`AedesTraits`: A global database of temperature–dependent trait responses in *Aedes* mosquitoes

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Abstract

Invasive Aedes mosquitoes are major vectors of arboviral diseases such as dengue, Zika, and chikungunya, posing an increasing threat to global public health. Their recent geographic expansion calls for predictive models to simulate population dynamics and transmission risk. Temperature is a key driver in these models, influencing traits that affect vector competence. While data on temperature–dependent traits are abundant for *Aedes aegypti* and *Ae. albopictus*, they remain scattered, inconsistent, and difficult to synthesise. For emerging species like *Ae. japonicu* and *Ae. koreicus*, data are even more limited.

To address these gaps, we developed `AedesTraits`, an open-access, machine-readable database aligned with VecTraits standards. It compiles and harmonises experimental data on temperature-dependent traits across these four Aedes species, covering life-history, morphological, physiological, and behavioural traits. Our synthesis highlights existing knowledge gaps and identifies under-studied species and traits. By promoting data harmonisation and accessibility, `AedesTraits` supports improved vector modelling and fosters international collaboration in the development of forecasting tools for arbovirus outbreaks.

Keywords: arboviruses, trait–based, vector-borne diseases, *Aedes*, mosquito, VecTraits

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Author Contributions Daniele Da Re, Veronica Andreo and Paul Huxley conceived the study; Paul Huxley led the literature review and digitisation efforts, with relevant contributions from Daniele Da Re, Veronica Andreo, Tomas San Miguel, Marharyta Blaha, Joe Harrison and Sean Sorek; Paul Huxley reviewed all the digitised information, ensuring that it adhered to the VectTraits standards. Daniele Da Re and Veronica Andreo analysed the digitised data; Daniele Da Re led the writing of the manuscript, with relevant contributions from Veronica Andreo and Paul Huxley. All authors contributed critically to the drafts and gave their final approval for publication.

Ethics declarations The authors declare no competing interests.

1 Background and Summary

Invasive mosquito species are of global public health concern because of their capacity to vector pathogens that cause substantial human mortality and morbidity (WHO, 2024). Among these species, those belonging to the *Aedes* genus have rapidly expanded their geographical range over the last few decades. Two of these, *Ae. aegypti* and *Ae. albopictus*, have been implicated as the main vectors in recent arboviral epidemic outbreaks around the world (Fauci and Morens, 2016; Estallo et al., 2024; Cattaneo et al., 2025).

The significant public health burden caused by these species has prompted the development of predictive mathematical models aimed at enhancing our understanding of mosquito population dynamics and vectorial capacity therefore enhancing our ability to anticipate associated arbovirus transmission risk (e.g., Otero et al., 2006; Erguler et al., 2017; Aguirre et al., 2021; Da Re et al., 2022; Brass et al., 2024). Most of these models are driven by environmental temperature because many processes involved in determining vector–borne pathogen transmission are sensitive to temperature variation (San Miguel et al., 2024). This biological understanding has led to growing recognition of the need for mosquito–borne disease models to be mechanism–based if the goal is to extrapolate their predictions reliably across space and time (Johnson et al., 2015; Mordecai et al., 2017; Molnár et al., 2017; Johnson et al., 2018; Cator et al., 2020).

As poikilothermic ectotherms, the biological rate processes that govern mosquito traits, such as survival, reproduction, and viral transmission rates, are strongly influenced by variation in environmental temperature (Amarasekare and Savage, 2012; Eisen et al., 2014; Gloria-Soria et al., 2017; Reinhold et al., 2018; Lahondère and Bonizzoni, 2022). However, although laboratory studies have provided valuable information on how temperature influences mosquito traits (e.g., larval development time, extrinsic incubation period), the current knowledge base remains fragmented. Thermal traits of *Aedes aegypti* and *Ae. albopictus* are comparatively well studied in some regions of the world (Eisen et al., 2014; Reinhold et al., 2018), while research on thermal traits of other *Aedes* species, such as *Ae. japonicus* and *Ae. koreicus*, is still in its infancy and are understudied (Scott, 2003; Ciocchetta et al., 2017; Marini et al., 2019; Reuss et al., 2018; Wieser et al., 2019).

Synthesis of thermal traits that underlie modelling efforts requires that data be readily available in consistent formats. However, published data is often presented in the tables and figures of scientific publications, mostly in summarised formats. Even when data are made available (as they increasingly are by default as a requirement for publication) upon publication the format and data standards are non–standardised (Moretti et al., 2017; Ryan et al., 2025). Together these factors require researchers who wish to synthesise information across studies to invest substantial time and effort in the manual extraction and management of the data into machine–readable formats.

In this study, we address this gap by compiling and standardising data extracted from the published literature on the temperature dependence of different types of traits in four *Aedes* species: *Ae. aegypti*, *Ae. albopictus*, *Ae. japonicus*, and *Ae. koreicus*. The traits of well–studied species such as *Ae. aegypti* and *Ae. albopictus* are represented as distinct sample populations from specific locations, along with detailed records of the experimental conditions under which these traits were measured. By creating a machine–readable database that encompasses multiple species, populations, and experimental settings, this work supports in–depth investigations into the biology of *Aedes* mosquitoes and provides the broad basis necessary to improve the accuracy and generalisability of predictive mechanistic models. Furthermore, it allows the identification of critical gaps in current knowledge, such as the need for more experimental data on understudied species, specific traits, and environmental conditions, guiding future research efforts to fill these voids. `AedesTraits` aims to assist the research community by providing a comprehensive basis for advancing our understanding of vector–borne disease risk and supporting the development of outbreak forecasting approaches.

