Evolution of host preference in mosquitoes and its impact on virus transmission

Matthew DeGennaro[a,b] **and Takeshi Morita**[a,b,*]
[a]Department of Biological Sciences, Florida International University, Miami, FL, United States
[b]Biomolecular Sciences Institute, Florida International University, Miami, FL, United States
*Corresponding author. e-mail address: tmorita@fiu.edu

Contents

1. Introduction 2
2. Evolutionary drivers of host preference in mosquitoes 4
   2.1 Ecological and selective drivers of host choice 4
   2.2 Genomic and sensory bases of host-linked divergence 5
   2.3 Comparative examples of host shifts across mosquito lineages 7
3. Mechanisms underlying host preference 8
   3.1 Olfactory cues and host odor discrimination 8
   3.2 Visual cues and odor-gated host detection 10
   3.3 Thermal, infrared, and humidity cues in close-range host localization 11
   3.4 Contact chemosensation and post-landing host evaluation 13
   3.5 Neural coding, integration, internal state, and learning 14
4. Host preference and mosquito-borne virus transmission 15
   4.1 Host specificity, amplification, and spillover 15
   4.2 Case studies: Aedes aegypti - Zika and Dengue, Culex spp. - West Nile virus 16
   4.3 Vectorial capacity, repeated feeding, and heterogeneity in host contact 18
5. Environmental and anthropogenic influences 20
   5.1 Urbanization, land-use change, and climate effects on host availability 20
   5.2 Human interventions and unintended evolutionary or behavioral consequences 23
6. Zoonoses and disease emergence 24
   6.1 Why host-use surveillance matters for predicting spillover 24
   6.2 Blood-meal analysis, metabarcoding, and xenosurveillance 26
   6.3 Toward network-based surveillance of host-vector-pathogen systems 27
7. Conclusion 28
Acknowledgements 29
References 29

Advances in Insect Physiology
ISSN 0065-2806, https://doi.org/10.1016/bs.aiip.2026.06.002
Copyright © 2026 Elsevier Ltd. All rights are reserved, including those for text and data mining, AI training, and similar technologies.

Abstract

Mosquito host preference plays a major role in viral persistence, zoonotic spillover, and urban transmission. This chapter synthesizes evidence from behavioral studies, molecular genetics, genomics, ecology, and field surveillance to explain how mosquitoes acquire host preferences, how their sensory systems guide host choice, and how these behaviors shape the transmission of viruses such as dengue, Zika, yellow fever, and West Nile. Attention is given to the evolution of human-seeking behavior in *Aedes aegypti*, the flexible feeding patterns of *Culex* mosquitoes, the ways urban environments drive behavioral and genetic change, and the growing use of molecular tools to identify blood-meal sources. Together, this chapter highlights findings that show that host preference is a dynamic ecological trait that must be accounted for in any effort to model or manage mosquito-borne virus transmission.

1. Introduction

Mosquito-borne viruses continue to impose a major burden on global public health. Dengue, Zika, chikungunya, yellow fever, West Nile, Japanese encephalitis, and Rift Valley fever repeatedly cause outbreaks that are associated with severe illness, long-term health effects, and substantial economic disruption (Kilpatrick and Randolph, 2012; Paixão et al., 2018; Wei et al., 2025). Despite their ecological and taxonomic diversity, all of these pathogens depend on a critical event for transmission, the mosquito blood meal. Each blood meal creates an opportunity for pathogens to pass between mosquitoes and vertebrate hosts, linking wildlife reservoirs, domestic animals, and human populations within a common transmission network. This includes any vertical transmission from infected adults to offspring, a rare and poorly studied aspect of disease endemicity, as these potential pathogen reservoirs must be transmitted to the human host to cause morbidity and mortality (Boyles et al., 2020; Ferreira-de-Lima and Lima-Camara, 2018).

A mosquito population's potential to transmit pathogens is its vectorial capacity, which integrates key factors such as population density, biting frequency, survival, and vector competence (Smith et al., 2012). Vectorial capacity also depends on mosquito population genetics, virus strain, and environmental conditions, as well as mosquito blood-feeding behavior (Kramer and Ciota, 2015). For this reason, mosquito host choice is not a minor behavioral detail but a core determinant of transmission. Mosquitoes that feed mainly on birds participate in transmission systems that differ markedly from those of mosquitoes that feed mainly on humans, and mosquitoes that feed across wildlife, livestock, and humans can connect otherwise

separate host communities and facilitate spillover. Although mosquito-borne disease dynamics depend on vector competence, abundance, survival, climate, host immunity, and human behavior, host preference remains a central mechanism by which mosquito biology shapes epidemiological contact (Abbasi, 2025; Coutinho-Abreu et al., 2022; Takken and Verhulst, 2013).

Host preference can be defined as the repeatable tendency of a mosquito species or population to seek out, approach, land on, and feed on particular host types more often than would be expected from host availability alone (McIver, 1968; Takken and Verhulst, 2013). This distinction is important because hosts may be bitten frequently either because mosquitoes actively prefer them or because they are abundant, accessible, or poorly defended. The motivation to bite a host is also likely dependent on their nutritional or mating status (Clifton and Noriega, 2012; League et al., 2021). A clear understanding of mosquito host choice, therefore, requires separating intrinsic attraction from realized host use in the field.

This distinction has important implications for disease ecology. A mosquito may have some innate attraction to humans, yet feed mostly on other hosts where humans are scarce or difficult to access. Conversely, a species with broad sensory capacity may appear highly anthropophilic in urban settings because local host availability and habitat structure channel feeding onto humans (Fikrig and Harrington, 2021; Takken and Verhulst, 2013). Host preference is therefore best understood as the interaction between evolved sensory and behavioral biases and the ecological settings in which mosquitoes encounter hosts (Gao et al., 2025; Stone and Gross, 2018; Yan et al., 2021). This interaction helps determine whether transmission remains largely within wildlife, spills over only occasionally, or becomes sustained within human populations.

The epidemiological importance of host preference is especially evident when contrasting major mosquito-borne virus systems. In West Nile virus ecology, transmission is maintained primarily between bird-feeding *Culex* mosquitoes and avian hosts, whereas human infections increase when *Culex* mosquitoes also feed on mammals, thereby functioning as bridge vectors (Kothera et al., 2020; Riccetti et al., 2022; Rizzoli et al., 2015; Wehmeyer et al., 2024). In contrast, dengue and Zika are transmitted mainly in human-dominated settings, where repeated human feeding by *Aedes aegypti* sustains urban transmission (McBride et al., 2014; Pruszynski et al., 2020; Tenywa et al., 2025). These contrasting systems show that host preference helps determine not only who is exposed but also whether pathogens remain enzootic, sporadically spill over, or circulate efficiently in human populations.

Mosquitoes exhibit host-use patterns that range from broad generalism to strong specialization. Generalist mosquitoes may distribute bites across several vertebrate groups, in some settings reducing human exposure and in others increasing spillover by linking host communities that would otherwise remain weakly connected (Kilpatrick and Randolph, 2012; Riccetti et al., 2022). Specialist mosquitoes, by contrast, concentrate bites within narrower transmission networks, which can either stabilize wildlife circulation or intensify transmission within human populations depending on the hosts involved (McBride et al., 2014; Rizzoli et al., 2015; Rose et al., 2020). The ecological and epidemiological consequences of host choice therefore depend not only on which hosts are preferred, but also on how strongly that preference is expressed under varying natural conditions (Fikrig and Harrington, 2021; Takken and Verhulst, 2013; Yan et al., 2021).

This chapter approaches host preference as an evolutionary, mechanistic, ecological, and epidemiological trait. The opening section examines the evolution of host preference, with emphasis on ecological opportunity, natural selection, genomic divergence, and host shifts across mosquito lineages. The next section considers the sensory and molecular basis of host seeking, including olfactory, visual, thermal, humidity, and contact-dependent cues. A subsequent section explores the role of host preference in virus amplification, spillover, and urban transmission, with particular emphasis on *Ae. aegypti* and *Culex* mosquitoes, as well as the contrasting ecologies of Zika and West Nile viruses. Another section addresses the effects of urbanization, land-use change, climate, and vector control on host availability and realized host use. The chapter then turns to blood-meal analysis, metabarcoding, and xenosurveillance as tools for improving surveillance of mosquito-borne zoonoses. Taken together, these perspectives support the argument that mosquito host preference is a dynamic trait shaped by both evolutionary history and ecological context, and that this host preference should be treated as a central component of any effort to understand, predict, or manage mosquito-borne virus transmission.

2. Evolutionary drivers of host preference in mosquitoes

2.1 Ecological and selective drivers of host choice

Mosquito host preference evolves through a combination of ecological opportunity and inherited genetic variation. For most medically important female mosquitoes, blood feeding is necessary for egg production, but hosts

differ in abundance, accessibility, defensive behavior, nutritional value, and the environments in which they are encountered. Selection therefore acts not simply on whether mosquitoes obtain a blood meal, but on whether they obtain blood in ways that maximize survival and reproductive success (Lyimo and Ferguson, 2009; Stone and Gross, 2018; Swart et al., 2023; Takken and Verhulst, 2013).

One of the strongest ecological drivers of host choice is the predictability of host access across space and time. Humans often live in dense settlements, follow fairly predictable daily routines, and create reliable mosquito breeding sites through stored water and household containers. In *Ae. aegypti*, this combination appears to have been central to the evolution of human preference and domestication. A stronger preference for humans has been associated with drier climates and more urbanized environments, consistent with the idea that dependence on human water storage made human-associated habitats more reliable and reinforced selection for human preference (Facchinelli et al., 2023; Powell and Tabachnick, 2013; Rose et al., 2023, 2020). In this framework, host preference evolves not only because a host is attractive, but because feeding on that host is repeatedly profitable under local ecological conditions.

Host choice is also shaped by broader ecological context. Host community diversity, habitat structure, competition, and the local spatial arrangement of vertebrates all influence which hosts mosquitoes encounter and how often they do so. Recent DNA-based diet studies suggest that mosquito feeding patterns are often more flexible than previously assumed, with local ecological conditions playing a major role in determining which hosts are used (Lee et al., 2025). Landscape and meteorological variables have likewise been linked to *Ae. aegypti* and *Aedes albopictus* infestation in urban settings, illustrating how ecological context shapes the circumstances under which host encounters occur (Costa-da-Silva et al., 2024). These findings suggest that evolution acts on host-seeking within real ecological mosaics, where host availability, habitat predictability, and environmental stress jointly determine the fitness consequences of feeding decisions.

2.2 Genomic and sensory bases of host-linked divergence

Ecological conditions can favor certain feeding strategies, but lasting host preference can evolve only when heritable variation is available for selection to shape. Chemosensory receptor evolution in insects has been linked to host specialization, particularly through gene duplication (McBride and Arguello, 2007; Robertson, 2018). In mosquitoes, some of the clearest

evidence for this variation comes from the sensory systems involved in host detection. In *Ae. aegypti*, preference for humans has been linked to divergence in odorant receptor pathways and broader differences in chemosensory gene expression, indicating that host specialization is associated with molecular changes in odor detection and processing rather than with human proximity alone (DeGennaro et al., 2013; McBride et al., 2014; Tallon et al., 2019; Wolff and Riffell, 2018; Zhao et al., 2022). Comparable evidence is now emerging in *Culex pipiens*, where differential expression of antennal chemosensory genes has been associated with host preference across biotypes, suggesting that sensory divergence may be a common route through which host use evolves across mosquito lineages (Menon et al., 2025).

Genomic studies further show that differences in host use can be detected across both recent and long evolutionary timescales. Early work using closely related species in the *Anopheles gambiae* complex suggested that chromosomal inversions were associated with differences in host preference (Coluzzi et al., 1977). Studies in *Anopheles* mosquitoes continue to work towards understanding the genetic basis of host preference and adaptation to host habitats (Ayala et al., 2017; Besansky et al., 2004; Main et al., 2016). Similarly, additional studies in *Ae. aegypti* suggests that chromosomal inversions and other features of genome structure may also contribute to host preference, helping maintain differences among populations even when they continue to exchange genes (Kent et al., 2025; Liang et al., 2025). In *Ae. aegypti*, genome-wide analyses have traced the spread of the human-preferring domestic form and identified adaptive genetic signatures linked to domestication, host seeking, and other ecologically important traits (Crawford et al., 2025; Lozada-Chávez et al., 2025). These findings indicate that host preference is not a purely plastic trait, but one that can leave detectable signatures in population history and genome structure.

Host specialization may also arise without relying entirely on new mutations. In *Ae. aegypti*, a recent genomic study suggests that domestication and preference for humans developed at least in part from genetic variation already present in ancestral populations, along with local adaptation and changes in the regulation of chemosensory, neuronal, and metabolic pathways (Lozada-Chávez et al., 2025). This helps explain why host preference can evolve repeatedly, sometimes quite rapidly, when ecological conditions favor a particular host. It also suggests that when mosquitoes invade new environments, already evolved host-seeking traits can spread into new regions and encounter new selective pressures and host

communities. In this way, genomic divergence, sensory evolution, and ecological context are best understood as closely connected parts of host-preference evolution rather than as separate processes.

