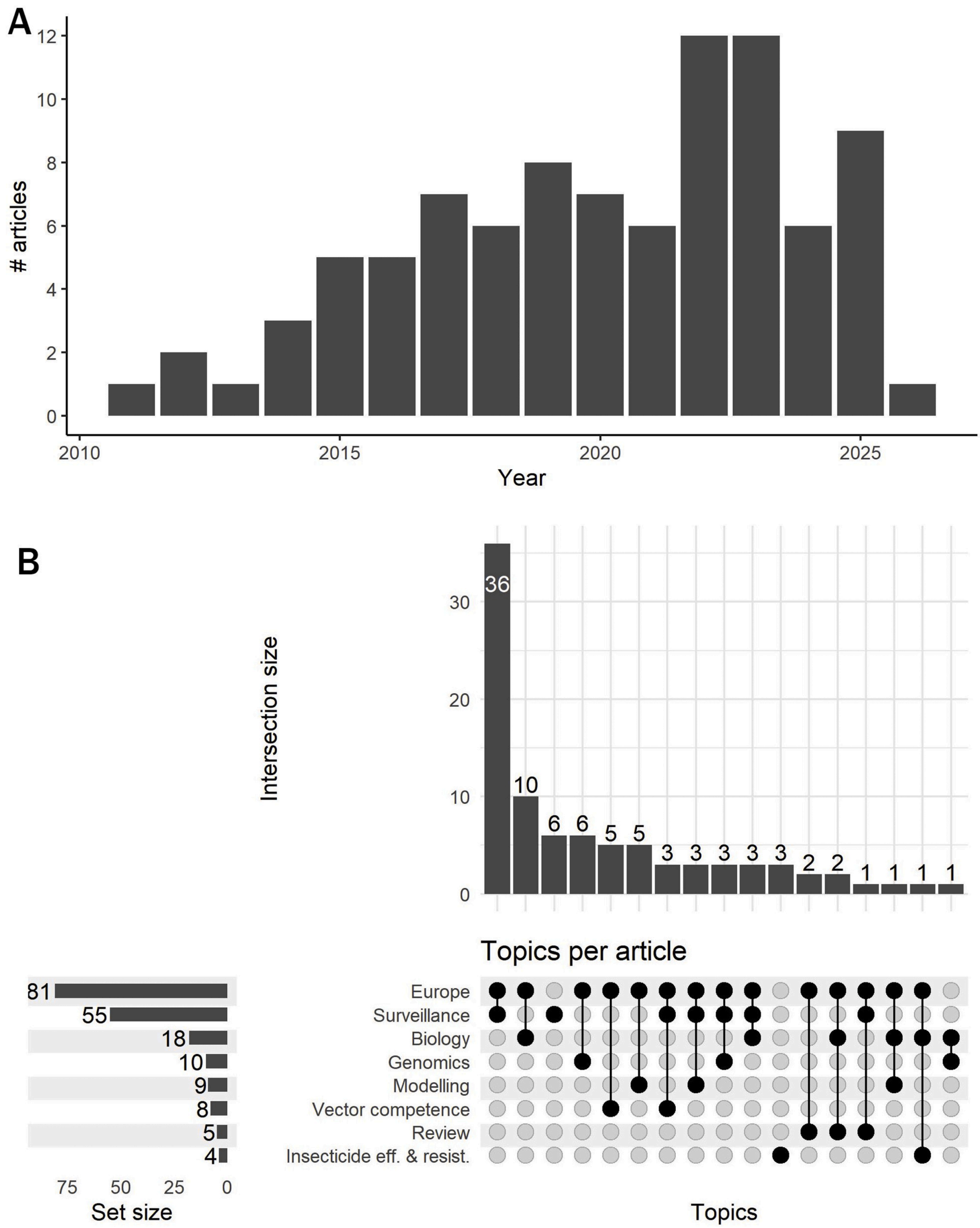

Fig. 1. Literature review results. A: number of articles by year of publication; B: articles by category: numbers (size) are provided for each category (set) (horizontal barplot) and for each identified combination of multiple categories (vertical histogram), as indicated by the connected filled dots below.

Centre for Disease Prevention and Control, 2012; Hohmeister et al., 2021), and with several *Aedes* species at the egg stage (Anicic et al., 2023). Standard ovitrap-based monitoring, the most widely deployed and cost-effective tool for tracking invasive *Aedes* mosquitoes across Europe, relies on the collection and counting of eggs under stereoscopic microscopy, a method that cannot reliably discriminate between the morphologically similar eggs of *Ae. koreicus, Ae. japonicus, Ae. albopictus*, and indigenous species such as *Ae. geniculatus* (Anicic et al., 2023). This limitation has direct operational consequences. Since *Ae. koreicus* is more cold-tolerant than *Ae. albopictus*, which remains the primary target of entomological surveillance across much of Europe, it tends to be active earlier in spring and later in autumn. In areas where the two species co-occur, ovitraps deployed at the beginning and end of the monitoring season may therefore collect *Ae. koreicus* eggs that are

Table 1
Detection of *Aedes koreicus* outside its native range, ordered by the year of first retrieval.