2 Methods

2.1 Literature search

To identify studies for inclusion, we followed the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta–Analyses; Moher et al., 2009) procedure, a structured approach to conduct and report systematic reviews and meta-analyses, ensuring transparency and consistency between studies. We conducted an extensive global literature search across multiple electronic databases, including Scopus, PubMed, and Web of Science. The last search was performed on January 28th, 2025. The search encompassed published journal articles without restrictions on date or language. We queried each database using Boolean operators with the following terms for each species to limit duplicates:

- (“Aedes aegypti” OR “Yellow fever mosquito”) AND temperature AND survival AND development

- (“Aedes albopictus” OR “Tiger mosquito” OR “Stegomyia albopicta”) AND temperature AND survival AND development
- “Aedes koreicus” AND temperature AND survival AND development
- “Aedes japonicus” AND temperature AND survival AND development

In addition, we manually searched for references to articles and relevant reviews for potential supplementary studies. The screening process comprised three sequential steps. First, duplicate records were eliminated. Subsequently, articles were screened by three authors based on title, abstract, and keywords, followed by a full-text evaluation to extract pertinent information. The inclusion criteria focused on studies examining the relationship between mosquito traits (e.g., life history, physiological, transmission) and temperature. This encompassed both laboratory and field experiments conducted in diverse experimental settings, and using specimens from various populations or geographic origins. To qualify for inclusion, studies had to meet four criteria: (1) they must be laboratory or field experiments, rather than surveillance-based entomological studies; (2) they must report measurable *Aedes* life-history traits, such as survival, developmental time, or size, as outcomes; (3) temperature must be the main environmental driver investigated; and (4) the data must provide sufficient detail to be standardized and integrated into a machine–readable format.

2.2 Data extraction

We requested raw data directly from the corresponding authors where possible. In cases where no response was received, we manually digitised the data and compiled it into tables. For data presented in figures, where raw data were not available, we used WebPlotDigitizer v4.8 (Rohatgi, 2020) to extract the data and convert it into table format. Throughout the process of building the database, we followed the standard format established by the VectorByte initiative (`https://www.vectorbyte.org/`), which is a global platform for open–access trait (VecTraits; Johnson et al., 2023) and abundance (VecDyn; Rund et al., 2023) data on disease vectors, alongside tools (e.g., Bayesian thermal performance curve fitting; Sorek et al., 2025) and training for researchers.

The information extracted from the literature includes species, life-history stage, location, GPS coordinates, experimental settings, and rearing conditions. This information was digitised according to the following rules: specimens reared in colonies for more than five generations in the laboratory were considered adapted to laboratory conditions and hence different from the field populations (Hoffmann and Ross, 2018). If coordinates for a specimen’s collection site were unavailable, the centroid of the administrative area provided in the study was selected.

3 Data Records

The initial search across the academic databases yielded a total of 510 studies: Scopus (78), PubMed (205), and Web of Science (227) (Fig. S1; Tab. S1). After removing duplicates, we screened the titles and abstracts of 324 studies, ultimately selecting 59 for digitisation. In addition, we identified and digitised 76 other studies sourced from Google Scholar and the reference lists of relevant articles. This search process resulted in a total of 135 digitised studies, distributed across species as follows: *Aedes aegypti* (86), *Aedes albopictus* (59), *Aedes japonicus japonicus* (1), and *Aedes koreicus* (1). During our search, we also encountered studies examining the temperature dependence of other *Aedes* species (Tab. S2). While these species are not included in the present description, the corresponding data are nonetheless included in the database.

`AedesTraits` currently hosts 31,840 rows of temperature–dependent *Aedes* trait observations, described through fields such as “originaltraitname”, “originaltraitdef”, which describe traits using their names (e.g., development time) and original definitions (e.g., mean duration of life stage). The values, units, and errors for these traits are stored in “originaltraitvalue”, “originaltraitunit”, and “originalerrorunit”, respectively.

Environmental and experimental contexts are described using fields such as “habitat”, “labfield”, “ambienttemp”, and “ambientlight”, among others, which capture the surrounding conditions and experimental setup under which the observations were collected. Geographical data is recorded in fields such as “locationtext”, “locationtype”, “latitude”, “longitude”. The specific temperatures that individuals were exposed to during experiments are stored in the “interactor1temp” and ‘interactor1tempunit” fields, respectively. Fields including “interactor1stage” and “interactor1sex” are used to indicate the life stage (e.g., larval, pupal, adult) and sex (female, male, indeterminate) of the species observed during experimentation. When publications studied the effect of temperature and additional variables, the latter is recorded in the “secondstressor” fields. Publication and data lineage are detailed in fields such as "figuretable", "citation", and "doi". The "notes" field provides options for extra metadata, ensuring each dataset's completeness and usability. All database fields are described in detail at `https://vectorbyte.crc.nd.edu/vectraits-columndefs`.

Following the guidelines provided in Moretti et al. (2017) and for clarity purposes, we summarise here the classification of traits in our database according to five overarching categories (Tab. S3): Behaviour, Infection & Transmission, Life History, Morphology, and Physiology. The original trait names, as reported in the studies, were nonetheless kept in the database to preserve transparency and facilitate traceability. In Fig. 1, we report the number of distinct trait types documented for each mosquito species across the five functional categories described above. It is important to note that this count reflects the diversity of traits, not the number of studies. Consequently, a single study may contribute data for multiple trait types, while for certain species, multiple traits may be documented within the same study. For instance, although all traits recorded for *Ae. koreicus* originate from a single study, they encompass multiple distinct traits within the Life History category (Marini et al., 2019). Overall, most traits are classified under Life History, with *Ae. aegypti* exhibiting 14 distinct traits and *Ae. albopictus*, 10. Infection & Transmission traits are also well-represented, with 6 traits for *Ae. aegypti* and 8 for *Ae. albopictus*. Morphological, Stress Tolerance & Physiological Performance traits, along with Behaviour traits, are comparatively under-represented. For *Ae. japonicus japonicus* and *Ae. koreicus*, a limited number of traits are currently documented, highlighting gaps in available trait information for these invasive species.