2.3 Comparative examples of host shifts across mosquito lineages

Ae. aegypti provides one of the clearest examples of a mosquito lineage that shifted toward humans. In this species, a strong preference for humans is closely linked to domestication, breeding in human-associated habitats, and sensory adaptation to human odor cues. Behavioral, ecological, and genomic evidence suggests that this specialization first evolved in Africa as mosquitoes became closely associated with human settlements, and that the human-adapted domestic form later spread worldwide (Crawford et al., 2025; Lozada-Chávez et al., 2025; McBride et al., 2014; Rose et al., 2023, 2020). The result is a mosquito lineage in which host preference, habitat use, and epidemiological importance have evolved together rather than independently.

Aedes albopictus provides a contrasting example of ecological flexibility. Unlike *Ae. aegypti*, this species often uses a broader range of hosts, and actual feeding patterns tend to vary with local host availability and habitat conditions. Field studies in suburban and invaded areas show that *Ae. albopictus* often feeds on humans, pets, and other vertebrates, depending on which hosts are locally available, rather than exhibiting strict host preference (Fikrig et al., 2022; Fikrig and Harrington, 2021; Richards et al., 2006). This flexibility may explain why invasion into a new region can quickly change the epidemiological importance of a population, even before longer-term evolutionary change occurs.

A third pattern is observed in the *Cx. pipiens* complex, where host use varies among biotypes, hybrids, and ecological settings. In general, feeding mainly on birds helps maintain West Nile virus and related flaviviruses in bird-mosquito cycles, whereas more frequent feeding on mammals raises the likelihood of spillover. Blood-meal and host-selection studies suggest that these differences are influenced by hybridization, urban habitats, and local host communities rather than by a fixed species-level preference (Apperson et al., 2004; Blom et al., 2024; Kothera et al., 2020; Molaei et al., 2006). In Europe, the underground form *molestus*, which is more associated with mammals, and the surface form *pipiens*, which is more associated with birds, illustrate how ecological divergence within a species complex can alter transmission potential (Farajollahi et al., 2011; Haba et al., 2025; Haba and McBride, 2022).

Mosquito host-preference evolution also extends beyond the familiar contrast between bird-feeding and mammal-feeding species. Some mosquitoes specialize on cold-blooded hosts such as amphibians, reptiles, or fish, demonstrating that host preference can evolve across diverse ecological contexts (Reinhold and Lahondère, 2024). Frog-biting mosquitoes are a good example. Some species, such as *Uranotaenia lowii*, feed mainly on amphibians, and mosquitoes may even specialize on different frog species within the same environment (Gould and Valdez, 2024; Silva et al., 2020). These cases show that specialization on humans is only one example of a broader evolutionary ability to diverge in host use.

These examples show that mosquito host preference can range from broad flexibility to strong specialization. Which pattern emerges depends on the combined effects of natural selection, sensory differences, genomic background, and ecological opportunity. Host preference is therefore best viewed as an adaptive trait shaped by both history and ecology, and one that can change with domestication, invasion, environmental change, and local host communities.

3. Mechanisms underlying host preference

Host preference in mosquitoes arises through a step-by-step sensory process in which mosquitoes detect, compare, and evaluate host cues at different distances. Host seeking does not depend on a single cue, but on the combined use of odors, visual signals, heat, humidity, and contact-dependent information gathered after landing. Because different cues matter more at different stages of approach, host preference reflects how mosquitoes combine and prioritize these signals in particular ecological settings rather than how they respond to any one cue alone (Coutinho-Abreu et al., 2022; Montell, 2025; Takken, 1990; Wolff and Riffell, 2018).

3.1 Olfactory cues and host odor discrimination

Olfaction provides the main basis for long-range host activation and discrimination. Carbon dioxide is one of the most important activators of mosquito host-seeking behavior (Dekker et al., 2005; McMeniman et al., 2014). Still, it does not by itself explain how mosquitoes distinguish among host species or among individual hosts. That discrimination depends on more complex blends of skin-, breath-, and microbiome-derived odorants. These odors arise from overlapping sources, including eccrine sweat, sebaceous

secretions, and microbial metabolism on the skin surface, and together they provide the chemical landscape through which mosquitoes identify hosts (Coutinho-Abreu et al., 2022; Montell, 2025; Takken, 1990).

In *Ae. aegypti*, several lines of evidence show that human attraction depends strongly on acidic skin volatiles and carboxylic acids. Behavioral studies and receptor-based experiments show that acidic odor compounds are important for normal attraction to human scent, and odor-coding studies indicate that certain classes of skin-derived acids contribute especially strongly to human attraction (Chen et al., 2019; Raji et al., 2019; Ray et al., 2023). Lactic acid alters how mosquitoes respond to human odor, indicating that certain chemicals in human sweat actively guide host-seeking behavior (Raji et al., 2019; Steib et al., 2001). More broadly, these studies show that mosquitoes do not respond to human odor as a single, uniform signal, but to complex chemical blends whose composition differs among host species.

The skin microbiome further modifies this process. Microbial metabolism converts host secretions into additional volatile compounds, and these microbiome-derived products can alter mosquito landing and feeding behavior. Experimental manipulation of skin-associated microbes has shown that reducing the production of certain attractive compounds can substantially reduce mosquito attraction and feeding, providing direct evidence that host-associated microbial communities shape mosquito host choice (Coutinho-Abreu et al., 2024; Liu et al., 2024; Lucas-Barbosa et al., 2023). A recent survey further suggests that some of the most distinctive features of human body odor derive from sebaceous secretions and their volatile derivatives, helping to explain why humans differ chemically from many other vertebrates in ways relevant to mosquito attraction (Zung and McBride, 2025).

Olfactory discrimination also operates within host species. Repeated behavioral assays have shown that some humans are consistently much more attractive to *Ae. aegypti* than others, and that these rankings remain stable across time. Furthermore, highly attractive individuals tend to produce higher levels of skin-derived carboxylic acids (Obaldia et al., 2022). This pattern is consistent with earlier evidence indicating that attractiveness to mosquitoes is partly inherited, suggesting that differences among hosts are biologically meaningful rather than temporary or environmentally driven (Fernández-Grandon et al., 2015). Recent evidence also suggests that different mosquito species do not rank the same humans in the same way, implying that host preference is shaped not only by host chemistry but also by species-specific

sensory interpretation of that chemistry (Marrero et al., 2026). Olfaction, therefore, contributes to both species-level host choice and fine-scale heterogeneity in host contact within human populations.

At the molecular level, olfactory-based behaviors depend on several classes of specialized receptors expressed in chemosensory appendages, primarily in the antenna, maxillary palp, and proboscis (Goldman et al., 2025; Herre et al., 2022; Matthews et al., 2016). In *Ae. aegypti*, a highly divergent family of chemosensory receptors called Odorant Receptors plays a critical role in detecting volatile odorants. Loss of the obligate co-receptor subunit, Orco, significantly reduces the strong preference for humans over guinea pigs, indicating that odorant receptor pathways play a major role in distinguishing hosts apart (DeGennaro et al., 2013). Acidic compounds associated with humans are detected in part through the Ionotropic Receptor pathways, helping to explain why carboxylic acids and related compounds are important for human attraction (Raji et al., 2019; Ray et al., 2023). Carbon dioxide is detected by gustatory receptor complexes, and disruption of the CO_2 receptor subunit Gr3 in *Ae. aegypti* greatly reduces attraction to host-related cues, showing that CO_2 detection is an important early step in multimodal host-seeking behavior (Kumar et al., 2020; McMeniman et al., 2014). Together, these studies show that mosquitoes distinguish hosts through the combined action of several receptor families rather than a single chemical pathway.

3.2 Visual cues and odor-gated host detection

Vision becomes especially important once odor has activated host seeking. Instead of acting independently, visual attraction is strongly shaped by olfactory context. In *Ae. aegypti*, wind-tunnel experiments showed that carbon dioxide exposure greatly increased attraction to certain wavelengths, especially cyan, orange, and red. That attraction to human skin tones disappeared when longer wavelengths were filtered out or when carbon dioxide detection or long-wavelength opsin function was disrupted (Alberto et al., 2022). These findings provide clear evidence that odor influences which visual cues become behaviorally important during host approach.

Visual responses are also flexible rather than fixed. When only carbon dioxide is present, *Ae. aegypti* shows a different pattern of color preference than when floral odors, egg-laying cues, or vertebrate host odors are also present, suggesting that visual evaluation depends on the wider sensory context in which a target is encountered (Blake and Riffell, 2025). Similar

species-specific color preferences have been reported in *Ae. albopictus* and *Cx. pipiens*, indicating that visual host orientation differs among mosquito taxa in ways that match broader differences in host use (Jung et al., 2021). Vision, therefore, does more than identify a host-like object by helping mosquitoes distinguish among targets together with odor-driven activation and the weighting of other cues.

This visual component also has a clear molecular basis. In *Ae. aegypti*, CRISPR-based disruption of long-wavelength opsin genes strongly reduced vision-guided attraction to visual targets, showing that host-related visual behavior depends on specific photoreceptor pathways rather than on a simple response to contrast alone (Zhan et al., 2021). The mosquito genome contains several opsin genes, and the long-wavelength opsins appear to be especially important for detecting the orange and red wavelengths associated with human skin. Disruption of both long-wavelength opsins had a stronger effect than disruption of either one alone, suggesting that these genes work in partly overlapping ways during visual host seeking (Zhan et al., 2021). These results match behavioral evidence that attraction to orange and red wavelengths depends on both smell and long-wavelength visual processing (Alberto et al., 2022). Visual host orientation is therefore best viewed as one part of a broader, context-dependent host-seeking process.

3.3 Thermal, infrared, and humidity cues in close-range host localization

As mosquitoes approach a host, heat, infrared radiation, and humidity become more important for pinpointing the target. These short-range cues help mosquitoes move from general host seeking to precise localization by detecting the warmth and moisture associated with a living host (Montell, 2025; Takken, 1990).

Experiments under semi-natural conditions show that heat alone is not enough to drive strong host attraction. In both *Ae. aegypti* and *An. gambiae*, mosquitoes were much more likely to orient to and land on warmed targets approximating human skin temperature when those targets were also presented with carbon dioxide and human odor. By contrast, heated targets without the appropriate odor context were only weakly attractive or unattractive, indicating that warmth is interpreted as a host cue only when paired with other signals that identify the target as biologically relevant (Giraldo et al., 2023; McMeniman et al., 2014). In *An. gambiae*, semi-field experiments further showed that the most attractive human subjects had odor

blends enriched in volatile carboxylic acids and certain microbiome-related compounds, reinforcing the close link between odor composition and thermotaxis during host selection (Giraldo et al., 2023). Recent work on *Ae. aegypti* has extended this picture by showing that thermal infrared radiation is part of the host-seeking repertoire and can serve as an effective mid-range directional cue when combined with carbon dioxide and other host-associated signals (Chandel et al., 2024). Together, these findings show that close-range host localization depends on the coordinated interpretation of odor, carbon dioxide, heat, humidity, and infrared radiation rather than on any single cue.

At the molecular level, thermal sensing in mosquitoes depends on specialized ion channels expressed in sensory appendages. One important component of this system is the ion channel TRPA1. In *Ae. aegypti*, female mosquitoes are attracted to targets with temperatures similar to those of vertebrate hosts. Still, they avoid targets that are too hot, showing that mosquitoes respond to a specific host-like temperature range rather than to heat in general. TRPA1 is required for this behavioral tuning because loss-of-function mosquitoes can no longer distinguish between harmless warmth and excessively hot surfaces (Corfas and Vosshall, 2015). More recent work also shows that TRPA1-dependent thermosensory neurons in the antennae contribute to infrared-guided approach to hosts, indicating that this pathway supports both temperature discrimination and host-directed orientation (Chandel et al., 2024; Corfas and Vosshall, 2015). Another class of ion channels shown to be important for mosquito thermotaxis is the ionotropic receptors. In *An. gambiae*, the ionotropic receptor subunit IR21a is required for heat-seeking and warmth-triggered blood-feeding behavior. This is especially notable because IR21a is related to a sensory pathway that functions as a cooling receptor in *Drosophila melanogaster*, suggesting that *An. gambiae* attraction to host heat may have evolved by modifying an evolutionarily more ancient temperature-sensing system for a new role in host-seeking behavior (Greppi et al., 2020; Laursen et al., 2023).

Humidity sensing provides an additional layer of close-range guidance in mosquitoes. In both *Ae. aegypti* and *An. gambiae*, IR93a-dependent sensory neurons are required for detecting nearby hosts and locating humid oviposition sites after blood feeding, thereby linking host-seeking and post-feeding behavior through shared hygrosensory pathways (Laursen et al., 2023). Additional work in *Ae. aegypti* has shown that dry-air-sensitive cells rely on IR40a, whereas humid-air-sensitive cells depend on IR68a, and that these pathways contribute differently to blood feeding and oviposition-site search

(Tang et al., 2024). Together, these findings indicate that mosquito humidity sensing is not a single uniform modality, but rather a set of molecularly and functionally distinct pathways that are differentially recruited across host-seeking and oviposition behaviors.