Country	Year of detection	Reference
Belgium	2008	(Versteirt et al., 2012a)
Italy	2011	(Capelli et al., 2011)
Russia	2013	(Bezzhonova et al., 2014)
Slovenia	2013	(Kalan et al., 2017)
Switzerland	2013	(Suter et al., 2015)
Germany	2015	(Pfitzner et al., 2018)
Hungary	2016	(Kurucz et al., 2016)
Austria	2018	(Fuehrer et al., 2020)
Kazakhstan	2018	(Andreeva et al., 2021)
Czech Republic	2021	(Vojtíšek et al., 2022)
Slovakia	2024	(Penazziová et al., 2026)

erroneously attributed to *Ae. albopictus*, generating false positives that could distort population density estimates and phenological assessments of the more epidemiologically prominent species. This risk is further compounded in localities where *Ae. japonicus* is also present, creating a three-way identification problem from a single trap sample.

Several approaches have been proposed to address this challenge. For example, MALDI-TOF MS has been proposed as a rapid complementary method for identifying invasive *Aedes* mosquitoes, particularly from eggs collected using ovitraps. Protein fingerprints obtained from individual eggs can distinguish *Ae. koreicus* from other container-breeding species, including the morphologically similar *Ae. japonicus*. In Schaffner et al. (2014), 18 species-specific biomarkers for nine *Aedes* species were identified, with all *Ae. koreicus* eggs correctly classified during blinded validation. MALDI-TOF MS can reduce the need to hatch and rear eggs and is useful when specimens are damaged or morphologically ambiguous. However, identification depends on the availability of validated reference spectra and can be affected by specimen preservation and sample quality. Moreover, pooled analysis provides mainly qualitative or semi-quantitative information: detection probability increases with species abundance, but peak intensity cannot be directly converted into the number or proportion of eggs in a pool. The method was subsequently applied to confirm *Ae. koreicus* detections during field surveillance and has also been used as a reference technique to assess the reliability of egg identification by microscopy. In fact, optical recognition of egg exochorionic membrane patterns, tested in Anicic et al. (2023) using a combination of high-resolution stereomicroscopy and expert and non-expert rater panels, demonstrated that *Ae. albopictus* and *Ae. geniculatus* could be reliably distinguished from other species, though discrimination between *Ae. japonicus* and *Ae. koreicus* remained problematic even for trained entomologists. Other approaches tried different targets rather than eggs, but their application may need a rethinking of surveillance design. For adult specimens, geometric wing morphometrics have shown considerable promise: Sauer et al. demonstrated that wing shape allows reliable discrimination between *Ae. japonicus* and *Ae. koreicus*, achieving reclassification accuracies of up to 96.5% for females and 91.3% for males, with low observer bias across independent landmark collectors (Sauer et al., 2023). Molecular methods offer greater specificity but at a higher cost and turnaround time; nonetheless, two emerging biotechnological approaches may eventually enable more scalable solutions. *Aedes koreicus, Ae. japonicus*, and *Ae. albopictus* could be detected from water samples using environmental DNA (eDNA) combined with high-throughput real-time PCR on a microfluidic platform, though non-reproducible detections and potential false positives due to eDNA degradation and assay sensitivity remain challenges to be resolved (Schneider et al., 2016; Wittwer et al., 2024). Loop-mediated isothermal amplification, developed for several invasive *Aedes* species, including *Ae. koreicus* (Schenkel et al., 2019), offers a rapid, low-cost, and potentially field-deployable alternative based on visually readable colorimetric results, with sensitivity sufficient to detect a single target egg among ninety-nine non-target eggs; however, sample preparation currently still requires laboratory steps that limit true field applicability. Taken together, these approaches share a common objective: to move beyond morphological ambiguity and enable species-level resolution from routine monitoring samples. Yet all remain at relatively early stages of development or operational validation, and the challenge is becoming increasingly acute as the distributional ranges of multiple invasive *Aedes* species continue to overlap across Europe.

Citizen science initiatives have proven a useful complement to classical entomological monitoring for tracking the distribution of invasive *Aedes* mosquitoes, primarily because they can extend spatial