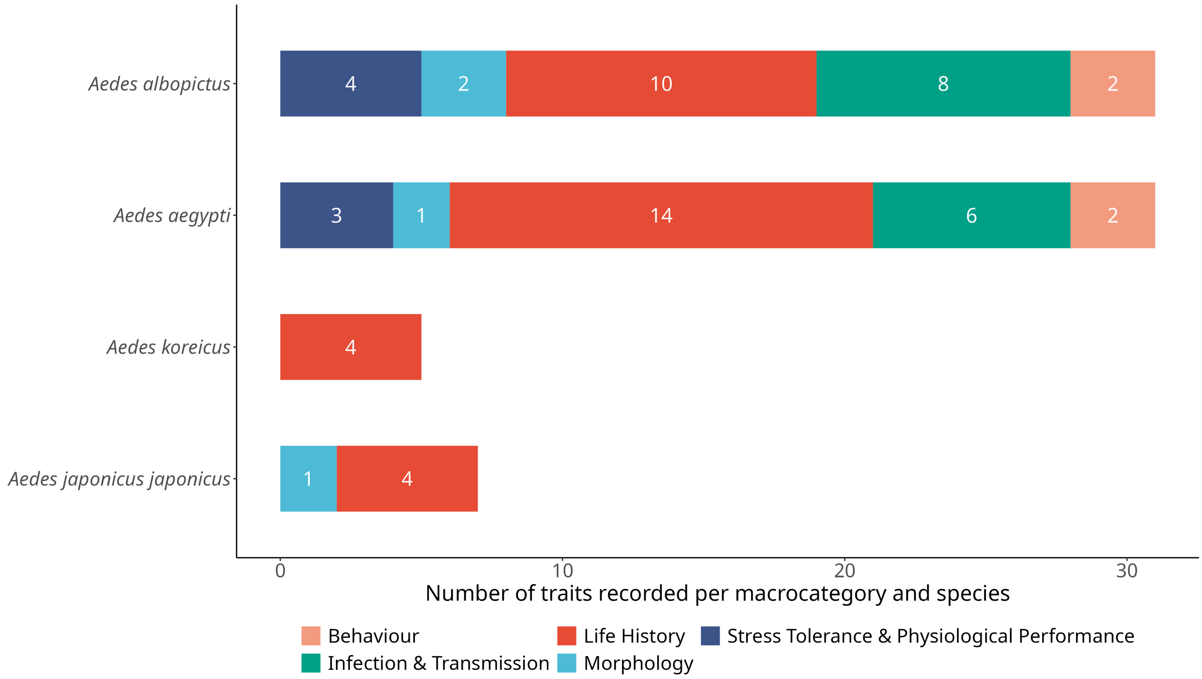

Figure 1: Number of distinct trait types reported for each mosquito species across five functional categories. Bars represent the diversity of traits reported rather than the number of studies. Note that multiple traits may originate from a single study.

Following data extraction, we categorised the origin of mosquito populations as either derived from laboratory colonies or field collections, based on information reported in the original studies. For *Ae. aegypti*, most populations originated from field collections (72 instances), while colony populations were used in 43 cases, and one study did not report the origin. Similarly, studies on *Ae. albopictus* showed a predominance of field–derived populations (80 instances), with colony populations used in 39 instances and two studies with unspecified origin. In contrast, data for *Ae. japonicus japonicus* and *Ae. koreicus* are more limited, with only field collections reported (4 and 1 instances, respectively).

Figure 2 illustrates the geographical distribution of experimental sites retrieved for *Ae. aegypti* and *Ae. albopictus*, encompassing both laboratory and field studies, overlaid on the DENV transmission suitability map using Index P (Nakase et al., 2023). This index represents a mechanistic measure of dengue transmission suitability for *Ae. aegypti* mosquitoes based on temperature and relative humidity. Experimental sites for *Ae. aegypti* are predominantly concentrated in tropical and subtropical regions where Index P values are higher. In contrast, *Ae. albopictus* experimental sites are primarily located in areas with low Index P values, specifically in Europe or the global North, as shown in Fig. S2, reflecting the more temperate range of *Ae. albopictus* compared to *Ae. ae-*

gypti. Due to limited data, *Ae. koreicus* and *Ae. japonicus* study locations are not displayed, with only two sites available: northern Italy and western Germany, respectively. It is striking that, despite their medical importance and widespread distribution, relatively few *Aedes* populations have been sampled in local areas denoted highly suitable for DENV transmission 2, likely underestimating the degree to which mosquito trait responses to temperature may vary across geographically distinct populations and species (Dennington et al., 2023; Couper et al., 2025).

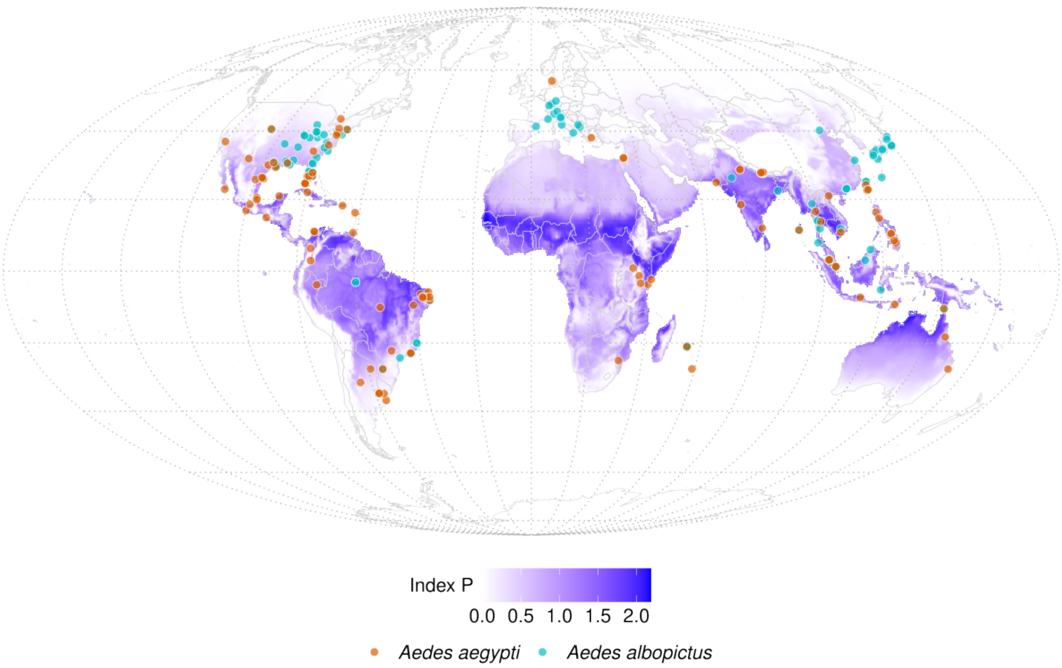

Figure 2: DENV transmission suitability Index P (from Nakase et al., 2023) and location of sampled population/-experiments of *Ae. aegypti* and *Ae. albopictus* (orange and light blue dots respectively) included in `AedesTraits`.