3.4 Contact chemosensation and post-landing host evaluation

Host choice does not end when a mosquito lands on a host. Once a mosquito reaches the skin surface, contact chemosensation helps determine whether probing continues, whether feeding begins, and whether the surface is accepted or rejected. This stage involves active sensory evaluation through structures such as the labellum, stylet, and legs rather than passive contact alone.

In *Ae. albopictus*, the labellum contains several classes of taste sensilla that respond to cues associated with humans, flowers, and oviposition sites. Experimental work shows that both excitatory and inhibitory responses occur at this stage and that inhibitory responses are especially informative, as they predict whether biting will continue (Baik et al., 2024). The same study found that some bitter compounds suppress both physiological and behavioral responses to sugar, whereas key tastants associated with human skin and sweat act together to promote biting. These findings suggest that post-landing decisions are controlled by a specialized gustatory system rather than by a simple continuation of earlier attraction.

Comparable evidence from *Ae. aegypti* shows that contact chemosensation is distributed across several peripheral structures. Functional studies have shown that the stylet and the proboscis can distinguish blood-like from nectar-like mixtures through combinatorial coding of contact cues. DEET can repel via olfactory detection or on contact by mosquito legs and suppress blood feeding before ingestion (DeGennaro et al., 2013; Dennis et al., 2019; Jové et al., 2020). At the molecular level, the TRP channel Painless1 has been implicated in gustatory avoidance of fatty acids on contact, extending the molecular basis of host evaluation beyond canonical gustatory receptors alone (Dhakal et al., 2026). Although similarly detailed work on other mosquito species remains limited, broader examination indicates that the labellum, stylet, and tarsi function as contact-sensing organs across mosquito genera, suggesting that post-landing evaluation is a general feature of mosquito feeding behavior (Coutinho-Abreu et al., 2022; Montell, 2025; Werner-Reiss et al., 1999). Host preference, therefore, does not end at the stage of long-range and mid-range attractive cues, but continues through contact-dependent acceptance or rejection at the host skin surface.

3.5 Neural coding, integration, internal state, and learning

The sensory systems involved in host-seeking behavior do not operate independently. Host preference emerges from the integration of multiple sensory inputs, and the outcome of that integration is shaped by physiological state, previous experience, and behavioral context. This helps explain why the same host cue can be evaluated differently across mosquito species, across individuals, and even across feeding states within the same individual.

Neural recording and imaging studies in *Ae. aegypti* show that the mosquito brain does not represent human odor through a simple labeled-line system, but through activity distributed across many neurons. Recordings from the antennal lobe indicate that a single odorant can activate multiple projection neurons in different glomeruli, and that both odor identity and behavioral relevance are encoded in these broader patterns of neural activity (Singh et al., 2023). Recent circuit and behavioral studies further suggest that *Ae. aegypti* processes human and animal odors differently, with dedicated olfactory glomeruli tuned to features that help distinguish humans from non-human hosts and are especially effective at driving host-seeking behavior (Zhao et al., 2022; Zhao and McBride, 2020). More recent work also shows that host-seeking behavior is not only multisensory but also flexible across sensory systems. In *Ae. aegypti*, impairment of one sensory pathway does not fully abolish attraction to humans, as mosquitoes can compensate by relying more heavily on other cues. The results indicate that host seeking is supported by cross-modal sensory compensation, with multiple sensory modalities working together to preserve attraction even when one pathway is disrupted (Morita et al., 2025). Together, these findings suggest that host preference depends not only on which odor molecules are detected but also on how the brain combines, compares, and prioritizes sensory information.

Internal state further shapes how mosquitoes respond to host cues. In *Ae. aegypti*, associative learning can change responses to those cues, and these effects depend on physiological condition and neuromodulatory signaling (Vinauger et al., 2018). Experimental work also shows that mating and sugar feeding alter blood-feeding physiology and behavior, indicating that the same host cues may be evaluated differently depending on energetic and reproductive state (League et al., 2021). Responses to humidity also vary with internal state, linking host-seeking to hydration status and to the later search for egg-laying sites (Laursen et al., 2023; Tang et al., 2024). Host seeking is

therefore not a fixed sensory reflex, but a flexible decision-making process shaped by sensory input, neural processing, physiological state, and prior experience.

Mosquito host preference emerges from the integrated action of multiple sensory systems. Smell, vision, heat, humidity, and contact cues are combined into a context-dependent behavioral decision. This process involves a wide range of molecular and neural components, including odorant receptors, ionotropic receptors, gustatory receptors, TRP channels, peripheral sensory pathways, and central neural circuits. Host preference is therefore not the result of a single cue or receptor, but the product of a flexible sensory system that mosquitoes use to identify and prioritize hosts.

4. Host preference and mosquito-borne virus transmission

4.1 Host specificity, amplification, and spillover

Host specificity shapes mosquito-borne virus transmission by determining which vertebrate hosts mosquitoes bite often enough to sustain pathogen circulation. In wildlife-associated systems, repeated feeding on competent reservoir or amplification hosts helps maintain enzootic transmission, whereas feeding that also connects those hosts to humans or livestock creates opportunities for bridge transmission and spillover. The epidemiological importance of a mosquito, therefore, depends not only on vector competence, abundance, or survival, but also on whether feeding remains concentrated within reservoir hosts or extends broadly enough to connect reservoir, amplification, and incidental hosts (Gao et al., 2025; Wu et al., 2025).

West Nile virus illustrates this pattern clearly, with transmission maintained mainly between bird-feeding *Culex* mosquitoes and birds, which serve as the main amplifying hosts. In contrast, humans and horses are usually incidental dead-end hosts that contribute little to onward transmission (Farajollahi et al., 2011; Riccetti et al., 2022; Rizzoli et al., 2015). In this system, the key epidemiological shift occurs when mosquito feeding crosses the bird-mammal boundary often enough to expose humans or other mammals to what is otherwise an avian transmission cycle. A broader survey of host-selection studies emphasizes that this shift depends on actual host use in local ecological settings rather than on a fixed species trait alone (Riccetti et al., 2022).

Japanese encephalitis follows a similar but more complex pattern. Ardeid wading birds, such as egrets and herons, help maintain the virus in nature, whereas pigs and livestock are especially important for viral amplification. When *Culex* mosquitoes feed frequently on birds and pigs and opportunistically on humans, these feeding links can connect enzootic and domestic transmission cycles, increasing spillover risk (Lindahl et al., 2012, 2013; Mulvey et al., 2021; Wu et al., 2025). In this type of system, transmission depends less on any single host class than on how mosquito feeding links several vertebrate compartments.

The same principle applies to other arboviruses. In Eastern Equine Encephalitis virus, strong feeding on birds by key vectors supports wildlife transmission cycles, reinforcing the broader point that bird-oriented feeding can stabilize enzootic amplification (Hassan et al., 2003; Simpson et al., 2009). In Rift Valley fever, mosquito feeding can focus transmission on livestock rather than on birds. Studies in Kenya found that mosquitoes frequently fed on cattle, sheep, and goats, indicating that domestic livestock can play a central role in shaping host contact and transmission. As a result, transmission may become organized mainly around farm animals rather than wildlife reservoirs (Tchouassi et al., 2016). Together, these examples show that host specificity helps determine which vertebrate carries most of the transmission burden and whether mosquitoes maintain enzootic cycles, generate bridge transmission, or support sustained amplification.

By contrast, in urban systems dominated by strongly human-preferring mosquitoes, repeated feeding on humans can maintain transmission largely within human populations. Dengue is the clearest example, and urban chikungunya, Zika, and yellow fever can follow the same pattern once those viruses enter densely populated settings where *Ae. aegypti* or other mosquitoes that frequently bite humans repeatedly encounter susceptible people (Weaver, 2005; Weaver and Forrester, 2015). In these systems, host preference influences not only who is exposed but also determines whether humans remain incidental hosts or become the primary amplifying population.

4.2 Case studies: Aedes aegypti - Zika and Dengue, Culex spp. - West Nile virus

Aedes aegypti illustrates why human-specialized mosquitoes are so effective in urban transmission. In many affected regions, this species served as the main urban vector because it combines a strong preference for humans, domestic breeding, a tendency to remain in and around human dwellings, and frequent human contact. Blood-meal analysis in the Florida Keys

showed that most identified meals in *Ae. aegypti* were human, consistent with the broader literature indicating that human blood indices are often very high in urban and peri-urban populations (Pruszynski et al., 2020). Similar patterns were reported in nonincorporated urban communities along the U.S.-Mexico border, where blood-meal analysis again showed strong feeding on humans despite lower-density urban conditions (Vera et al., 2023). Earlier field studies from Latin America, Southeast Asia, and Africa likewise found that *Ae. aegypti* commonly feeds predominantly on humans in domestic settings, with human feeding approaching near-exclusivity in some densely inhabited neighborhoods (Liebman et al., 2014; Ponlawat and Harrington, 2005; Scott et al., 1993). Together, these studies help explain why *Ae. aegypti* is quite effective at sustaining urban transmission once a human-amplified virus is introduced.

Zika provides a particularly clear example of this process. Because *Ae. aegypti* feeds repeatedly on humans, frequent human contact can facilitate rapid urban spread when mosquito populations are also highly susceptible to infection. Experimental infections showed that globally invasive *Ae. aegypti* populations were more susceptible to Zika virus than several noninvasive populations, suggesting that invasion history can further increase epidemic potential when repeated human feeding is already present (Aubry et al., 2020). The Cape Verde Zika epidemic provides another example in which epidemic intensity was argued to depend on enhanced vectorial capacity rather than on host contact alone (Rose et al., 2022).

A similar interaction between host preference and competence has also been reported more broadly in *Ae. aegypti* arbovirus systems. More recent surveillance in Dar es Salaam detected DENV-2 circulation in highly human-preferential, outdoor-biting *Ae. aegypti*, indicating that strong human feeding can sustain intense arbovirus circulation even when most host contact occurs outdoors rather than indoors (Tenywa et al., 2025). Similar patterns have been reported for dengue and Zika with substantial population-level and strain-specific differences in susceptibility (Gonçalves et al., 2014; Souza-Neto et al., 2019). Taken together, these studies show that *Ae. aegypti* populations become especially dangerous when frequent human contact coincides with high viral susceptibility.

West Nile virus provides a contrasting model because transmission is maintained mainly in a bird-mosquito cycle. In both North America and Europe, bird-feeding *Culex* mosquitoes play a central role in maintenance. At the same time, birds serve as the primary amplifying hosts, and humans and horses are usually incidental dead-end hosts that contribute little to onward

transmission (Farajollahi et al., 2011; Riccetti et al., 2022; Rizzoli et al., 2015). In this system, the key epidemiological question is not simply whether mosquitoes can bite humans, but how often feeding crosses from birds to mammals. Blood-meal studies show that *Culex* feeding often remains strongly focused on birds during enzootic amplification, but that host use can vary substantially across ecological settings. Classic studies from North America found that *Culex* vectors frequently fed predominantly on birds, while the degree of avian specialization varied by locality, season, host availability, and mosquito taxon (Apperson et al., 2004; Kilpatrick et al., 2006; Molaei et al., 2006). A broader survey reached the same general conclusion, emphasizing that realized host use depends heavily on local ecological conditions rather than on a single fixed species trait (Riccetti et al., 2022).

Human risk increases when feeding becomes more mixed and crosses the bird-mammal boundary often enough to create bridge transmission. Within the *Cx. pipiens* complex, blood-meal sources, and host-selection patterns have been associated with biotype identity and genetic admixture, suggesting that relatively small shifts in host use can alter the likelihood of spillover to humans (Kothera et al., 2020). More recent work in the Eastern Balkans and Camargue likewise showed that local *Cx. pipiens* host-feeding patterns have important implications for avian pathogen circulation and flavivirus risk, again underscoring that bridge transmission emerges from ecological variation in host feeding (Bobeva et al., 2025; Rodríguez-Valencia et al., 2025). Other field studies reached similar conclusions, indicating that spillover risk is shaped less by a fixed species-level tendency than by the timing and location of mosquito shifts from birds to mammals (Julian et al., 2010; Oduola and Awe, 2006). Taken together, these studies show that West Nile risk increases when bird-focused feeding broadens enough to connect avian amplification hosts to mammals.

4.3 Vectorial capacity, repeated feeding, and heterogeneity in host contact

Traditional studies of vectorial capacity emphasize mosquito density, biting rate, survival, competence, and how often humans are bitten (Smith et al., 2012). A mosquito may be abundant and competent yet contribute little to human transmission if most of its bites occur on non-human hosts. Conversely, a less abundant but strongly anthropophilic mosquito can have a disproportionate effect on human disease because its bites are concentrated on epidemiologically relevant hosts. Understanding how host preference can vary across vector species can improve the accuracy of models of vectorial capacity.

Repeated feeding behavior can amplify these effects by increasing both host contact and survival under stressful conditions. Modeling and experimental work showed that multiple blood-feeding bouts prolonged mosquito survival during dry periods and were predicted to increase viral transmission, indicating that host preference has stronger epidemiological consequences when feeding is frequent and repetitive rather than limited to one blood meal per gonotrophic cycle (Holmes et al., 2025). Earlier experimental work likewise showed that *Ae. aegypti* commonly take multiple blood meals within a single gonotrophic cycle, increasing opportunities for both acquisition and onward transmission (Ponlawat and Harrington, 2005; Scott et al., 1993). In highly anthropophilic mosquitoes, repeated or interrupted feeding can therefore place high-contact behavior directly into the human transmission network.