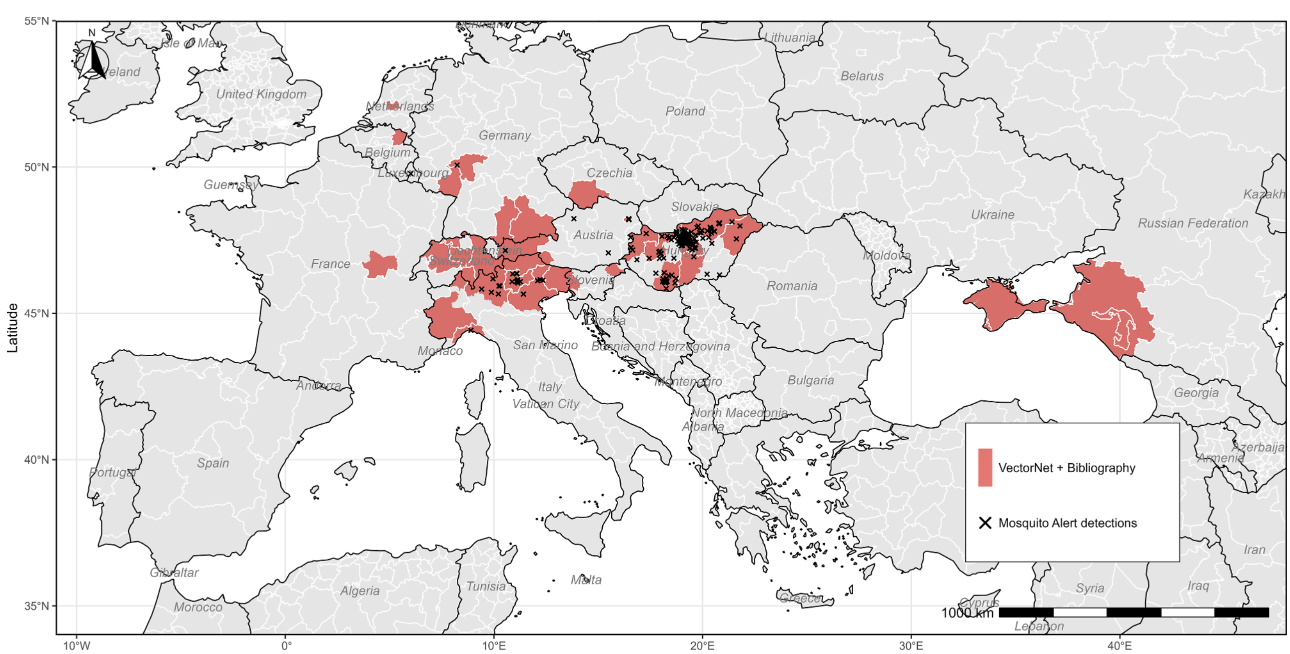

Fig. 2. Distribution of *Ae. koreicus* in the European continent. Red areas: NUTS3 regions where *Ae. koreicus* has been reported in the literature and ECDC-VectorNet. Black crosses: Mosquito Alert detections.

coverage well beyond what professional surveillance networks can realistically achieve. The German Mueckenatlas project demonstrated that public submissions of mosquito specimens could flag new populations of *Ae. japonicus* and *Ae. koreicus* in areas not covered by active monitoring, prompting targeted follow-up field work that confirmed their presence (Walther and Kampen, 2017). Similarly, iNaturalist observations have been shown to broadly match known distributions of invasive *Aedes* species across Europe while occasionally identifying potential new areas of establishment ahead of formal monitoring records (Cull, 2025). Mosquito Alert is a citizen science system aimed at investigating and managing disease-carrying mosquitoes, operational since 2014 (Južnič-Zonta et al., 2022). Initially, most participants were located in Spain, but since 2020 participation has expanded worldwide, particularly in Europe, triggering many *Ae. koreicus* detections, as shown in Fig. 2. In Hungary, a dedicated citizen science programme based on Mosquito Alert generated approximately 3000 validated reports of invasive *Aedes* species over three years, and showed that citizen-derived data can be broadly consistent with conventional trapping results when reporting intensity is sufficient (Garamszegi et al., 2023b, 2023a). However, the morphological identification difficulties described above are likely to be even more consequential in citizen science-based monitoring, where species records rely on photographs instead of collected specimens, and where the images submitted by participants rarely, if ever, capture the diagnostic characters required to distinguish *Ae. koreicus* reliably from *Ae. japonicus* (Cull, 2025). Also, a recurring limitation across these initiatives is the highly uneven and unpredictable level of public engagement, which tends to be strongly dependent on the visibility and sustained promotion of the programme rather than on the actual distribution of the target species and might need adequate methods to account for potential reporting bias (Virgillito et al., 2024). This spatio-temporal bias in reporting means that citizen science data are on one hand effective in improving species detection and on the other best interpreted as a qualitative signal to guide professional surveillance efforts, rather than as a standalone source for rigorous ecological or epidemiological inference.

3.4. Genetics

Genetic research on *Ae. koreicus* has advanced considerably in recent years, although it still lags behind that of other invasive *Aedes* species. Many investigations primarily relied on barcoding, using mitochondrial markers, particularly the cytochrome oxidase I (COI) or NADH dehydrogenase subunit 4 (ND4) genes, to explore genetic homology between populations (Hohmeister et al., 2021; Kurucz et al., 2016; Pfitzner et al., 2018; Versteirt et al., 2012a; Werner et al., 2016). A pan-European analysis, based on COI sequences, revealed a considerably high haplotype diversity across the known populations by identifying at least five major haplotype groups (Kurucz et al., 2022). Along with further population genetic analysis, based on microsatellite markers (Soresinetti et al., 2025), these findings suggest multiple introductions from different source regions in Asia, followed by local dispersal and subsequent admixture among populations, pointing to a complex dispersal history of the species in Europe. This was corroborated by a modelling study suggesting China as an additional potential origin of non-native population in Europe (Seok et al., 2026). A barcoding analysis of 145 COI samples mainly from Europe (Zadra et al., 2023) revealed the existence of an *Ae. koreicus* haplotype (sampled so far in Austria and Belgium) characterised by a high genetic distance to all other haplotypes: according to barcoding-gap, this distance is compatible with a distinct species or at least with a subspecies. This paves the way for the possibility of two cryptic species, or two extremely distinct genetic lineages of *Ae. koreicus*, currently circulating in Europe that may be characterised by different biological and epidemiological traits.