We retrieved studies spanning nearly a century, with publication years ranging from 1930 to 2024. For *Ae. aegypti*, studies date back as early as 1930, while for *Ae. albopictus*, the earliest studies were published from 1969 onwards. However, most studies for both species are concentrated from 2000 onwards, reflecting the increased research attention over recent decades. In contrast, studies on *Ae. japonicus japonicus* and *Ae. koreicus* are much more recent, first appearing in 2018 and 2019 respectively, consistent with their more recent recognition as invasive vector species. A detailed overview of the temporal distribution of studies on *Ae. aegypti* and *Ae. albopictus* is provided in Fig. S3.

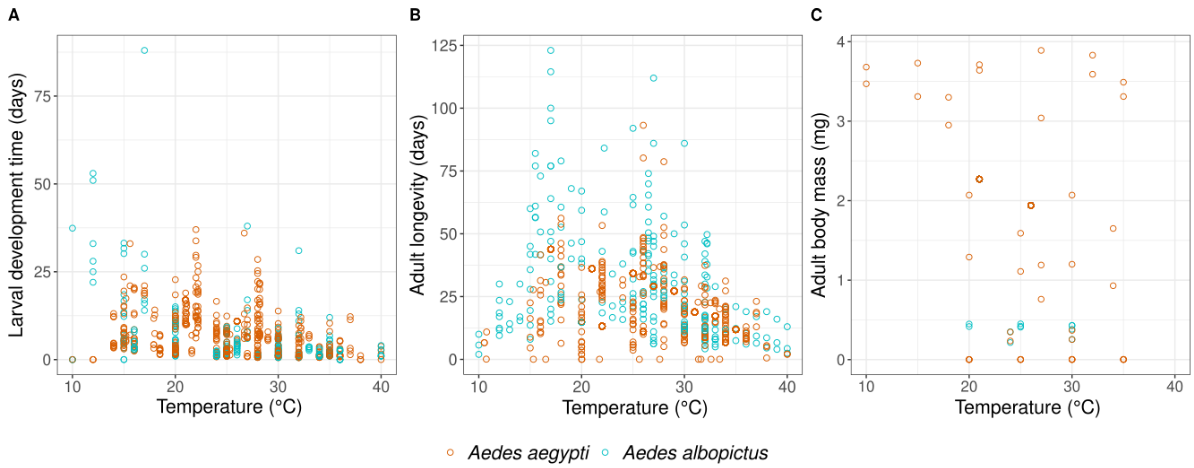

Figure 3: *Ae. aegypti* and *Ae. albopictus* (orange and light blue dots respectively) larval development time(A), adult longevity (B), and adult body mass (C) variability according to temperature.

`AedesTraits` includes observations on several traits – such as longevity, biting rate, flight capacity, and extrinsic incubation period – but for brevity, we focus here solely on larval development time, adult longevity, and adult body mass data for *Ae. aegypti* and *Ae. albopictus* (Fig. 3). The observations shown in Fig. 3 exhibit considerable variation in longevity across both species, likely reflecting differences in experimental protocols such as temperature, humidity, and resource availability (Huxley et al., 2021, 2022), as well as inherent ecological plasticity and potential local adaptation in *Aedes* populations (*sensu* Kramer et al., 2021). This pronounced variation emphasises the challenge of isolating intrinsic biological traits from external experimental factors and underscores the importance of adopting standardised methodologies to improve cross–study comparability (Ryan et al., 2025).

4 Data availability

`AedesTraits` adheres to the FAIR principles (Findable, Accessible, Interoperable, and Reusable; Wilkinson et al., 2016) and is permanently archived in a Zenodo repository (DOI: 10.5281/zenodo.15149903). All analyses conducted for this study are fully reproducible, with the corresponding code also available in Zenodo. Finally, `AedesTraits` is also deposited in and available for download from the VecTraits database (Johnson et al., 2023). Depositing `AedesTraits` in VecTraits allows other contributors to add data from new studies to further expand the knowledge base on this group of mosquito vectors. VecTraits submission requirements are minimal and fully described at `https://www.vectorbyte.org`.

5 Technical validation

Manual input of large volumes of data is likely to introduce errors. To minimise such errors during data entry, each life-history trait variable was checked using frequency histograms, box plots, and/or scatter plots in R (R Core Team, 2024). Any outliers identified in these plots were cross–checked against the source publications, and discrepancies were corrected accordingly.

6 Usage notes

Mechanism–informed models have a pivotal role in implementing robust surveillance systems and forecasting approaches capable of estimating vector abundance and seasonality (Caputo and Manica, 2020; Da Re et al., 2025). The absence of standardised and comprehensive datasets of mosquito species traits likely hinders the reliability and broader applicability of these model predictions, particularly across diverse spatial and temporal contexts.

To address this limitation, we have gathered the widest range of studies on the thermal biology of four *Aedes* species – *Ae. aegypti*, *Ae. albopictus*, *Ae. japonicus*, and *Ae. koreicus* – compiling and standardising the data into an open–access and machine–readable database that adheres to VecTraits standards (Johnson et al., 2023). Further, `AedesTraits` provides researchers, policymakers, and public health professionals with access to comprehensive data on mosquito biology. It can serve as a critical resource for the development and validation of predictive models on mosquito population dynamics and arbovirus transmission. Further, `AedesTraits` promotes data harmonization and sharing across regions, fostering collaboration, and enhancing the quality of global scientific investigations on vector–borne diseases.