Environmental conditions further modify this relationship. Experimental studies found that higher temperatures reduced the vectorial capacity of *Aedes* mosquitoes for Zika virus, indicating that environmental stress can alter the relationships among host contact, survival, and competence (Onyango et al., 2020). A broader survey of *Ae. aegypti* vector competence similarly concluded that competence data must be interpreted alongside biting behavior, host contact, and ecology rather than in isolation (Souza-Neto et al., 2019). These findings reinforce the point that host preference is not an isolated behavioral parameter but rather one component of a larger transmission system in which environmental conditions influence how feeding behavior translates into epidemic potential.

Transmission consequences may also depend on how the infection alters mosquito behavior after exposure. Experimental work has shown that viral infection can interfere with mosquito host-seeking behavior, raising the possibility that pathogens may modify vector contact patterns in ways that alter onward transmission (Vogels et al., 2017). Although the magnitude and direction of such effects likely vary among systems, they reinforce the broader point that transmission depends not only on baseline host preference but also on the interaction between infection state and host-seeking behavior.

Taken together, these studies show that host preference affects far more than simple host identity. It shapes how vector competence is deployed across host populations, how often bridges form between host species, how repetitive feeding behavior amplifies contact, and how unevenly exposure is distributed within communities. Host preference is therefore one of the main behavioral pathways by which mosquito biology translates into transmission intensity.

5. Environmental and anthropogenic influences

Mosquito host preference is continually reshaped by urbanization, land-use change, climatic variation, and human interventions that alter host availability, habitat structure, and the costs and benefits of feeding on different hosts. For this reason, host preference is best understood not as a fixed species attribute, but as a dynamic ecological trait embedded in changing human landscapes (Takken and Verhulst, 2013; Vinauger and Chandrasegaran, 2024; Yan et al., 2021).

5.1 Urbanization, land-use change, and climate effects on host availability

Urbanization is one of the strongest present-day drivers of mosquito host preference because it alters both the host community and the physical environment in which host-seeking occurs. Cities concentrate humans, reduce many large vertebrate populations, elevate local temperatures, and create abundant artificial larval habitat through water storage, containers, drainage systems, and other infrastructure. These conditions often favor mosquitoes that are well adapted to locating and exploiting humans, especially the anthropophilic mosquito species such as *Ae. aegypti*. Across African populations of *Ae. aegypti*, stronger preference for humans has been associated with hotter, drier climates and more urbanized environments, supporting the view that human specialization is linked to human-dominated habitats rather than occurring equally across the species range (Rose et al., 2020). More broadly, ecological studies of urban mosquitoes have concluded that rapid urbanization can promote both the spread of *Aedes* mosquitoes and the persistence of the diseases they transmit by creating predictable access to hosts and persistent larval habitats (Kolimenakis et al., 2021).

Urban adaptation involves more than host choice alone. Urban adaptation also includes the physiological and life-history traits that allow mosquitoes to persist in human-modified habitats. Recent work on *Ae. aegypti* has shown that egg thermal tolerance is linked to urban adaptation and to traits that support persistence near humans, suggesting that cities may select not only for a stronger preference for humans but also for the ability to survive in hot, dry, and thermally variable environments (Chakraborty et al., 2025). This interpretation is consistent with the broader view arguing that thermotolerance is becoming increasingly important in blood-feeding arthropods as climate change, urban heat islands, and global movement reshape vector distributions and seasonal

persistence (Bonizzoni and Lahondère, 2026). Climatic adaptation may therefore reinforce host specialization by allowing mosquitoes to remain active and abundant where humans are most concentrated.

Urban areas contain many different habitat types, and those differences influence where mosquitoes thrive. Studies from coastal cities have shown that *Aedes* infestation is not evenly distributed across urban space, but instead varies with combinations of vegetation, built cover, moisture, and weather conditions (Costa-da-Silva et al., 2024; Sallam et al., 2017). Work in northern Spain documented medically important mosquitoes in urban green spaces and cemeteries, showing that important urban vector habitats extend beyond houses and household containers (Goiri et al., 2024). Comparable studies have identified storm drains, catch basins, vacant lots, construction sites, and refuse around homes as productive habitats for urban mosquitoes, including *Ae. aegypti*, *Ae. albopictus*, and *Culex* species (Paploski et al., 2016; Unlu et al., 2013; Wilke et al., 2019). Together, these findings show that urban transmission risk arises from a patchwork of habitat types in which human-dominated and wildlife-associated host communities may overlap.

Human-built environments can also support less obvious mosquito ecologies with distinct evolutionary histories. An ancient urban underground mosquito lineage has been linked to subterranean human-made habitats, showing that adaptation to built environments can have deep historical roots rather than being only a recent response to modern cities (Haba et al., 2025). This interpretation is consistent with earlier work on the *Cx. pipiens* complex, which has long documented associations of the *molestus* form with underground and enclosed urban habitats and has shown that belowground and aboveground populations can differ in ecology and host use (Byrne and Nichols, 1999; Epstein et al., 2021; Farajollahi et al., 2011). More broadly, sewers, flooded basements, stormwater systems, urban water bodies, cemeteries, and peri-urban wetlands can support mosquito populations exposed to different host communities, thermal conditions, and control pressures (Crocker et al., 2017; Goiri et al., 2024; Unlu et al., 2013). These findings complicate any simple distinction between "domestic" and "wild" mosquitoes and suggest that host preference may evolve across a wider range of human-made habitats than is often assumed.

Land-use change outside cities can be just as important, as it reshapes the host communities and habitats that arboviral vectors such as *Aedes* and *Culex* encounter. Deforestation, irrigation, agriculture, livestock farming, and wetland modification often bring wildlife, domestic animals, and

humans into closer contact while also creating or stabilizing larval habitat. Studies of *Aedes* and *Culex* in transformed landscapes show that host use often shifts with local vertebrate community structure, water management, and the arrangement of houses, animals, and breeding sites rather than remaining fixed at the species level (Cebrián-Camisón et al., 2020; Froxán-Grabalosa et al., 2025). More recent work in Kenya likewise found that land-use change shaped mosquito assemblages, host-feeding patterns, and arbovirus infection in landscapes where *Cx. pipiens sensu lato* and *Ae. aegypti* were both present, reinforcing the view that host contact in arboviral systems depends strongly on how land use reorganizes hosts, water, and opportunities for encounter (Getugi et al., 2026). Together, these studies show that land-use change can alter arbovirus risk not only by changing vector abundance but also by changing which hosts *Aedes* and *Culex* mosquitoes encounter and connect with.

Agricultural and livestock systems can be especially important because these systems can reorganize transmission around domestic amplifying hosts. In Kenya, host-choice experiments and blood-meal analysis showed substantial feeding on cattle, sheep, and goats by *Aedes*, *Culex*, and *Anopheles* species, demonstrating that domestic ungulates can strongly shape mosquito host choice and arbovirus ecology (Tchouassi et al., 2016). Experimental transmission work in a lamb-mosquito-lamb system further showed that successful mosquito feeding directly led to measurable onward transmission, linking host contact and feeding success to transmission efficiency (Bron et al., 2023). A similar logic applies to Japanese encephalitis and other multi-host systems in which pigs, birds, and humans occur close together, because land use can alter spillover risk by changing which host groups mosquitoes encounter most often and how frequently mosquitoes move between the hosts (Bouyer et al., 2025; Lindahl et al., 2012, 2013; Mulvey et al., 2021). Together, these examples show that farming systems can shape transmission not only by changing mosquito abundance but also by changing which domestic and wild hosts mosquitoes connect with.

These patterns are further complicated by climate change, which interacts with urbanization and land-use change and is predicted to alter the distribution of *Aedes* mosquitoes (Ryan et al., 2019). Temperature can affect mosquito development, survival, activity, gonotrophic timing, and biting frequency, whereas rainfall and humidity influence breeding-site persistence and the spatial distribution of hosts. Heat stress and altered rainfall can therefore shift both mosquito abundance and the relative

advantages of feeding on different hosts. Experimental work has shown that temperature can alter feeding-related components of transmission potential in *Aedes* mosquitoes, including survival and vectorial capacity for arboviruses (Onyango et al., 2020). More broadly, climate change, urban warming, altered precipitation, and infrastructure-mediated microclimates are likely to reshape the biology of blood-feeding arthropods, affecting both behavior and distribution (Bonizzoni and Lahondère, 2026). These findings suggest that host preference is embedded within broader environmental change, because warming and climatic stress not only alter mosquito abundance but also change which hosts mosquitoes encounter, when those hosts are available, and how favorable different feeding choices become.

5.2 Human interventions and unintended evolutionary or behavioral consequences

Human interventions can also reshape host preference, either directly or indirectly. Population control, water management, housing modification, screening, insecticide use, and other control measures can all change the costs and benefits of feeding on different hosts. Under these conditions, mosquitoes may shift the timing, location, or target of host-seeking; over longer timescales, these altered costs may impose selection on host-related behavior. Work on *Ae. aegypti* and other urban arboviral vectors has emphasized that control effectiveness depends heavily on mosquito behavior in the human environment, including where mosquitoes rest, where they bite, and how they exploit indoor and outdoor spaces (Achee et al., 2019; Facchinelli et al., 2023; Pates and Curtis, 2005). Evolutionary arguments have therefore suggested that mosquitoes with strong human preference may evolve away from human feeding if attacking humans becomes sufficiently costly due to insecticides, physical barriers, or other control measures (Stone and Gross, 2018). Housing improvements and integrated environmental interventions may likewise alter host contact by reducing mosquito access to humans or by changing the availability of larval habitat near homes (Alqassim, 2024; Bouzid et al., 2016). This possibility is important because control tools may have consequences that extend beyond immediate reductions in mosquito density, potentially altering how arboviral vectors encounter and prioritize hosts.

Behavioral evidence is consistent with this broader framework. Host use and biting behavior can vary substantially even in highly urban settings, indicating that preference for humans is not expressed in the same way

across all populations or contexts (Oduola and Awe, 2006; Pruszynski et al., 2020; Vera et al., 2023). At the same time, work on *Ae. aegypti* in Florida and East Africa shows that strongly human-preferring populations can remain epidemiologically important even when substantial biting occurs outdoors or across heterogeneous environments around homes (Pruszynski et al., 2020; Tenywa et al., 2025; Vera et al., 2023). These findings suggest that *Aedes* mosquito interventions focused only on indoor exposure leave a substantial fraction of transmission intact. More broadly, studies of arboviral vectors indicate that biting time, resting site, feeding location, and host use can all shape how mosquito populations respond to sustained control pressure, especially in human-dominated environments where indoor and outdoor host access differ (Achee et al., 2019; Facchinelli et al., 2023; Pates and Curtis, 2005; Vinauger and Chandrasegaran, 2024).

Human-associated environmental change also affects host behavior, which then feeds back into mosquito feeding patterns. Sleep schedules, outdoor evening activity, proximity to livestock, housing design, window and door screening, fan use, and household structure can all influence when and where mosquitoes encounter hosts. Studies of arbovirus transmission in changing human environments emphasize that these behavioral and infrastructural factors are central to realized exposure, especially in urban and peri-urban settings where *Aedes* and *Culex* mosquitoes exploit fine-scale differences in host accessibility, water storage, housing quality, and movement patterns (Cofone et al., 2025; Eder et al., 2018; Kolimenakis et al., 2021; Renard et al., 2023). From this perspective, host preference is not simply a property of the mosquito but rather a property of the mosquito–host encounter system, shaped jointly by mosquito and host behavior, infrastructure, and environmental change.

6. Zoonoses and disease emergence

6.1 Why host-use surveillance matters for predicting spillover

Host-use surveillance is vital for predicting spillover because it reveals whether mosquitoes feed on wildlife, domestic animals, or humans, influencing disease emergence. Mosquito-borne zoonoses often emerge at ecological interfaces where vectors, wildlife, domestic animals, and humans overlap. At these interfaces, host use helps determine whether mosquitoes remain within wildlife transmission cycles or connect those

cycles to humans. For this reason, understanding disease emergence requires more than documenting vector presence or pathogen prevalence. It also requires identifying which hosts mosquitoes are actually feeding on in the field to determine whether transmission remains concentrated within reservoir communities or spills into human populations (Kilpatrick and Randolph, 2012).

This point is especially important because many arboviruses circulate silently in wildlife for long periods before recognized human outbreaks occur. Spillover may follow environmental disruption, shifts in host communities, climatic anomalies, or increases in bridge-vector abundance. In these situations, surveillance based solely on mosquito abundance or virus detection can miss the central ecological question of whether mosquitoes are actually transmitting pathogens between host groups. Work in disturbed rainforest systems has shown that combining host-selection analysis with flavivirus screening can reveal multiple plausible transmission pathways operating simultaneously, including links among wildlife, domestic animals, and humans that would not be apparent from vector detection alone (Hoyos et al., 2021). Integrated molecular studies of wildlife-associated mosquito communities have similarly shown that identifying both blood-meal origin and pathogen presence can clarify host-vector-pathogen interactions far better than taxonomic surveillance alone (Hernández-Triana et al., 2020). These findings suggest that host-use data are essential for understanding not only where mosquitoes occur but also the epidemiological role they play.