Moreover, the genetic basis of phenotypic variability within *Ae. koreicus* is also poorly understood. This is particularly relevant given the existence of distinct morphological forms, originally described from mainland Korea and Jeju Island (Tanaka et al., 1979; Versteirt et al., 2012b). However, comprehensive analyses using multiple mitochondrial and nuclear markers revealed no detectable genetic differentiation at the population level between these morphotypes (Kurucz et al., 2026).

Complete mitochondrial and draft nuclear genome assemblies (generated using combined long- and short-read sequencing approaches) enabled more detailed analyses of population structure, adaptive variation, and phylogenetic relationships (Kurucz et al., 2022; Nagy et al., 2024; Zadra et al., 2023). Genome-wide data indicate that *Ae. koreicus* shares key features with its close relative *Ae. japonicus*, including genes potentially associated with cold tolerance and environmental adaptation, which may facilitate its establishment in temperate regions (Nagy et al., 2024). Also, phylogenomic studies support a close evolutionary relationship between these species, hypothesising that *Ae. koreicus* diverged relatively recently from *Ae. japonicus*, likely during the Oligocene, while clearly distinguishing them at the genomic level (Zadra et al., 2023). Earlier studies based on three gene markers (Cameron et al., 2010) have suggested that *Ae. koreicus* may belong to an *Ae. japonicus* species complex, leaving space for possible hybridisation events between *Ae. koreicus* and the 3–4 recognised subspecies of *Ae. japonicus*. However, the high genetic distances from the barcoding analysis of (Zadra et al., 2023), together with some evidence of mating incompatibility (Miyagi and Lee, 1975) point toward two distinct species (i.e., *Ae. koreicus* and *Ae. japonicus)*. As stated above, it remains unclear if *Ae. koreicus* is a single species, or there are distinct genetic identities of either two cryptic species or two Evolutionary Significant Units (Zadra et al., 2023).

Genetic studies are still limited and important knowledge gaps remain particularly for what concerns the functional significance of identified genetic variants, the genetic basis of vector competence, climate adaptation, and invasion success. We advocate that a substantial amount of genomic resources (for example the genome resequencing of many populations sampled worldwide) may open the way for future studies on phenotypic plasticity, adaptive evolution, population connectivity, and invasion dynamics of the species. Future research integrating high-resolution genomic data, transcriptomics, and ecological approaches will be essential to elucidate the mechanisms underlying the public health relevance of this "emerging" alien mosquito species.

3.5. Fundamental biology

3.5.1. Thermal response

All participants agreed that temperature is a key ecological and physiological determinant of *Ae. koreicus* performance, shaping its life history traits, population dynamics, and invasion potential. Thermal effects act across all life stages, from egg overwintering to adult survival and reproduction (Bahrami et al., 2026; Da Re et al., 2026; Marini et al., 2022, 2019).

The establishment of *Ae. koreicus* in temperate regions, supported by both field observations and experimental evidence, highlights its capacity to overwinter successfully and maintain adult performance under relatively cool conditions (Marini et al., 2019). The species exhibits an optimal temperature range generally between 20 and 28°C, although performance declines near the upper thermal limit, with negative effects on survival and fecundity, especially above 30°C (Bahrami et al., 2026; Marini et al., 2019). At the lower end, temperatures below 10°C are largely unfavourable for development and activity (Marini et al., 2019).

Importantly, thermal optima vary across life stages: juvenile stages tend to perform better at slightly higher temperatures than adults (Bahrami et al., 2026). This mismatch has important ecological implications, as adult survival is often a stronger driver of population growth than developmental rates (Mordecai et al., 2017; Pawar et al., 2024). Such dynamics may contribute to the persistence and spread of *Ae. koreicus* in cooler environments and at higher latitudes. Consistent with this, recent evidence suggests that adult performance peaks around

20°C, with relatively stable survival up to ~28°C, indicating a thermal profile distinct from that of *Ae. albopictus*. Under future climate scenarios, these traits may facilitate extended seasonal activity and increased population abundance, thereby enhancing invasion potential, particularly at temperate latitudes, although extremely high summer temperature might be very detrimental for the adults (Marini et al., 2019).

Diapause further strengthens the species' thermal resilience by enabling eggs to withstand adverse environmental conditions. While hatching success under mild cold conditions (e.g., ~5°C) appears similar between diapausing and non-diapausing eggs, exposure to subzero temperatures reveals a clear advantage of diapause, with higher survival and hatching success (Da Re et al., 2026). This enhanced cold tolerance represents a critical adaptation supporting overwintering success and long-term establishment of this species in temperate and colder regions.