In this study, we primarily focused on experimental studies in which temperature was the main, but not necessarily the only, variable influencing traits of four *Aedes* species. For example, the database includes studies that explore the interaction of temperature and resource availability. We recognise that other factors, such as precipitation and humidity, can act independently and interactively with other environmental factors to influence mosquito traits involved in disease transmission. However, if temperature was not concurrently manipulated then traits that vary with other factors would not have met our inclusion criteria. Although not included here, some trait data from such studies is currently held in VecTraits (Johnson et al., 2023), and it can uploaded from future studies when it becomes available to complement the current study. In conclusion, the summary analysis of this database highlights gaps in the current knowledge on temperature–dependent mosquito traits, identifying which species and specific traits require further experimental investigation. Furthermore, our work fosters data harmonization and international collaboration to support global efforts in developing outbreak forecasting systems

References

Aguirre, E., Andreo, V., Porcasi, X., Lopez, L., Guzman, C., González, P., and Scavuzzo, C. M. (2021). Implementation of a proactive system to monitor aedes aegypti populations using open access historical and forecasted meteorological data. *Ecological Informatics*, 64:101351.

Amarasekare, P. and Savage, V. (2012). A framework for elucidating the temperature dependence of fitness. *The American Naturalist*, 179(2):178–191.

Brass, D. P., Cobbold, C. A., Purse, B. V., Ewing, D. A., Callaghan, A., and White, S. M. (2024). Role of vector phenotypic plasticity in disease transmission as illustrated by the spread of dengue virus by aedes albopictus. *Nature Communications*, 15(1):7823.

Caputo, B. and Manica, M. (2020). Mosquito surveillance and disease outbreak risk models to inform mosquito-control operations in europe. *Current opinion in insect science*, 39:101–108.

Cator, L. J., Johnson, L. R., Mordecai, E. A., El Moustaid, F., Smallwood, T. R., LaDeau, S. L., Johansson, M. A., Hudson, P. J., Boots, M., Thomas, M. B., et al. (2020). The role of vector trait variation in vector-borne disease dynamics. *Frontiers in ecology and evolution*, 8:189.

Cattaneo, P., Salvador, E., Manica, M., Barzon, L., Castilletti, C., Di Gennaro, F., Huits, R., Merler, S., Poletti, P., Riccardo, F., et al. (2025). Transmission of autochthonous aedes-borne arboviruses and related public health challenges in europe 2007–2023: a systematic review and secondary analysis. *The Lancet Regional Health–Europe*.

Ciocchetta, S., Darbro, J. M., Frentiu, F. D., Montarsi, F., Capelli, G., Aaskov, J. G., and Devine, G. J. (2017). Laboratory colonization of the European invasive mosquito *Aedes (Finlaya) koreicus*. *Parasites & vectors*, 10(1):1–6.

Couper, L. I., Dodge, T. O., Hemker, J. A., Kim, B. Y., Exposito-Alonso, M., Brem, R. B., Mordecai, E. A., and Bitter, M. C. (2025). Evolutionary adaptation under climate change: Aedes sp. demonstrates potential to adapt to warming. *Proceedings of the National Academy of Sciences*, 122(2):e2418199122.

Da Re, D., Marini, G., Bonannella, C., Laurini, F., Manica, M., Anicic, N., Albieri, A., Angelini, P., Arnoldi, D., Bertola, F., et al. (2025). Modelling the seasonal dynamics of aedes albopictus populations using a spatio-temporal stacked machine learning model. *Scientific Reports*, 15(1):3750.

Da Re, D., Van Bortel, W., Reuss, F., Müller, R., Boyer, S., Montarsi, F., Ciocchetta, S., Arnoldi, D., Marini, G., Rizzoli, A., et al. (2022). dynamaedes: a unified modelling framework for invasive aedes mosquitoes. *Parasites & vectors*, 15(1):414.

Dennington, N. L., Grossman, M. K., Ware-Gilmore, F., Teeple, J. L., Johnson, L. R., Shocket, M. S., McGraw, E. A., and Thomas, M. B. (2023). Phenotypic adaptation to temperature in the mosquito vector, aedes aegypti. *Global Change Biology*, 30(1):e17041. e17041 GCB-23-2108.R1.

Eisen, L., Monaghan, A. J., Lozano-Fuentes, S., Steinhoff, D. F., Hayden, M. H., and Bieringer, P. E. (2014). The impact of temperature on the bionomics of *Aedes (Stegomyia) aegypti* , with special reference to the cool geographic range margins. *Journal of medical entomology*, 51(3):496–516.

Erguler, K., Chandra, N. L., Proestos, Y., Lelieveld, J., Christophides, G. K., and Parham, P. E. (2017). A large-scale stochastic spatiotemporal model for aedes albopictus-borne chikungunya epidemiology. *PloS one*, 12(3):e0174293.

Estallo, E. L., López, M. S., Ludueña-Almeida, F., Madelón, M. I., Layún, F., and Robert, M. A. (2024). Increased risks of mosquito-borne disease emergence in temperate regions of South America. *The Lancet Regional Health - Americas*, 40:100946.

Fauci, A. S. and Morens, D. M. (2016). Zika virus in the americas—yet another arbovirus threat. *New England journal of medicine*, 374(7):601–604.

Gloria-Soria, A., Armstrong, P., Powell, J., and Turner, P. (2017). Infection rate of aedes aegypti mosquitoes with dengue virus depends on the interaction between temperature and mosquito genotype. *Proceedings of the Royal Society B: Biological Sciences*, 284(1864):20171506.

Hoffmann, A. A. and Ross, P. A. (2018). Rates and patterns of laboratory adaptation in (mostly) insects. *Journal of Economic Entomology*, 111(2):501–509.

Huxley, P. J., Murray, K. A., Pawar, S., and Cator, L. J. (2021). The effect of resource limitation on the temperature dependence of mosquito population fitness. *Proceedings of the Royal Society B*, 288(1949):20203217.

Huxley, P. J., Murray, K. A., Pawar, S., and Cator, L. J. (2022). Competition and resource depletion shape the thermal response of population fitness in aedes aegypti. *Communications biology*, 5(1):66.

Johnson, L. R., Ben-Horin, T., Lafferty, K. D., McNally, A., Mordecai, E., Paaijmans, K. P., Pawar, S., and Ryan, S. J. (2015). Understanding uncertainty in temperature effects on vector-borne disease: a bayesian approach. *Ecology*, 96(1):203–213.

Johnson, L. R., Cator, L., Rund, S. S. C., Ryan, S., Huxley, P. J., and Pawar, S. (2023). Vectraits explorer.