Host-use surveillance is particularly valuable in systems where environmental change and behavioral plasticity occur together. In a disturbed tropical forest, joint analysis of host selection and flavivirus occurrence revealed several potential transmission pathways operating simultaneously, supporting the view that ecological disruption can increase the number of host links available to mosquitoes rather than simply increasing mosquito abundance (Hoyos et al., 2021). Similar logic likely applies in suburban landscapes, irrigated agricultural systems, fragmented forests, and expanding cities, where mosquitoes may move among wildlife, livestock, and humans in ways that increase spillover probability even without dramatic changes in total vector density (Rizzoli et al., 2015; Rose et al., 2020; Tchouassi et al., 2016). From a surveillance perspective, the crucial question is therefore not only how many mosquitoes are present, but whether local ecological change is increasing the frequency of bridge feeding across host groups.

6.2 Blood-meal analysis, metabarcoding, and xenosurveillance

Blood-meal analysis remains one of the most direct ways to reconstruct actual mosquito-host contact. Host use in the field often differs from host preference measured under laboratory or semi-field conditions, so direct evidence of feeding is essential. Recent studies from dengue-endemic and arbovirus-prone settings have documented substantial geographic variation in the realized host use of *Ae. aegypti* and *Ae. albopictus*, including strong human feeding in some urban settings and more mixed feeding where domestic animals or other vertebrates are readily available (Dias et al., 2025; Gonçalves et al., 2023; Jeyaprakasam et al., 2024). Earlier field studies reached similar conclusions, showing that blood-feeding patterns in *Aedes* and *Culex* are highly context-dependent and can shift with host density, habitat type, season, and local vertebrate community structure (Apperson et al., 2004; Liebman et al., 2014; Molaei et al., 2006). Blood-meal analysis, therefore, provides a direct view of actual transmission pathways rather than inferred ones.

Recent methodological advances have expanded this approach beyond simple host identification. Mosquito blood meals can now be used to assess vertebrate diversity, infer pathogen exposure, and reconstruct aspects of local host-contact networks in both humans and wildlife (Vieira et al., 2024). Recent studies further support the feasibility of using mosquito blood meals for wildlife pathogen surveillance. However, those studies also emphasize important constraints related to blood-meal digestion, sample quality, and the probabilistic nature of pathogen detection (Wisely et al., 2025). These approaches are especially valuable where direct sampling of wildlife or humans is logistically difficult, expensive, or ethically constrained.

Xenosurveillance extends this logic by using blood-feeding arthropods to recover information about pathogens circulating in host populations. Foundational work has shown that mosquito blood meals can be used to detect human bacteria, parasites, and viruses, providing proof of principle for mosquito-based surveillance of the human pathogen landscape (Fauver et al., 2017; Grubaugh et al., 2015). Related studies of viral metagenomics and molecular xenomonitoring have shown that blood-feeding arthropods can provide access to host and pathogen information that might otherwise be missed by conventional sampling (Brinkmann et al., 2016; Cameron and Ramesh, 2021). Although xenosurveillance does not replace direct epidemiological or veterinary surveillance, it offers a practical, complementary strategy for detecting pathogen circulation and potential spillover signals in complex ecological settings.

Metabarcoding approaches have further increased the information yield of these methods. Instead of identifying only the mosquito or only the host, integrated workflows can now recover information on the mosquito species, the vertebrate host, and associated pathogens from the same blood-fed individual (Johnson et al., 2025). This is especially important for emergence studies because it allows surveillance to move beyond parallel data streams and toward more direct reconstruction of host–vector–pathogen linkages. In rapidly changing environments, where assumptions about host use may quickly become outdated, such integrated approaches are likely to become increasingly valuable.

6.3 Toward network-based surveillance of host-vector-pathogen systems

Traditional vector surveillance often asks whether a known vector species is present or whether a pathogen has been detected in mosquitoes. A more informative approach asks which hosts local mosquitoes use, how those contacts are distributed across the landscape, and whether pathogens are detectable in the same blood-fed individuals (Hernández-Triana et al., 2020; Johnson et al., 2025; Vieira et al., 2024). In this framework, emergence risk depends not only on vector presence but also on the structure of the interaction network connecting vectors, hosts, and pathogens.

This network perspective also has implications for spatial scale. Standard mosquito surveillance often treats the human population as a relatively uniform host category, but growing evidence suggests that this assumption is too coarse. Experimental work in *Ae. aegypti* showed stable and repeatable differences in human attractiveness over time and linked high attractiveness to elevated levels of skin-derived carboxylic acids (Obaldia et al., 2022). Broader studies likewise conclude that mosquito attraction to humans is highly heterogeneous and that this heterogeneity can have important consequences for transmission by concentrating bites on particular individuals or groups (Martinez et al., 2021). Additional work suggests that mosquito species do not necessarily rank hosts in the same way, opening the possibility that host-contact structure may vary at fine spatial scales even within the same household or neighborhood environment (Marrero et al., 2026). These patterns suggest that emergence risk may cluster much more locally than standard trap counts reveal. A more informative surveillance framework would therefore combine blood-meal analysis with host-odor ecology, fine-scale vector mapping, and environmental data on host accessibility.

Another reason to integrate host-use data into surveillance is that infection itself may alter mosquito behavior. Experimental work has shown that viral infection can interfere with mosquito host-seeking behavior, suggesting that pathogen detection and host-use data should ideally be interpreted together whenever possible (Vogels et al., 2017). If infected mosquitoes contact hosts differently from uninfected mosquitoes, then surveillance based solely on baseline feeding patterns may miss important heterogeneities in transmission. This reinforces the value of approaches that capture mosquitoes, hosts, and pathogens within a single analytical framework, rather than treating them as separate monitoring targets.

These approaches support a more informative form of surveillance in which hosts, vectors, and pathogens are monitored as parts of a single interaction network. Blood-meal analysis, metabarcoding, xenosurveillance, and molecular xenomonitoring now make this increasingly feasible and, in many settings, may offer the clearest way to identify which host contacts are sustaining local transmission and where the next spillover event is most likely to emerge.

7. Conclusion

Host preference is a central determinant of mosquito-borne virus transmission because host preference governs which hosts mosquitoes contact, how often those contacts occur, and whether transmission remains confined to animal reservoirs or extends into human populations. Across the evidence reviewed in this chapter, host preference emerges not as a minor behavioral characteristic but as a key factor linking mosquito evolution, sensory biology, ecology, and disease transmission.

Host preference is an evolving trait shaped by ecological opportunity, natural selection, and heritable variation rather than a fixed property of a species. Host preference is also expressed through a flexible sensory and behavioral system in which odor, vision, heat, humidity, contact cues, neural processing, and internal state are integrated into context-dependent host choice. Because host use helps determine whether pathogens remain in enzootic cycles, spill over only occasionally, or circulate efficiently in human populations, host preference has direct epidemiological consequences. Host preference is continually reshaped by urbanization, land-use change, climate, and intervention, which alter host availability, habitat structure, and the costs and benefits of feeding on different hosts. Because

the hosts mosquitoes actually feed on in the wild often differ from the hosts they appear to prefer under laboratory conditions, direct evidence of feeding is essential for both surveillance and prediction.

To understand, predict, and manage mosquito-borne virus transmission, host preference must be treated as a central component of the system rather than as a background trait. Future progress will depend on integrating genomics, sensory biology, blood-meal ecology, experimental transmission, and fine-scale surveillance of host-vector contact. Host preference is not simply one trait among many in mosquito biology, but one of the clearest mechanisms by which ecological change translates into epidemic risk.

Acknowledgements

The development of this chapter was partially supported by the National Institute of Allergy and Infectious Diseases of the National Institutes of Health awards R01AI148551 and R01AI165560 (M.D.). We also thank the Centers for Disease Control and Prevention (CDC), Southeastern Center of Excellence in Vector-borne Disease (U01CK000662) for support to M.D. The funders did not have a role in the selection of studies for this review chapter, in the interpretation of literature, or in writing the manuscript.

References

Abbasi, E., 2025. *Aedes aegypti* and dengue: insights into transmission dynamics and viral lifecycle. Epidemiol. Infect. 153, e88. https://doi.org/10.1017/s0950268825100320.

Achee, N.L., Grieco, J.P., Vatandoost, H., Seixas, G., Pinto, J., Ching-NG, L., et al., 2019. Alternative strategies for mosquito-borne arbovirus control. PLoS Neglected Trop. Dis. 13, e0006822. https://doi.org/10.1371/journal.pntd.0006822.

Alberto, D.A.S., Rusch, C., Zhan, Y., Straw, A.D., Montell, C., Riffell, J.A., 2022. The olfactory gating of visual preferences to human skin and visible spectra in mosquitoes. Nat. Commun. 13, 555. https://doi.org/10.1038/s41467-022-28195-x.

Alqassim, A.Y., 2024. Social, behavioral and environmental determinants of vector-borne diseases: a narrative review of evidence and implications for integrated control approaches. J. Vector Borne Dis. 61, 525–535. https://doi.org/10.4103/jvbd.jvbd_34_24.

Apperson, C.S., Hassan, H.K., Harrison, B.A., Savage, H.M., Aspen, S.E., Farajollahi, A., et al., 2004. Host feeding patterns of established and potential mosquito vectors of west Nile Virus in the Eastern United States. Vector-Borne Zoonotic Dis. 4, 71–82. https://doi.org/10.1089/153036604773083013.

Aubry, F., Dabo, S., Manet, C., Filipović, I., Rose, N.H., Miot, E.F., et al., 2020. Enhanced Zika virus susceptibility of globally invasive *Aedes aegypti* populations. Science 370, 991–996. https://doi.org/10.1126/science.abd3663.

Ayala, D., Acevedo, P., Pombi, M., Dia, I., Boccolini, D., Costantini, C., et al., 2017. Chromosome inversions and ecological plasticity in the main African malaria mosquitoes. Evolution 71, 686–701. https://doi.org/10.1111/evo.13176.

Baik, L.S., Talross, G.J.S., Gray, S., Pattisam, H.S., Peterson, T.N., Nidetz, J.E., et al., 2024. Mosquito taste responses to human and floral cues guide biting and feeding. Nature 635, 639–646. https://doi.org/10.1038/s41586-024-08047-y.

Besansky, N.J., Hill, C.A., Costantini, C., 2004. No accounting for taste: host preference in malaria vectors. Trends Parasitol. 20, 249–251. https://doi.org/10.1016/j.pt.2004.03.007.

Blake, A.J., Riffell, J.A., 2025. Spectral preferences of mosquitos are altered by odors. J. Exp. Biol. 228, jeb250318. https://doi.org/10.1242/jeb.250318.

Blom, R., Krol, L., Langezaal, M., Schrama, M., Trimbos, K.B., Wassenaar, D., et al., 2024. Blood-feeding patterns of *Culex pipiens* biotype pipiens and pipiens/molestus hybrids in relation to avian community composition in urban habitats. Parasites Vectors 17, 95. https://doi.org/10.1186/s13071-024-06186-9.

Bobeva, A., Marinov, M.P., Klayn, S., Ilieva, M., Dimitrov, D., Zehtindjiev, P., 2025. Feeding preferences of mosquitoes (Culicidae) from the Eastern balkans and their role in transmission of avian Malaria. Integr. Zoöl. 21, 17–27. https://doi.org/10.1111/1749-4877.70018.

Bonizzoni, M., Lahondère, C., 2026. Blood-sucking arthropods in the Anthropocene: climate change thermotolerance, and global disease risks. Curr. Opin. Insect Sci. 75, 101506. https://doi.org/10.1016/j.cois.2026.101506.

Bouyer, J., Gil, D.A., Mora, I.P., Sorlí, V.D., Maiga, H., Mamai, W., et al., 2025. Suppression of *Aedes* mosquito populations with the boosted sterile insect technique in tropical and Mediterranean urban areas. Sci. Rep. 15, 17648. https://doi.org/10.1038/s41598-025-02795-1.

Bouzid, M., Brainard, J., Hooper, L., Hunter, P.R., 2016. Public health interventions for *Aedes* control in the time of Zikavirus– a meta-review on effectiveness of vector control strategies. PLoS Neglected Trop. Dis. 10, e0005176. https://doi.org/10.1371/journal.pntd.0005176.

Boyles, S.M., Mavian, C.N., Finol, E., Ukhanova, M., Stephenson, C.J., Hamerlinck, G., et al., 2020. Under-the-radar dengue virus infections in natural populations of *Aedes aegypti* mosquitoes. mSphere 5. https://doi.org/10.1128/msphere.00316-20.

Brinkmann, A., Nitsche, A., Kohl, C., 2016. Viral metagenomics on blood-feeding arthropods as a tool for human disease surveillance. Int. J. Mol. Sci. 17, 1743. https://doi.org/10.3390/ijms17101743.

Bron, G.M., Schreur, P.J.W., Jong, M.C.M. de, Keulen, L. van, Vloet, R.P.M., Koenraadt, C.J.M., et al., 2023. Quantifying Rift Valley fever virus transmission efficiency in a lamb-mosquito-lamb model. Front. Cell. Infect. Microbiol. 13, 1206089. https://doi.org/10.3389/fcimb.2023.1206089.