3.5.2. Interspecific competition at the larval stage and sex competition

There was consensus that laboratory studies investigating interspecific interactions between *Ae. koreicus* and *Ae. albopictus* remain extremely limited, and virtually no data exist from natural settings. In controlled experiments, (Baldacchino et al., 2017a) reported weak larval competition between the two species, with *Ae. albopictus* larvae generally develop faster and maintain higher survivorship across varying densities and diet levels, while *Ae. koreicus* performance was slightly reduced in mixed-species treatments; notably, the presence of *Ae. albopictus* was associated with larger emerging *Ae. koreicus* females, suggesting complex interactions beyond simple competitive suppression.

Laboratory investigations have also shown that *Ae. koreicus* exhibits mating traits consistent with other *Aedes* mosquitoes, including rapid copulation and the potential for male competition under confined conditions (Ciocchetta et al., 2023). The study also suggested that mating may be facilitated by behaviours displayed in the wild, such as swarming. Consistent with this hypothesis, preliminary unpublished observations reported by some of the workshop participants (CD and RS) indicate that large-cage conditions can support male swarming in *Ae. koreicus*. Such systems may provide a promising experimental platform for future studies on mating behaviour, mate choice, and intra- or interspecific mating competition in this species. Mating success may be influenced by factors such as male density and sex ratio, highlighting the presence of intra-sexual competition that could affect reproductive output (Ciocchetta et al., 2023). Interestingly, heterospecific mating attempts by *Ae. albopictus* males appear largely ineffective, as *Ae. koreicus* females do not store sperm in their spermatheca following such encounters. However, compared to well-studied species like *Ae. aegypti* and *Ae. albopictus*, the mating system of *Ae. koreicus* remains insufficiently characterized, particularly under natural conditions. Overall, these findings underscore that current knowledge of *Ae. koreicus* ecology is based on a few laboratory studies, with no direct evidence from field populations, emphasizing the urgent need for comprehensive experimental and observational studies to clarify the ecological and reproductive dynamics of this invasive species.

3.5.3. Host preference

Aedes koreicus exhibits a complex host preference in its biting behavior, largely shaped by local ecological conditions. Evidence from (Montarsi et al., 2022), which provides the first and to date only quantitative assessment of its blood-feeding patterns in Europe, indicates a predominantly mammalophilic but opportunistic feeding strategy. Molecular analysis of blood meals revealed that the majority of feedings were derived from wild ungulates, particularly European roe deer (*Capreolus capreolus*, ~63%), followed by humans (~15%), with negligible contributions from avian or other vertebrate hosts. Importantly, this pattern appears to reflect host availability rather than strict intrinsic preference: in forested environments, feedings are mainly directed toward wildlife, whereas in urban or peri-urban settings, anthropophagy increases significantly. Such flexibility suggests that *Ae. koreicus* adopts an opportunistic host-seeking strategy, modulating its biting behaviour according to host abundance and accessibility. From an epidemiological perspective, the predominance of mammalian hosts supports a potential role in maintaining transmission cycles among mammals, while the limited involvement of avian hosts may reduce its relevance as a bridge vector for bird-associated arboviruses. Overall, current evidence highlights the trophic plasticity of *Ae. koreicus* and underscores the importance of environmental context when assessing its public health risk.

3.5.4. Microbiota

The microbiota of *Ae. koreicus* remains comparatively underexplored, yet available studies suggest a relatively simple and environmentally driven bacterial community consistent with other container-breeding *Aedes*. The gut microbiota is typically dominated by a limited number of taxa, with *Asaia* and *Pseudomonas* frequently reported as the most abundant bacterial genera, with *Asaia* representing a stable and pervasive symbiont characterized by high prevalence, transtadial transmission, and effective colonization of multiple host tissues (Alfano et al., 2019). This marked dominance may contribute to shaping the overall microbial structure and potentially constrains the establishment of other symbionts. Indeed, *Ae. koreicus* has generally been described as lacking natural *Wolbachia* infections, in contrast with several other mosquito species of medical relevance (Rosso et al., 2018). Although a recent study reported the detection of *Wolbachia* DNA in a very small number of field-collected individuals, the extremely low prevalence and absence of evidence for stable vertical transmission suggest that these findings should be interpreted with caution and may reflect transient, environmentally acquired, or low-density infections rather than a true symbiotic association (Damiani et al., 2022). In this context, the ecological and functional relevance of *Wolbachia* in *Ae. koreicus* remains unclear, particularly when compared to the consistently high abundance of *Asaia*, which may play a more central role in host–microbe interactions. More broadly, the composition of the microbiota is strongly influenced by the larval aquatic environment and undergoes substantial restructuring during metamorphosis and adulthood, reflecting ecological transitions and dietary shifts. Despite pronounced inter-individual variability, a partially conserved core microbiota persists across developmental stages and geographic populations, with a considerable proportion of taxa shared with closely related invasive species such as *Ae. albopictus* (Rosso et al., 2018) and *Ae. japonicus* (Zadra et al., 2023). While the microbiota is expected to influence host physiology, immunity, and vector competence, direct functional evidence in *Ae. koreicus* is still lacking. Overall, the current literature is largely descriptive and highlights the need for integrative and experimental approaches to clarify the ecological roles of dominant symbionts and to assess whether microbiota-based control strategies can be realistically implemented in this species.