Johnson, L. R., Gramacy, R. B., Cohen, J., Mordecai, E., Murdock, C., Rohr, J., Ryan, S. J., Stewart-Ibarra, A. M., and Weikel, D. (2018). Phenomenological forecasting of disease incidence using heteroskedastic gaussian processes: A dengue case study. *The Annals of Applied Statistics*, 12(1):27.

Kramer, I. M., Pfeiffer, M., Steffens, O., Schneider, F., Gerger, V., Phuyal, P., Braun, M., Magdeburg, A., Ahrens, B., Groneberg, D. A., et al. (2021). The ecophysiological plasticity of *Aedes aegypti* and *Aedes albopictus* concerning overwintering in cooler ecoregions is driven by local climate and acclimation capacity. *Science of The Total Environment*, 778:146128.

Lahondère, C. and Bonizzoni, M. (2022). Thermal biology of invasive aedes mosquitoes in the context of climate change. *Current Opinion in Insect Science*, 51:100920.

Marini, G., Arnoldi, D., Baldacchino, F., Capelli, G., Guzzetta, G., Merler, S., Montarsi, F., Rizzoli, A., and Rosà, R. (2019). First report of the influence of temperature on the bionomics and population dynamics of *Aedes koreicus*, a new invasive alien species in Europe. *Parasites & vectors*, 12(1):1–12.

Moher, D., Liberati, A., Tetzlaff, J., and Altman, D. G. (2009). The prisma statement for reporting systematic reviews and meta-analyses of studies that evaluate health care interventions: Explanation and elaboration. *Annals of Internal Medicine*, 151(4):W–65–W–94.

Molnár, P. K., Sckrabulis, J. P., Altman, K. A., and Raffel, T. R. (2017). Thermal performance curves and the metabolic theory of ecology—a practical guide to models and experiments for parasitologists. *Journal of Parasitology*, 103(5):423–439.

Mordecai, E. A., Cohen, J. M., Evans, M. V., Gudapati, P., Johnson, L. R., Lippi, C. A., Miazgowicz, K., Murdock, C. C., Rohr, J. R., Ryan, S. J., et al. (2017). Detecting the impact of temperature on transmission of zika, dengue, and chikungunya using mechanistic models. *PLoS neglected tropical diseases*, 11(4):e0005568.

Moretti, M., Dias, A. T., De Bello, F., Altermatt, F., Chown, S. L., Azcárate, F. M., Bell, J. R., Fournier, B., Hedde, M., Hortal, J., et al. (2017). Handbook of protocols for standardized measurement of terrestrial invertebrate functional traits. *Functional Ecology*, 31(3):558–567.

Nakase, T., Giovanetti, M., Obolski, U., and Lourenço, J. (2023). Global transmission suitability maps for dengue virus transmitted by aedes aegypti from 1981 to 2019. *Scientific Data*, 10(1):275.

Otero, M., Solari, H. G., and Schweigmann, N. (2006). A stochastic population dynamics model for *Aedes aegypti*: formulation and application to a city with temperate climate. *Bulletin of mathematical biology*, 68(8):1945–1974.

R Core Team (2024). *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria.

Reinhold, J. M., Lazzari, C. R., and Lahondère, C. (2018). Effects of the environmental temperature on aedes aegypti and aedes albopictus mosquitoes: a review. *Insects*, 9(4):158.

Reuss, F., Wieser, A., Niamir, A., Bálint, M., Kuch, U., Pfenninger, M., and Müller, R. (2018). Thermal experiments with the asian bush mosquito (*Aedes japonicus japonicus*)(Diptera: Culicidae) and implications for its distribution in Germany. *Parasites & vectors*, 11(1):1–10.

Rohatgi, A. (2020). *Webplotdigitizer: Version 4.4*.

Rund, S. S. C., Ryan, S. J., Huxley, P. J., A., L. C., Cator, L., Pawar, S., and Johnson, L. R. (2023). Vecdyn explorer.

Ryan, S. J., Huxley, P. J., Lippi, C. A., Pawar, S., Cator, L., Rund, S. S., and Johnson, L. R. (2025). Mirevtd, a minimum information standard for reporting vector trait data. *bioRxiv*, pages 2025–01.

San Miguel, T. V., Daniele, D. R., and Verónica, A. (2024). A systematic review of aedes aegypti population dynamics models based on differential equations. *Acta Tropica*, page 107459.

Scott, J. (2003). *The Ecology of the Exotic Mosquito* Ochlerotatus (Finlaya) japonicus japonicus *(Theobald 1901) (Diptera: Culicidae) and an Examination of its Role in the West Nile Virus Cycle in New Jersey*. Ph.D. thesis, Rutgers University, New Brunswick, NJ.

Sorek, S., Smith Jr., J. W., Huxley, P. J., and Johnson, L. R. (2025). bayestpc: Bayesian inference for thermal performance curves in r. *Methods in Ecology and Evolution*.

WHO, G. A. I. (2024). Preparing for the next pandemic by tackling mosquito-borne viruses with epidemic and pandemic potential. *WHO: Geneva, Switzerland*.

Wieser, A., Reuss, F., Niamir, A., Müller, R., O'Hara, R. B., and Pfenninger, M. (2019). Modelling seasonal dynamics, population stability, and pest control in *Aedes japonicus japonicus* (Diptera: Culicidae). *Parasites & vectors*, 12(1):1–12.

Wilkinson, M. D., Dumontier, M., Aalbersberg, I. J., Appleton, G., Axton, M., Baak, A., Blomberg, N., Boiten, J.-W., da Silva Santos, L. B., Bourne, P. E., et al. (2016). The fair guiding principles for scientific data management and stewardship. *Scientific data*, 3(1):1–9.