Byrne, K., Nichols, R.A., 1999. Culex pipiens in London underground tunnels: differentiation between surface and subterranean populations. Heredity 82, 7–15. https://doi.org/10.1046/j.1365-2540.1999.00412.x.

Cameron, M.M., Ramesh, A., 2021. The use of molecular xenomonitoring for surveillance of mosquito-borne diseases. Philos. Trans. R. Soc. B 376, 20190816. https://doi.org/10.1098/rstb.2019.0816.

Cebrián-Camisón, S., Puente, J.M. la, Figuerola, J., 2020. A literature review of host feeding patterns of invasive *Aedes* mosquitoes in Europe. Insects 11, 848. https://doi.org/10.3390/insects11120848.

Chakraborty, S., Zigmond, E., Shah, S., Dayal, D., Sylla, M., Akorli, J., et al., 2025. Thermal tolerance of *Aedes aegypti* mosquito eggs is associated with urban adaptation and human interactions. J. Therm. Biol. 131, 104167. https://doi.org/10.1016/j.jtherbio.2025.104167.

Chandel, A., DeBeaubien, N.A., Ganguly, A., Meyerhof, G.T., Krumholz, A.A., Liu, J., et al., 2024. Thermal infrared directs host-seeking behaviour in *Aedes aegypti* mosquitoes. Nature 633, 615–623. https://doi.org/10.1038/s41586-024-07848-5.

Chen, Z., Liu, F., Liu, N., 2019. Human odour coding in the yellow fever mosquito, *Aedes aegypti*. Sci. Rep., 13336. https://doi.org/10.1038/s41598-019-49753-2.

Clifton, M.E., Noriega, F.G., 2012. The fate of follicles after a blood meal is dependent on previtellogenic nutrition and juvenile hormone in *Aedes aegypti*. J. Insect Physiol. 58, 1007–1019. https://doi.org/10.1016/j.jinsphys.2012.05.005.

Cofone, L., Sabato, M., Paolo, C.D., Giovanni, S.D., Donato, M.A., Paglione, L., 2025. Urban, architectural, and socioeconomic factors contributing to the concentration of potential arbovirus vectors and arbovirosis in urban environments from a one health perspective: a systematic review. Sustainability 17, 4077. https://doi.org/10.3390/su17094077.

Coluzzi, M., Sabatini, A., Petrarca, Vi, Deco, M.A.D., 1977. Behavioural divergences between mosquitoes with different inversion karyotypes in polymorphic populations of the *Anopheles gambiae* complex. Nature 266, 832–833. https://doi.org/10.1038/266832a0.

Corfas, R.A., Vosshall, L.B., 2015. The cation channel TRPA1 tunes mosquito thermotaxis to host temperatures. Elife 4, e11750. https://doi.org/10.7554/elife.11750.

Costa-da-Silva, A.L., Dye-Braumuller, K.C., Wagner-Coello, H.U., Li, H., Johnson-Carson, D., Gunter, S.M., et al., 2024. Landscape and meteorological variables associated with *Aedes aegypti* and *Aedes albopictus* mosquito infestation in two southeastern U.S.A. coastal cities. J. Vector Ecol. 50, 28–38. https://doi.org/10.52707/1081-1710-50.1-28.

Coutinho-Abreu, I.V., Jamshidi, O., Raban, R., Atabakhsh, K., Merriman, J.A., Akbari, O.S., 2024. Identification of human skin microbiome odorants that manipulate mosquito landing behavior. Sci. Rep. 14, 1631. https://doi.org/10.1038/s41598-023-50182-5.

Coutinho-Abreu, I.V., Riffell, J.A., Akbari, O.S., 2022. Human attractive cues and mosquito host-seeking behavior. Trends Parasitol. 38, 246–264. https://doi.org/10.1016/j.pt.2021.09.012.

Crawford, J.E., Balcazar, D., Redmond, S., Rose, N.H., Youd, H.A., Lucas, E.R., et al., 2025. 1206 genomes reveal origin and movement of *Aedes aegypti* driving increased dengue risk. Science 389, eads3732. https://doi.org/10.1126/science.ads3732.

Crocker, W., Maute, K., Webb, C., French, K., 2017. Mosquito assemblages associated with urban water bodies; implications for pest and public health threats. Landsc. Urban. Plan 162, 115–125. https://doi.org/10.1016/j.landurbplan.2017.02.006.

DeGennaro, M., McBride, C.S., Seeholzer, L., Nakagawa, T., Dennis, E.J., Goldman, C., et al., 2013. *Orco* mutant mosquitoes lose strong preference for humans and are not repelled by volatile DEET. Nature 498, 487–491. https://doi.org/10.1038/nature12206.

Dekker, T., Geier, M., Cardé, R.T., 2005. Carbon dioxide instantly sensitizes female yellow fever mosquitoes to human skin odours. J. Exp. Biol. 208, 2963–2972. https://doi.org/10.1242/jeb.01736.

Dennis, E.J., Goldman, O.V., Vosshall, L.B., 2019. *Aedes aegypti* mosquitoes use their legs to sense DEET on contact. Curr. Biol. 29, 1551–1556.e5. https://doi.org/10.1016/j.cub.2019.04.004.

Dhakal, S., Bontempo, A.E., Singh, R., Dhavan, P., Montell, C., 2026. Gustatory avoidance of fatty acids by *Aedes aegypti* depends on an arthropod-specific TRP channel. Proc. Natl. Acad. Sci. 123, e2522818123. https://doi.org/10.1073/pnas.2522818123.

Dias, H.G., Garrido, I.O., Câmara, D.C.P., Stenn, T.M.S., Burkett-Cadena, N., Honório, N.A., et al., 2025. Blood-feeding patterns of mosquitoes (Diptera: Culicidae) collected in an area of high arbovirus transmission in West-Central Brazil. J. Méd. Èntomol. 62, 914–920. https://doi.org/10.1093/jme/tjaf041.

Eder, M., Cortes, F., Filha, N.T. de S., França, G.V.A. de, Degroote, S., Braga, C., et al., 2018. Scoping review on vector-borne diseases in urban areas: transmission dynamics, vectorial capacity and co-infection. Infect. Dis. Poverty 7, 90. https://doi.org/10.1186/s40249-018-0475-7.

Epstein, N.R., Saez, K., Polat, A., Davis, S.R., Aardema, M.L., 2021. The urban-adapted underground mosquito *Culex pipiens* form molestus maintains exogenously influenceable circadian rhythms. J. Exp. Biol. 224. https://doi.org/10.1242/jeb.242231.

Facchinelli, L., Badolo, A., McCall, P.J., 2023. Biology and behaviour of *Aedes aegypti* in the human environment: opportunities for vector control of arbovirus transmission. Viruses 15, 636. https://doi.org/10.3390/v15030636.

Farajollahi, A., Fonseca, D.M., Kramer, L.D., Kilpatrick, A.M., 2011. "Bird biting" mosquitoes and human disease: a review of the role of *Culex pipiens* complex mosquitoes in epidemiology. Infect., Genet. Evol. 11, 1577–1585. https://doi.org/10.1016/j.meegid.2011.08.013.

Fauver, J.R., Gendernalik, A., Weger-Lucarelli, J., Grubaugh, N.D., Brackney, D.E., Foy, B.D., et al., 2017. The use of xenosurveillance to detect human bacteria, parasites, and viruses in mosquito bloodmeals. Am. Soc. Trop. Med. Hyg. 97, 324–329. https://doi.org/10.4269/ajtmh.17-0063.

Fernández-Grandon, G.M., Gezan, S.A., Armour, J.A.L., Pickett, J.A., Logan, J.G., 2015. Heritability of attractiveness to mosquitoes. PLoS One 10, e0122716. https://doi.org/10.1371/journal.pone.0122716.

Ferreira-de-Lima, V.H., Lima-Camara, T.N., 2018. Natural vertical transmission of dengue virus in *Aedes aegypti* and *Aedes albopictus*: a systematic review. Parasites Vectors 11, 77. https://doi.org/10.1186/s13071-018-2643-9.

Fikrig, K., Harrington, L.C., 2021. Understanding and interpreting mosquito blood feeding studies: the case of *Aedes albopictus*. Trends Parasitol. 37, 959–975. https://doi.org/10.1016/j.pt.2021.07.013.

Fikrig, K., Martin, E., Dang, S., Fleur, K.S., Goldsmith, H., Qu, S., et al., 2022. The effects of host availability and fitness on *Aedes albopictus* blood feeding patterns in New York. Am. J. Trop. Med. Hyg. 106, 320–331. https://doi.org/10.4269/ajtmh.21-0157.

Froxán-Grabalosa, J., Mariani, S., Cerecedo-Iglesias, C., Richter-Boix, A., Torner, A.O., Pla, M., et al., 2025. Ecological drivers of arboviral disease risk: vector-host interfaces in a Mediterranean wetland of Northeastern Spain. PLOS Neglected Trop. Dis. 19, e0013447. https://doi.org/10.1371/journal.pntd.0013447.

Gao, H., Hu, W., Cui, C., Wang, Y., Zheng, Y., Jacobs-Lorena, M., et al., 2025. Emerging challenges for mosquito-borne disease control and the promise of symbiont-based transmission-blocking strategies. PLOS Pathog. 21, e1013431. https://doi.org/10.1371/journal.ppat.1013431.

Getugi, C., Kokwaro, E., Nyamache, A., Slothouwer, I., Rotich, G., Sang, R., et al., 2026. Land-use changes shape mosquito assemblages, host-feeding and arbovirus infection in Baringo County, Kenya. Infect., Genet. Evol. 139, 105913. https://doi.org/10.1016/j.meegid.2026.105913.

Giraldo, D., Rankin-Turner, S., Corver, A., Tauxe, G.M., Gao, A.L., Jackson, D.M., et al., 2023. Human scent guides mosquito thermotaxis and host selection under naturalistic conditions. Curr. Biol. 33, 2367–2382.e7. https://doi.org/10.1016/j.cub.2023.04.050.

Goiri, F., González, M.A., Cevidanes, A., Barandika, J.F., García-Peréz, A.L., 2024. Mosquitoes in urban green spaces and cemeteries in northern Spain. Parasites Vectors 17, 168. https://doi.org/10.1186/s13071-024-06263-z.

Goldman, O.V., DeFoe, A.E., Qi, Y., Jiao, Y., Weng, S.-C., Wick, B., et al., 2025. A single-nucleus transcriptomic atlas of the adult Aedes aegypti mosquito. Cell 188, 7267–7290.e26. https://doi.org/10.1016/j.cell.2025.10.008.

Gonçalves, A.A.L.M., Dias, A.H.C., Monteiro, D.D.S., Varela, I.B.F., Leal, S. da V., 2023. Blood meal survey reveals insights into mosquito-borne diseases on the island of Santiago, Cape Verde. Front. Trop. Dis. 4. https://doi.org/10.3389/fitd.2023.1070172.

Gonçalves, C.M., Melo, F.F., Bezerra, J.M., Chaves, B.A., Silva, B.M., Silva, L.D., et al., 2014. Distinct variation in vector competence among nine field populations of *Aedes aegypti* from a Brazilian dengue-endemic risk city. Parasites Vectors 7, 320. https://doi.org/10.1186/1756-3305-7-320.

Gould, J., Valdez, J.W., 2024. A little on the nose: a mosquito targets the nostrils of tree frogs for a blood meal. Ethology 130. https://doi.org/10.1111/eth.13424.

Greppi, C., Laursen, W.J., Budelli, G., Chang, E.C., Daniels, A.M., Giesen, L. van, et al., 2020. Mosquito heat seeking is driven by an ancestral cooling receptor. Science 367, 681–684. https://doi.org/10.1126/science.aay9847.

Grubaugh, N.D., Sharma, S., Krajacich, B.J., Fakoli III, L.S., Bolay, F.K., Diclaro II, J.W., et al., 2015. Xenosurveillance: a novel mosquito-based approach for examining the human-pathogen landscape. PLoS Neglected Trop. Dis. 9, e0003628. https://doi.org/10.1371/journal.pntd.0003628.

Haba, Y., Consortium‡, P., Korlević, P., McAlister, E., Lawniczak, M.K.N., Schumer, M., et al., 2025. Ancient origin of an urban underground mosquito. Science 390, eady4515. https://doi.org/10.1126/science.ady4515.

Haba, Y., McBride, L., 2022. Origin and status of *Culex pipiens* mosquito ecotypes. Curr. Biol. 32, R237–R246. https://doi.org/10.1016/j.cub.2022.01.062.

Hassan, H.K., Cupp, E.W., Hill, G.E., Katholi, C.R., Klingler, K., Unnasch, T.R., 2003. Avian host preference by vectors of eastern equine encephalomyelitis virus. Am. J. Trop. Med. Hyg. 69, 641–647. https://doi.org/10.4269/ajtmh.2003.69.641.

Hernández-Triana, L.M., Garza-Hernández, J.A., Morales, A.I.O., Prosser, S.W.J., Hebert, P.D.N., Nikolova, N.I., et al., 2020. An integrated molecular approach to untangling host-vector-pathogen interactions in mosquitoes (Diptera: Culicidae) from sylvan communities in Mexico. Front. Vet. Sci. 7, 564791. https://doi.org/10.3389/fvets.2020.564791.