3.6. Vector competence

Despite the ongoing expansion of *Ae. koreicus* across Europe, we collectively agreed that its epidemiological role remains poorly characterized. As found by some of the workshop participants, experimental evidence indicates that this species can become infected with nematodes such as *Dirofilaria immitis* (Montarsi et al., 2015a) and arboviruses, such as Sindbis, dengue, chikungunya and Zika (Ciocchetta et al., 2018; Jansen et al., 2022, 2021; Montarsi et al., 2026) and may support transmission under specific conditions, suggesting a potential epidemiological role. As observed in other *Aedes* species, vector competence of *Ae. koreicus* for chikungunya and Zika viruses appears to be temperature-dependent, with transmission generally remaining low, typically below 10%, but tending to increase under warmer conditions, around 27°C, compared with cooler regimes. A recent study (Bahrami et al., 2026) further supports this temperature-dependent pattern, showing that *Ae. koreicus* can transmit both chikungunya and dengue under laboratory conditions, but with distinct thermal profiles: chikungunya transmission was detected at 24°C, whereas dengue transmission was observed only at 28°C. Although transmission rates remain low across studies, the high chikungunya infection rates reported in this recent work suggest that *Ae. koreicus* can sustain efficient viral infection, even if progression to transmission appears constrained and strongly temperature-dependent (Bahrami et al., 2026). This species was shown to be susceptible to dengue infection also at a slightly lower temperature (26°C) and capable of transmitting the virus, although with low efficiency (20%) and a long extrinsic incubation period (at least three weeks, (Montarsi et al., 2026)). Conversely, larger transmission efficiency values were observed for Sindbis virus (67–100%), though with relatively limited samples (Jansen et al., 2022). Field data collected in the 1960s by Russian researchers hinted that *Ae. koreicus* could be a vector for the Japanese encephalitis virus, and experimental virus transmission was reported a few years later, but never confirmed afterwards (Ganassi et al., 2022; Miles, 1964). Finally, *Ae. koreicus* failed to transmit both West Nile and Tahyna viruses in laboratory conditions (Höller et al., 2025; Jansen et al., 2021). Overall, these findings suggest that *Ae. koreicus* may support arbovirus transmission under specific conditions, but they should be interpreted considering some general limitations. For temperature-based studies, experimental designs remain heterogeneous, often differing in viral strains, mosquito populations, and thermal regimes, with some studies focusing primarily on adult exposure while largely overlooking thermal conditions experienced during juvenile development. For field-based studies, available data are still limited to a small number of mosquito populations and geographic areas, making it difficult to assess how vector competence may vary across the species' invasive range. For example, in (Höller et al., 2025), vector competence for Tahyna virus was assessed using the Bardos92 strain, a historical isolate obtained several decades ago and extensively passaged in cell culture, which may not fully represent the phenotypic characteristics of contemporary circulating strains.

Importantly, vector competence alone does not determine transmission risk, which depends on multiple biotic and abiotic factors such as the genetic background of both mosquitoes and viruses involved, vector density, host availability, feeding behaviour, survival, and environmental conditions. In Europe, outbreaks of dengue and chikungunya have typically been spatially localized and driven by high densities of a competent vector (*Ae. albopictus*) combined with favourable climatic conditions. Although host-vector interaction is constrained by the biological capacity of the vector to sustain viral replication and transmission, high vector abundance can partially compensate for lower intrinsic competence by increasing the overall vector capacity as demonstrated in both theoretical and empirical arbovirus systems (Cator et al., 2020; Miller et al., 1989; Scott and Morrison, 2010).

Within this framework, we argue that *Ae. koreicus*, which appears to exhibit moderate and temperature-dependent competence, is unlikely to act as a primary arbovirus vector. However, under conditions of high local abundance and suitable environmental context, it might contribute to transmission, particularly in localized outbreak scenarios.

3.7. Control

Very few studies evaluated insecticide resistance and effectiveness for this mosquito species. Genotype analysis revealed no pyrethroid resistant individuals reared from immature stages collected in 2017 in Ansan (Republic of Korea) (Ryu et al., 2019). However, using the Centers for Disease Control and Prevention (CDC) bottle bioassay, adults reared from immature collected in US army garrisons in the same country were found to be resistant to etofenprox and permethrin with possible resistance to deltamethrin but were susceptible to chlorpyrifos in 2022 (Stoops et al., 2023). On the other hand, in 2023 and 2024, no resistance to chlorpyrifos, deltamethrin, or permethrin was detected but resistance to etofenprox was confirmed (Stoops et al., 2023). To date, the only study evaluating insecticide effectiveness outside *Ae. koreicus* native range was carried out in Italy and it provides the first confirmation of this species' susceptibility, at the larval stage, to the bioinsecticide *Bacillus thuringiensis*, though at a lower rate with respect to *Ae. albopictus* (Negri et al., 2024).