A Supplementary materials

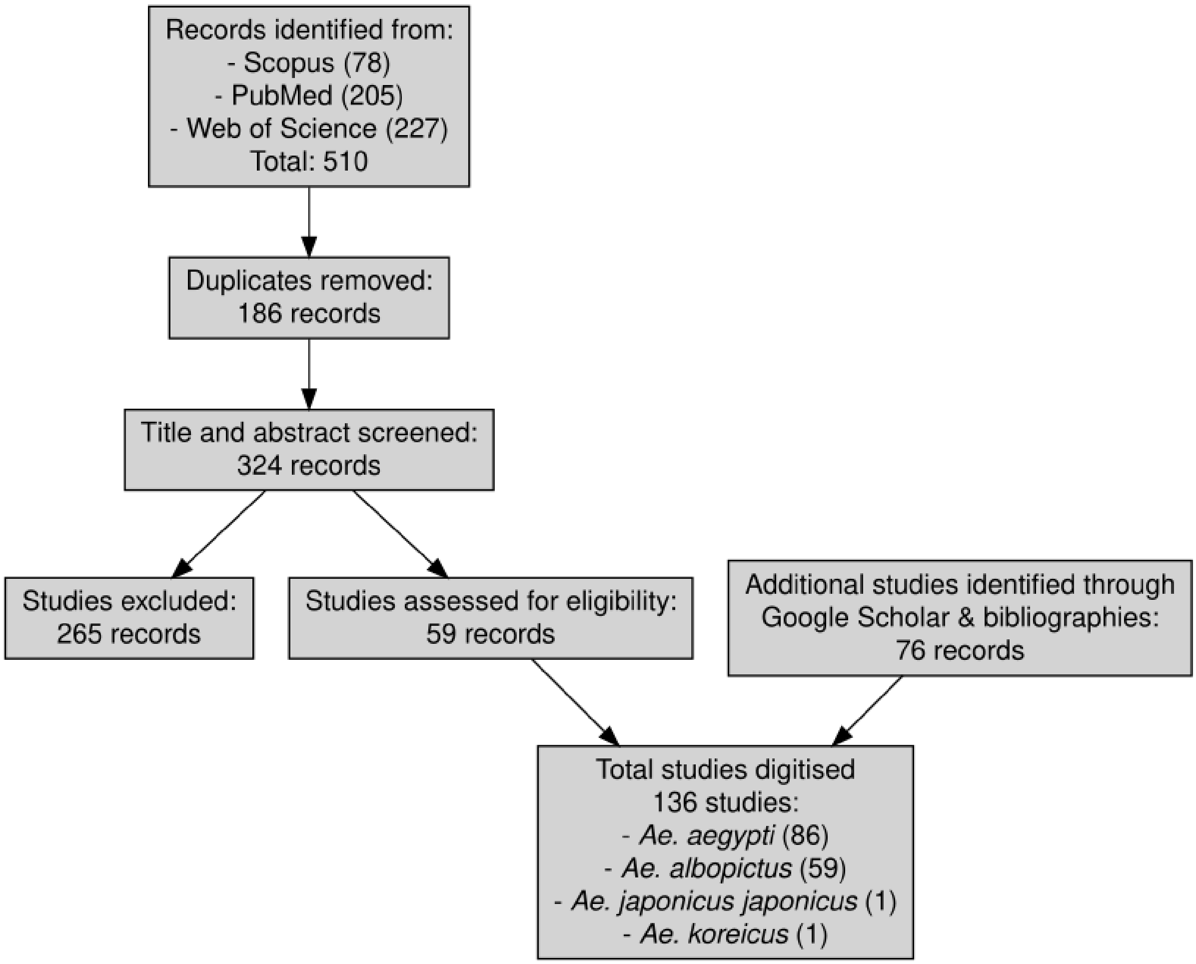

Figure S1: PRISMA flow diagram illustrating the selection process of studies included in `AedesTraits` following an initial search across three databases (Scopus, PubMed, and Web of Science). Note that some studies investigated more than one species.

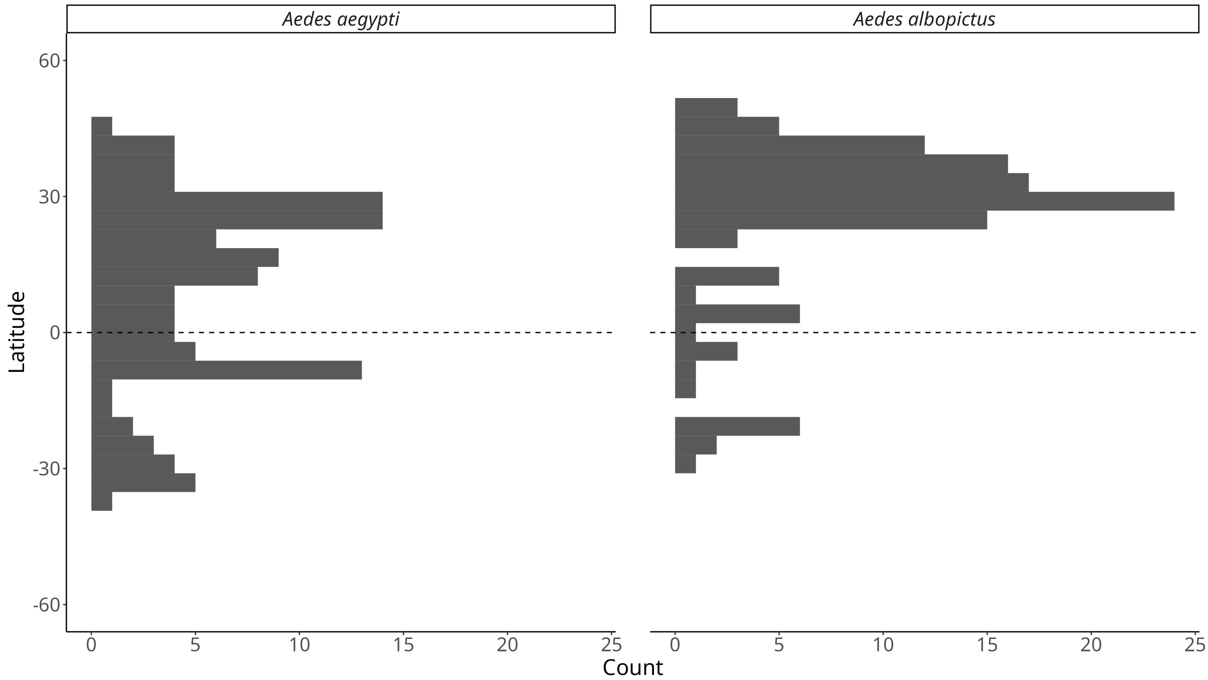

Figure S2: Latitudinal distribution of *Ae. aegypti* and *Ae. albopictus* experiments included in `AedesTraits`. The bars represent the number of digitised studies conducted at different latitudes, illustrating the geographic trends in experimental coverage for both species.