Herre, M., Goldman, O.V., Lu, T.-C., Caballero-Vidal, G., Qi, Y., Gilbert, Z.N., et al., 2022. Non-canonical odor coding in the mosquito. Cell 185, 3104–3123.e28. https://doi.org/10.1016/j.cell.2022.07.024.

Holmes, C.J., Chakraborty, S., Ajayi, O.M., Uhran, M.R., Frigard, R., Stacey, C.L., et al., 2025. Multiple blood feeding bouts in mosquitoes allow for prolonged survival and are predicted to increase viral transmission during dry periods. iScience 28, 111760. https://doi.org/10.1016/j.isci.2025.111760.

Hoyos, J., Carrasquilla, M.C., León, C., Montgomery, J.M., Salyer, S.J., Komar, N., et al., 2021. Host selection pattern and flavivirus screening of mosquitoes in a disturbed Colombian rainforest. Sci. Rep. 11, 18656. https://doi.org/10.1038/s41598-021-98076-8.

Jeyaprakasam, N.K., Naidu, V.T.V., Vythilingam, I., Saeung, A., 2024. Blood meal analysis: unveiling the feeding preferences of *Aedes aegypti* and *Aedes albopictus* in a dengue-endemic area. Trop. Biomed. 41, 518–525. https://doi.org/10.47665/tb.41.4.013.

Johnson, B.J., Graham, M.C., Panahi, E., Vieira, C.J.S.P., Nath, N.S., Mason, P., et al., 2025. An all-in-one metabarcoding approach to mosquito and arbovirus xenosurveillance. Mol. Ecol. Resour. 25, e70022. https://doi.org/10.1111/1755-0998.70022.

Jové, V., Gong, Z., Hol, F.J.H., Zhao, Z., Sorrells, T.R., Carroll, T.S., et al., 2020. Sensory discrimination of blood and floral nectar by *Aedes aegypti* mosquitoes. Neuron. 108, 1163–1180.e12. https://doi.org/10.1016/j.neuron.2020.09.019.

Julian, E.G.-R., Bradley, J.B., Jose, A.F.-A., Maria, A.L.-P., Wilberth, A.C.C., Luis, F.F.-F., et al., 2010. Host-feeding preference of the mosquito, *Culex quinquefasciatus*, in Yucatan State, Mexico. J. Insect Sci. 10, 32. https://doi.org/10.1673/031.010.3201.

Jung, S.H., Kim, D., Jung, K.-S., Lee, D.-K., 2021. Color preference for host-seeking activity of *Aedes albopictus* and *Culex pipiens* (Diptera: Culicidae). J. Med. Entomol. 58, 2446–2452. https://doi.org/10.1093/jme/tjab100.

Kent, T.V., Schrider, D.R., Matute, D.R., 2025. Demographic history, genetic load, and the efficacy of selection in the globally invasive mosquito *Aedes aegypti*. Genome Biol. Evol. 17, evaf066. https://doi.org/10.1093/gbe/evaf066.

Kilpatrick, A.M., Kramer, L.D., Jones, M.J., Marra, P.P., Daszak, P., 2006. West Nile virus epidemics in north America are driven by shifts in mosquito feeding behavior. PLoS Biol. 4, e82. https://doi.org/10.1371/journal.pbio.0040082.

Kilpatrick, A.M., Randolph, S.E., 2012. Drivers, dynamics, and control of emerging vector-borne zoonotic diseases. Lancet 380, 1946–1955. https://doi.org/10.1016/s0140-6736(12)61151-9.

Kolimenakis, A., Heinz, S., Wilson, M.L., Winkler, V., Yakob, L., Michaelakis, A., et al., 2021. The role of urbanisation in the spread of *Aedes* mosquitoes and the diseases they transmit—A systematic review. PLoS Neglected Trop. Dis. 15, e0009631. https://doi.org/10.1371/journal.pntd.0009631.

Kothera, L., Mutebi, J.-P., Kenney, J.L., Saxton-Shaw, K., Ward, M.P., Savage, H.M., 2020. Bloodmeal, host selection, and genetic admixture analyses of *Culex pipiens* complex (Diptera: Culicidae) mosquitoes in Chicago, IL. J. Méd. Èntomol. 57, 78–87. https://doi.org/10.1093/jme/tjz158.

Kramer, L.D., Ciota, A.T., 2015. Dissecting vectorial capacity for mosquito-borne viruses. Curr. Opin. Virol 15, 112–118. https://doi.org/10.1016/j.coviro.2015.10.003.

Kumar, A., Tauxe, G.M., Perry, S., Scott, C.A., Dahanukar, A., Ray, A., 2020. Contributions of the conserved insect carbon dioxide receptor subunits to odor detection. Cell Rep. 31, 107510. https://doi.org/10.1016/j.celrep.2020.03.074.

Laursen, W.J., Budelli, G., Tang, R., Chang, E.C., Busby, R., Shankar, S., et al., 2023. Humidity sensors that alert mosquitoes to nearby hosts and egg-laying sites. Neuron 111, 874–887.e8. https://doi.org/10.1016/j.neuron.2022.12.025.

League, G.P., Degner, E.C., Pitcher, S.A., Hafezi, Y., Tennant, E., Cruz, P.C., et al., 2021. The impact of mating and sugar feeding on blood-feeding physiology and behavior in the arbovirus vector mosquito *Aedes aegypti*. PLoS Neglected Trop. Dis. 15, e0009815. https://doi.org/10.1371/journal.pntd.0009815.

Lee, M., O'Rorke, R., Clark, N.J., Webster, T.U., Wells, K., 2025. Diversity and plasticity in mosquito feeding patterns: a meta-analysis of 'Universal' DNA diet studies. Glob. Ecol. Biogeogr. 34. https://doi.org/10.1111/geb.70077.

Liang, J., Rose, N.H., Brusentsov, I.I., Lukyanchikova, V., Karagodin, D.A., Feng, Y., et al., 2025. Chromosomal inversions and their potential impact on the evolution of arboviral vector *Aedes aegypti*. Genome Biol. Evol. 17, evaf118. https://doi.org/10.1093/gbe/evaf118.

Liebman, K.A., Stoddard, S.T., Reiner, R.C., Perkins, T.A., Astete, H., Sihuincha, M., et al., 2014. Determinants of heterogeneous blood feeding patterns by *Aedes aegypti* in Iquitos, Peru. PLoS Neglected Trop. Dis. 8, e2702. https://doi.org/10.1371/journal.pntd.0002702.

Lindahl, J., Chirico, J., Boqvist, S., Thu, H.T.V., Magnusson, U., 2012. Occurrence of Japanese encephalitis virus mosquito vectors in relation to urban pig holdings. Am. J. Trop. Med. Hyg. 87, 1076–1082. https://doi.org/10.4269/ajtmh.2012.12-0315.

Lindahl, J.F., Ståhl, K., Chirico, J., Boqvist, S., Thu, H.T.V., Magnusson, U., 2013. Circulation of Japanese encephalitis virus in pigs and mosquito vectors within Can Tho City, Vietnam. PLoS Neglected Trop. Dis. 7, e2153. https://doi.org/10.1371/journal.pntd.0002153.

Liu, F., Coutinho-Abreu, I.V., Raban, R., Nguyen, T.T.D., Dimas, A.R., Merriman, J.A., et al., 2024. Engineered skin microbiome reduces mosquito attraction to mice. PNAS Nexus 3, pgae267. https://doi.org/10.1093/pnasnexus/pgae267.

Lozada-Chávez, A.N., Lozada-Chávez, I., Alfano, N., Palatini, U., Sogliani, D., Elfekih, S., et al., 2025. Adaptive genomic signatures of globally invasive populations of the yellow fever mosquito *Aedes aegypti*. Nat. Ecol. Evol. 9, 652–671. https://doi.org/10.1038/s41559-025-02643-5.

Lucas-Barbosa, D., Balvers, C., Bellantuono, A.J., Castillo, J.S., Costa-da-Silva, A.L., Moraes, C.M.D., et al., 2023. Competition matters: using in vitro community models to study the impact of human skin bacteria on mosquito attraction. Front. Ecol. Evol. 11, 1156311. https://doi.org/10.3389/fevo.2023.1156311.

Lyimo, I.N., Ferguson, H.M., 2009. Ecological and evolutionary determinants of host species choice in mosquito vectors. Trends Parasitol. 25, 189–196. https://doi.org/10.1016/j.pt.2009.01.005.

Main, B.J., Lee, Y., Ferguson, H.M., Kreppel, K.S., Kihonda, A., Govella, N.J., et al., 2016. The genetic basis of host preference and resting behavior in the major African Malaria vector, *Anopheles arabiensis*. PLoS Genet. 12, e1006303. https://doi.org/10.1371/journal.pgen.1006303.

Marrero, K.M., Castillo, J.S., Barbosa, D.L., Bellantuono, A.J., Marrero, M.A., Cid, D., et al., 2026. Individual humans attract different mosquito species. bioRxiv. https://doi.org/10.64898/2026.01.30.702931.

Martinez, J., Showering, A., Oke, C., Jones, R.T., Logan, J.G., 2021. Differential attraction in mosquito–human interactions and implications for disease control. Philos. Trans. R. Soc. B. 376, 20190811. https://doi.org/10.1098/rstb.2019.0811.

Matthews, B.J., McBride, C.S., DeGennaro, M., Despo, O., Vosshall, L.B., 2016. The neurotranscriptome of the *Aedes aegypti* mosquito. BMC Genomics 17, 32. https://doi.org/10.1186/s12864-015-2239-0.

McBride, C.S., Arguello, J.R., 2007. Five Drosophila genomes reveal nonneutral evolution and the signature of host specialization in the chemoreceptor superfamily. Genetics 177, 1395–1416. https://doi.org/10.1534/genetics.107.078683.

McBride, C.S., Baier, F., Omondi, A.B., Spitzer, S.A., Lutomiah, J., Sang, R., et al., 2014. Evolution of mosquito preference for humans linked to an odorant receptor. Nature 515, 222–227. https://doi.org/10.1038/nature13964.

McIver, S.B., 1968. Host preferences and discrimination by the mosquitoes *Aedes aegypti* and *Culex tarsali* (Diptera: Culicidae). J. Med. entomology 5, 422–428.

McMeniman, C.J., Corfas, R.A., Matthews, B.J., Ritchie, S.A., Vosshall, L.B., 2014. Multimodal integration of carbon dioxide and other sensory cues drives mosquito attraction to humans. Cell 156, 1060–1071. https://doi.org/10.1016/j.cell.2013.12.044.

Menon, R., Ignell, R., Hill, S.R., 2025. Differential expression of antennal chemosensory genes related to host preference of *Culex pipiens* biotypes. Parasites Vectors 18, 372. https://doi.org/10.1186/s13071-025-07028-y.

Molaei, G., Andreadis, T.G., Armstrong, P.M., Anderson, J.F., Vossbrinck, C.R., 2006. Host feeding patterns of culex mosquitoes and west Nile Virus transmission, northeastern United States - volume 12, number 3—March 2006 - emerging infectious diseases Journal - CDC. Emerg. Infect. Dis. 12, 468–474. https://doi.org/10.3201/eid1203.051004.

Montell, C., 2025. The sensory arsenal mosquitoes use to find us. Trends Parasitol 41, 591–602. https://doi.org/10.1016/j.pt.2025.05.004.

Morita, T., Lyn, N.G., Heynitz, R.K. von, Goldman, O.V., Sorrells, T.R., DeGennaro, M., et al., 2025. Cross-modal sensory compensation increases mosquito attraction to humans. Sci. Adv. 11, eadn5758. https://doi.org/10.1126/sciadv.adn5758.

Mulvey, P., Duong, V., Boyer, S., Burgess, G., Williams, D.T., Dussart, P., et al., 2021. The ecology and evolution of Japanese encephalitis virus. Pathogens 10, 1534. https://doi.org/10.3390/pathogens10121534.

Obaldia, M.E.D., Morita, T., Dedmon, L.C., Boehmler, D.J., Jiang, C.S., Zeledon, E.V., et al., 2022. Differential mosquito attraction to humans is associated with skin-derived carboxylic acid levels. Cell 185, 4099–4116.e13. https://doi.org/10.1016/j.cell.2022.09.034.

Oduola, A.O., Awe, O.O., 2006. Behavioural biting preference of *Culex quinquefasciatus* in human host in Lagos metropolis Nigeria. J. Vector Borne Dis. 43, 16–20.

Onyango, M.G., Bialosuknia, S.M., Payne, A.F., Mathias, N., Kuo, L., Vigneron, A., et al., 2020. Increased temperatures reduce the vectorial capacity of *Aedes* mosquitoes for Zika virus. Emerg. Microbes & Infect. 9, 67–77. https://doi.org/10.1080/22221751.2019.1707125.

Paixão, E.S., Teixeira, M.G., Rodrigues, L.C., 2018. Zika, chikungunya and dengue: the causes and threats of new and re-emerging arboviral diseases. BMJ Glob. Heal. 3, e000530. https://doi.org/10.1136/bmjgh-2017-000530.