3.8. Modelling

Most of the modelling studies we identified aimed at assessing the suitability of a particular area of interest for *Ae. koreicus* establishment. Specifically, (Marcantonio et al., 2016) represents the first quantitative evaluation of the potential invasion of this species, focusing on North-Eastern Italy, followed by a similar study covering whole Europe (Arnoldi et al., 2022). Using the same correlative modelling techniques, (Liu et al., 2023; Seok et al., 2023) assessed suitability at global level. All the above-mentioned studies adopted MaxEnt models, considering similar environmental or bioclimatic variables. On the other hand, different statistical models were implemented to predict *Ae. koreicus* occurrence in Hungary considering mainly citizen science data (Garamszegi et al., 2025, 2023b) and to quantify and compare the environmental niches of native and non-native populations of *Ae. koreicus* and *Ae. japonicus* (Seok et al., 2026). Conversely, a mechanistic model, which mimics the whole mosquito life cycle, was first proposed in (Marini et al., 2019), and model temperature-dependent parameters were informed by ad-hoc laboratory experiments. This model was then adopted to investigate *Ae. koreicus* population dynamics in a Hungarian city (Kurucz et al., 2020). Finally, a similar mechanistic model is provided within the *dynamaedes* R library (Da Re et al., 2022), built upon (Marini et al., 2019), offering the option to consider mosquito dispersal and different spatial resolutions.

Modellers attending the workshop concluded that the ecological modelling of *Ae. koreicus* is still in its infancy, not for the lack of questions and tools, but rather for the limited amount of data (species abundance time series, extensive life-history tables, etc.) that make it difficult to inform and calibrate subtler modelling approaches than those already explored.

3.9. Communication and education

Workshop participants converged on the importance of transparent, calibrated communication with both the public and policymakers, with a strong emphasis on avoiding alarmist tones. A central message that emerged from discussions is that the public health relevance of *Ae. koreicus* remains genuinely uncertain: its vectorial capacity is poorly characterised, and any claims about its potential role in disease transmission to humans and domestic animals in Europe are, at present, speculative. Communicating this uncertainty honestly, rather than extrapolating from the better-known risks associated with *Ae. albopictus*, was seen as both scientifically responsible and strategically important to maintain public trust. A recurring concern was the risk of triggering disproportionate alarm or indiscriminate chemical control responses; awareness campaigns should therefore promote informed, integrated mosquito management, making clear that the presence of *Ae. koreicus* is currently better understood as a nuisance issue than a sanitary emergency, even if some concerns have been raised regarding its potential veterinary threat as vector of *Dirofilaria* (Montarsi et al., 2015a). Participants highlighted younger generations as a priority audience, advocating for educational outreach embedded within the school system through laboratory activities, guided field visits, and summer camps designed to foster active and sustained engagement with mosquito monitoring.

A particularly productive framing that emerged was repositioning *Ae. koreicus* research and surveillance as a "biodiversity watch" initiative, deliberately decoupled from the public health urgency associated with *Ae. albopictus*. In peri-urban and montane contexts, where mosquito biting nuisance might directly affect the tourism sector, participants saw an opportunity to link control activities to outreach efforts, creating a practical case for sustained local funding and stakeholder engagement. This framing also carries a forward-looking rationale: building surveillance and research capacity around *Ae. koreicus* now, while substantial knowledge gaps remain, could help prevent a future *Ae. albopictus*-like scenario, in which a species spreads widely before adequate monitoring and response infrastructures are established.

4. Conclusion and future perspectives

This scoping review and expert workshop have collectively highlighted that, nearly two decades after its first detection in Europe, *Ae. koreicus* remains a substantially understudied species, especially with respect to *Ae. albopictus*. Indeed, some recent literature reviews retrieved 59 studies investigating the effect of temperature on this latter species' bionomics (Da Re et al., 2025), 38 studies identifying field-collected blood meals (Fikrig and Harrington, 2021) and 17 evaluating its competence for chikungunya, dengue, and Zika viruses (Delrieu et al., 2023).

The evidence base assembled here provides a useful baseline, though it should be interpreted with an important caveat: the literature on *Ae. koreicus* is likely underrepresented in standard bibliographic databases, partly because older records are not indexed in current databases or were published under the former synonyms *Ochlerotatus koreicus* and *Hulecoeteomyia koreica*, and partly because earlier studies did not consistently distinguish *Ae. koreicus* from *Ae. japonicus*, treating them as a single taxonomic unit (Ganassi et al., 2022; Seok et al., 2024). These indexing and taxonomic inconsistencies introduce a degree of incompleteness into any scoping review of this species and underscore the need for greater terminological standardisation in future publications.