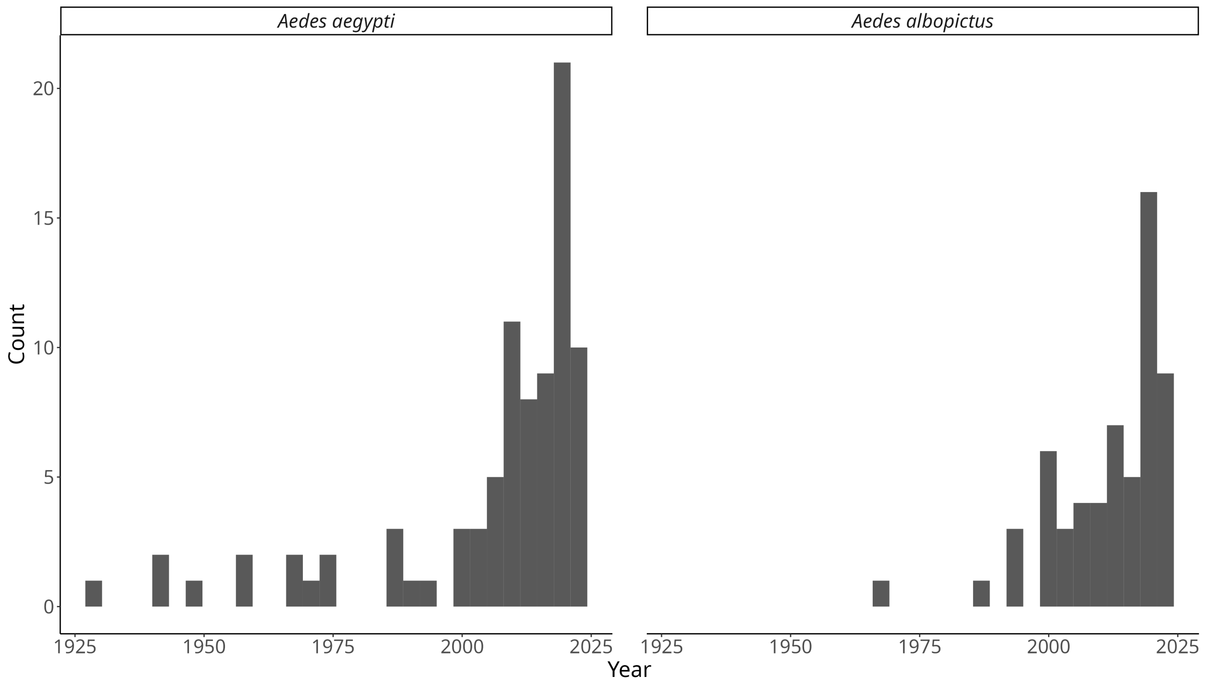

Figure S3: emporal distribution of textitAe. aegypti and *Ae. albopictus* experiments included in `AedesTraits`. The bars show the number of studies published per year, highlighting temporal trends in research activity across both species.

Table S1: Number of studies per Aedes species retrieved from each citation database source (Scopus, Web of Science, and PubMed).

Species	**Scopus**	**WoS**	**PubMed**
Aedes aegypti	10	140	118
Aedes albopictus	63	83	81
Aedes japonicus	4	3	5
Aedes koreicus	1	1	1

Table S2: List of species present in `AedesTraits`.

Species	**Number of studies**
Aedes aegypti	86
Aedes alboannulatus	1
Aedes albopictus	59
Aedes atropalpus	1
Aedes camptorhynchus	1
Aedes japonicus japonicus	1
Aedes koreicus	1
Aedes krombeini	1
Aedes nigromaculis	1
Aedes notoscriptus	2
Aedes sagax	1
Aedes togoi	1
Aedes triseriatus	3
Aedes vigilax	1
Aedes vixans	1

Table S3: Summary of trait diversity grouped into five macrocategories, following the classification framework of Moretti et al., 2017. This organisation highlights the variability of traits described in the `AedesTraits`.

Trait Category	Trait Examples
Morphology	- Body size (mean dry weight, wing length, wing size, wet mass, cephalothorax length, head width, live body weight, body length, wing area) - Egg size (non-diapause/diapause egg length and width under different conditions)
Life History	- Development time (mean, median, min, max duration, hatch to pupation, under stressors like temperature, food quantity, competition) - Fecundity (mean lifetime eggs, eggs per cycle, individual-level lifetime eggs, ovariole count, eggs post blood meal) - Gonotrophic cycle length (duration, number of cycles) - Longevity (mean, max, min lifespan, days when X% population alive) - Survival (percent surviving life stage, egg hatching, pupation rate, survival to adulthood, survival under stressors, mean survival probability) - Blood feeding frequency (mean number of blood meals, percent taking one/two meals) - Pre-bloodmeal period, pre-oviposition period, incubation period, juvenile life span - Sex ratio (as function of temperature, larval food type)
Physiology	- Temperature tolerance (percent survival after extreme temperatures, knock-down time, chill coma onset/recovery, chill injury) - Energy reserves (glucose, glycogen, trehalose content) - Hemolymph composition (Na^+, K^+ concentrations after cold stress) - Weight loss during exhaustive flight - Critical photoperiod period (minimum light exposure for egg hatching)
Behaviour	- Biting rate (time to first bite, number of bites, time between bites) - Feeding preference (preference for protein-rich vs. sucrose meals) - Mating capacity (mean % females inseminated by one male)
Infection & Transmission	- Infection rate (percent infected after exposure to DENV, ZIKV, CHIKV, Wolbachia, body/head/salivary gland/midgut presence) - Dissemination rate (percent dissemination to body parts like legs, heads, salivary glands) - Transmission rate & efficiency (vertical/horizontal transmission, progeny infection, transmission to hosts) - Viral titers & viral load ($\log_{10}$ plaque forming units, virus concentration in body, legs, salivary glands) - Extrinsic incubation period & rate (time until transmission potential) - Viral replication rate (as a function of temperature/post-infection days)