From an operational standpoint, a central priority emerging from both the review and the workshop is the revision of existing monitoring frameworks. Current *Aedes* surveillance programmes across Europe are predominantly designed around *Ae. albopictus* and are poorly equipped to account for the presence of *Ae. koreicus*, whose greater cold tolerance allows it to remain active outside the core monitoring season and at elevations typically excluded from standard surveillance grids. Developing reliable tools to distinguish the two species from routine trap samples is therefore an urgent practical need. Among the approaches currently available, optical recognition of egg exochorionic patterns appears to be a promising solution, though it still struggles to discriminate *Ae. koreicus* from *Ae. japonicus*. Molecular and eDNA-based methods hold longer-term promise but require further validation before operational deployment, while the most immediately scalable approach is still the classical morphological determination of adult mosquitoes.

Modelling efforts face a related but distinct bottleneck. The workshop discussions made clear that the main constraint on improving predictive models of *Ae. koreicus* distribution and population dynamics, is not the availability of analytical tools, as both correlative and mechanistic frameworks are well developed, but rather the scarcity and inconsistency of the underlying biological and surveillance data needed to parameterise and validate them. Investing in harmonised, long-term monitoring datasets, particularly across montane and peri-alpine areas where the species displays its most distinctive ecological traits, should therefore be considered a prerequisite for any meaningful advancement in modelling the species distribution. The same applies when considering other modeling applications such as the role of interspecific competition with *Ae. albopictus*.

Beyond its direct management relevance, *Ae. koreicus* may also offer a valuable model system for understanding broader questions in mosquito biology. Drawing on the analogy of comparative research in *Anopheles*, studying species with lower or poorly characterised vector competence can illuminate the chemical and physiological mechanisms that underpin vectorial capacity, potentially identifying targets applicable to more competent species and contributing to novel strategies for reducing pathogen transmission.

Finally, communicating the status of *Ae. koreicus* to the public and to policymakers requires a carefully calibrated framing. At present, the species could be characterised primarily as a significant nuisance rather than an established public health threat, given the limited evidence for its role in arbovirus transmission to humans in Europe but the veterinary aspect should not be underestimated. However, this view should be accompanied by an honest acknowledgement that the species is heavily understudied, that its feeding behaviour and potential impacts on wildlife remain poorly quantified, and that its public health relevance could be revised as evidence accumulates. Citizen science engagement, clearly focused around nuisance monitoring and species reporting, represents both a pragmatic surveillance tool and an opportunity for transparent public communication about the evolving status of invasive *Aedes* mosquitoes in Europe.

CRediT authorship contribution statement

Giovanni Marini: Writing – review & editing, Writing – original draft, Visualization, Investigation, Formal analysis, Conceptualization. **Maria Vittoria Mancini:** Writing – review & editing, Writing – original draft, Conceptualization. **Claudia Damiani:** Writing – review & editing, Writing – original draft, Conceptualization. **Kornélia Kurucz:** Writing – review & editing. **Alessandro Albieri:** Writing – review & editing. **Daniele Arnoldi:** Writing – review & editing. **Romina Bahrami:** Writing – review & editing. **Giulia Battistin:** Writing – review & editing. **Margo Blaha:** Writing – review & editing. **Davide Bonetto:** Writing – review & editing. **Lidia Iustina Danca:** Writing – review & editing. **Sofia Di Castri:** Writing – review & editing. **Carmela Di Santo:** Writing – review & editing. **Kamil Erguler:** Writing – review & editing. **Nicola Ferrari:** Writing – review & editing. **Eleonora Flacio:** Writing – review & editing. **Alessandra Franceschini:** Writing – review & editing. **Daniel Gingell:** Writing – review & editing. **Federica Gobbo:** Writing – review & editing. **Francesco Gradoni:** Writing – review & editing. **Annalisa Grisendi:** Writing – review & editing. **Ayda Khorramnejad:** Writing – review & editing. **Eleonora Longo:** Writing – review & editing, Visualization. **Mattia Manica:** Writing – review & editing. **Mario Marinozzi:** Writing – review & editing. **Cedric Marsboom:** Writing – review & editing. **Stefania Melillo:** Writing – review & editing. **Fabrizio Montarsi:** Writing – review & editing. **Moh Mirza Nuryady:** Writing – review & editing. **Francesca Paoli:** Writing – review & editing. **Roberto Rosà:** Writing – review & editing. **Omar Rota-Stabelli:** Writing – review & editing. **Mara Scremin:** Writing – review & editing. **Tanto Situmorang:** Writing – review & editing. **Davide Sogliani:** Writing – review & editing. **Roberta Spaccapelo:** Writing – review & editing. **Wim Van Bortel:** Writing – review & editing. **Rodolfo Veronesi:** Writing – review & editing. **Patrizia Visentin:** Writing – review & editing. **Valeria Lencioni:** Writing – review & editing, Writing – original draft, Conceptualization. **Daniele Da Re:** Writing – review & editing, Writing – original draft, Investigation, Formal analysis, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.actatropica.2026.108302.

Data availability

No data was used for the research described in the article.

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