Paploski, I.A.D., Rodrigues, M.S., Mugabe, V.A., Kikuti, M., Tavares, A.S., Reis, M.G., et al., 2016. Storm drains as larval development and adult resting sites for *Aedes aegypti* and *Aedes albopictus* in Salvador, Brazil. Parasites Vectors 9, 419. https://doi.org/10.1186/s13071-016-1705-0.

Pates, H., Curtis, C., 2005. Mosquito behavior and vector control. Annu. Rev. Entomol. 50, 53–70. https://doi.org/10.1146/annurev.ento.50.071803.130439.

Ponlawat, A., Harrington, L.C., 2005. Blood feeding patterns of *Aedes aegypti* and *Aedes albopictus* in Thailand. J. Méd. Èntomol. 42, 844–849. https://doi.org/10.1093/jmedent/42.5.844.

Powell, J.R., Tabachnick, W.J., 2013. History of domestication and spread of *Aedes aegypti* - a review. Memórias Inst. Oswaldo Cruz 108, 11–17. https://doi.org/10.1590/0074-0276130395.

Pruszynski, C.A., Stenn, T., Acevedo, C., Leal, A.L., Burkett-Cadena, N.D., 2020. Human blood feeding by *Aedes aegypti* (Diptera: Culicidae) in the Florida Keys and a review of the literature. J. Med. Entomol. 57, 1640–1647. https://doi.org/10.1093/jme/tjaa083.

Raji, J.I., Melo, N., Castillo, J.S., Gonzalez, S., Saldana, V., Stensmyr, M.C., et al., 2019. *Aedes aegypti* mosquitoes detect acidic volatiles found in human odor using the IR8a pathway. Curr. Biol. 29, 1253–1262.e7. https://doi.org/10.1016/j.cub.2019.02.045.

Ray, G., Huff, R.M., Castillo, J.S., Bellantuono, A.J., DeGennaro, M., Pitts, R.J., 2023. Carboxylic acids that drive mosquito attraction to humans activate ionotropic receptors. PLOS Neglected Trop. Dis. 17, e0011402. https://doi.org/10.1371/journal.pntd.0011402.

Reinhold, J.M., Lahondère, C., 2024. Mosquitoes feeding on ectothermic hosts: from host seeking to pathogen transmission. Curr. Opin. Insect Sci. 66, 101273. https://doi.org/10.1016/j.cois.2024.101273.

Renard, A., Lombardini, F.P., Zapata, M.P., Porphyre, T., Bento, A., Suzán, G., et al., 2023. Interaction of human behavioral factors shapes the transmission of arboviruses by *Aedes* and *Culex* mosquitoes. Pathogens 12, 1421. https://doi.org/10.3390/pathogens12121421.

Riccetti, N., Fasano, A., Ferraccioli, F., Gomez-Ramirez, J., Stilianakis, N.I., 2022. Host selection and forage ratio in West Nile virus–transmitting *Culex* mosquitoes: challenges and knowledge gaps. PLOS Neglected Trop. Dis. 16, e0010819. https://doi.org/10.1371/journal.pntd.0010819.

Richards, S.L., Ponnusamy, L., Unnasch, T.R., Hassan, H.K., Apperson, C.S., 2006. Host-feeding patterns of *Aedes albopictus* (Diptera: Culicidae) in relation to availability of human and domestic animals in suburban landscapes of central North Carolina. J. Med. Entomol. 43, 543–551. https://doi.org/10.1093/jmedent/43.3.543.

Rizzoli, A., Bolzoni, L., Chadwick, E.A., Capelli, G., Montarsi, F., Grisenti, M., et al., 2015. Understanding west Nile virus ecology in Europe: *Culex pipiens* host feeding preference in a hotspot of virus emergence. Parasites Vectors 8, 213. https://doi.org/10.1186/s13071-015-0831-4.

Robertson, H.M., 2018. Molecular evolution of the major arthropod chemoreceptor gene families. Annu. Rev. Entomol. 64, 1–16. https://doi.org/10.1146/annurev-ento-020117-043322.

Rodríguez-Valencia, V., Olive, M., Goff, G.L., Faisse, M., Bourel, M., L'Ambert, G., et al., 2025. Host-feeding preferences of *Culex pipiens* and its potential significance for flavivirus transmission in the Camargue, France. Med. Vet. Entomol. 39, 614–625. https://doi.org/10.1111/mve.12802.

Rose, N.H., Badolo, A., Sylla, M., Akorli, J., Otoo, S., Gloria-Soria, A., et al., 2023. Dating the origin and spread of specialization on human hosts in *Aedes aegypti* mosquitoes. eLife 12, e83524. https://doi.org/10.7554/elife.83524.

Rose, N.H., Dabo, S., Leal, S. da V., Sylla, M., Diagne, C.T., Faye, Oumar, et al., 2022. Enhanced mosquito vectorial capacity underlies the Cape Verde Zika epidemic. PLOS Biol. 20, e3001864. https://doi.org/10.1371/journal.pbio.3001864.

Rose, N.H., Sylla, M., Badolo, A., Lutomiah, J., Ayala, D., Aribodor, O.B., et al., 2020. Climate and urbanization drive mosquito preference for humans. Curr. Biol. 30, 3570–3579.e6. https://doi.org/10.1016/j.cub.2020.06.092.

Ryan, S.J., Carlson, C.J., Mordecai, E.A., Johnson, L.R., 2019. Global expansion and redistribution of *Aedes*-borne virus transmission risk with climate change. PLoS Neglected Trop. Dis. 13, e0007213. https://doi.org/10.1371/journal.pntd.0007213.

Sallam, M.F., Fizer, C., Pilant, A.N., Whung, P.-Y., 2017. Systematic review: land cover, meteorological, and socioeconomic determinants of *Aedes* mosquito habitat for risk mapping. Int. J. Environ. Res. Public. Heal. 14, 1230. https://doi.org/10.3390/ijerph14101230.

Scott, T.W., Clark, G.G., Lorenz, L.H., Amerasinghe, P.H., Reiter, P., Edman, J.D., 1993. Detection of multiple blood feeding in *Aedes aegypti* (Diptera: Culicidae) during a single gonotrophic cycle using a histologic technique. J. Méd. Èntomol. 30, 94–99. https://doi.org/10.1093/jmedent/30.1.94.

Silva, W.A.P.P. de, Bernal, X.E., Chathuranga, W.G.D., Herath, B.P., Ekanayake, C., Abeysundara, H.T.K., et al., 2020. Feeding patterns revealed host partitioning in a community of frog-biting mosquitoes. Ecol. Entomol. 45, 988–996. https://doi.org/10.1111/een.12874.

Simpson, J.E., Folsom-O'Keefe, C.M., Childs, J.E., Simons, L.E., Andreadis, T.G., Diuk-Wasser, M.A., 2009. Avian host-selection by culex pipiens in experimental trials. PLoS ONE 4, e7861. https://doi.org/10.1371/journal.pone.0007861.

Singh, P., Goyal, S., Gupta, S., Garg, S., Tiwari, A., Rajput, V., et al., 2023. Combinatorial encoding of odors in the mosquito antennal lobe. Nat. Commun. 14, 3539. https://doi.org/10.1038/s41467-023-39303-w.

Smith, D.L., Battle, K.E., Hay, S.I., Barker, C.M., Scott, T.W., McKenzie, F.E., 2012. Ross, Macdonald, and a theory for the dynamics and control of mosquito-transmitted pathogens. PLoS Pathog. 8, e1002588. https://doi.org/10.1371/journal.ppat.1002588.

Souza-Neto, J.A., Powell, J.R., Bonizzoni, M., 2019. *Aedes aegypti* vector competence studies: a review. Infect., Genet. Evol. 67, 191–209. https://doi.org/10.1016/j.meegid.2018.11.009.

Steib, B.M., Geier, M., Boeckh, J., 2001. The effect of lactic acid on odour-related host preference of yellow fever mosquitoes. Chem. Senses 26, 523–528. https://doi.org/10.1093/chemse/26.5.523.

Stone, C., Gross, K., 2018. Evolution of host preference in anthropophilic mosquitoes. Malar. J. 17, 257. https://doi.org/10.1186/s12936-018-2407-1.

Swart, M.M. de, Balvers, C., Verhulst, N.O., Koenraadt, C.J.M., 2023. Effects of host blood on mosquito reproduction. Trends Parasitol. 39, 575–587. https://doi.org/10.1016/j.pt.2023.04.003.

Takken, W., 1990. The role of olfaction in host-seeking of mosquitoes: a review. Int. J. Trop. Insect Sci. 12, 287–295. https://doi.org/10.1017/s1742758400020816.

Takken, W., Verhulst, N.O., 2013. Host preferences of blood-feeding mosquitoes. Annu. Rev. Entomol. 58, 433–453. https://doi.org/10.1146/annurev-ento-120811-153618.

Tallon, A.K., Hill, S.R., Ignell, R., 2019. Sex and age modulate antennal chemosensory-related genes linked to the onset of host seeking in the yellow-fever mosquito, *Aedes aegypti*. Sci. Rep-uk 9, 43. https://doi.org/10.1038/s41598-018-36550-6.

Tang, R., Busby, R., Laursen, W.J., Keane, G.T., Garrity, P.A., 2024. Functional dissection of mosquito humidity sensing reveals distinct dry and moist cell contributions to blood feeding and oviposition. Proc. Natl. Acad. Sci. 121, e2407394121. https://doi.org/10.1073/pnas.2407394121.

Tchouassi, D.P., Okiro, R.O.K., Sang, R., Cohnstaedt, L.W., McVey, D.S., Torto, B., 2016. Mosquito host choices on livestock amplifiers of Rift Valley fever virus in Kenya. Parasites Vectors 9, 184. https://doi.org/10.1186/s13071-016-1473-x.

Tenywa, F.S.C., Hälg, S., Makame, H., Moore, J., Dogan, O., Mapipi, H.I., et al., 2025. DENV-2 circulation and host preference among highly anthropophilic, outdoor-biting *Aedes aegypti* in Dar es Salaam, Tanzania. Viruses 17, 818. https://doi.org/10.3390/v17060818.

Unlu, I., Farajollahi, A., Strickman, D., Fonseca, D.M., 2013. Crouching tiger, hidden trouble: urban sources of *Aedes albopictus* (Diptera: Culicidae) refractory to source-reduction. PLoS ONE 8, e77999. https://doi.org/10.1371/journal.pone.0077999.

Vera, A.J., Soliz, A.G., Mora-Covarrubias, A.D., la, Watts, D.M., 2023. Host feeding preference by Aedes aegypti at two nonincorporated urban communities along the U.S.-Mexico border. Southwest. Entomol. 48, 563–568. https://doi.org/10.3958/059.048.0307.

Vieira, C.J.S.P., Gyawali, N., Onn, M.B., Shivas, M.A., Shearman, D., Darbro, J.M., et al., 2024. Mosquito bloodmeals can be used to determine vertebrate diversity, host preference, and pathogen exposure in humans and wildlife. Sci. Rep. 14, 23203. https://doi.org/10.1038/s41598-024-73820-y.

Vinauger, C., Chandrasegaran, K., 2024. Context-specific variation in life history traits and behavior of *Aedes aegypti* mosquitoes. Front. Insect Sci. 4, 1426715. https://doi.org/10.3389/finsc.2024.1426715.

Vinauger, C., Lahondère, C., Wolff, G.H., Locke, L.T., Liaw, J.E., Parrish, J.Z., et al., 2018. Modulation of host learning in *Aedes aegypti* mosquitoes. Curr. Biol. 28, 333–344.e8. https://doi.org/10.1016/j.cub.2017.12.015.

Vogels, C.B.F., Fros, J.J., Pijlman, G.P., Loon, J.J.A. van, Gort, G., Koenraadt, C.J.M., 2017. Virus interferes with host-seeking behaviour of mosquito. J. Exp. Biol. 220, 3598–3603. https://doi.org/10.1242/jeb.164186.

Weaver, S.C., 2005. Infectious diseases from nature: mechanisms of viral emergence and persistence. Arch. Virol. Suppl. 33–44. https://doi.org/10.1007/3-211-29981-5_4.

Weaver, S.C., Forrester, N.L., 2015. Chikungunya: evolutionary history and recent epidemic spread. Antivir. Res. 120, 32–39. https://doi.org/10.1016/j.antiviral.2015.04.016.

Wehmeyer, M.L., Jaworski, L., Jöst, H., Şuleşco, T., Rauhöft, L., Afonso, S.M.M., et al., 2024. Host attraction and host feeding patterns indicate generalist feeding of *Culex pipiens s.s.* and *Cx. torrentium*. Parasites Vectors 17, 369. https://doi.org/10.1186/s13071-024-06439-7.

Wei, Y.-L., Wu, Z., Li, R.-L., Tang, F., 2025. Review of selected mosquito-borne diseases: arboviruses (dengue, chikungunya, Zika, West Nile, Japanese encephalitis, yellow fever) and parasitic diseases (malaria, lymphatic Filariasis). Front. Public. Heal. 13, 1712094. https://doi.org/10.3389/fpubh.2025.1712094.

Werner-Reiss, U., Galun, R., Crnjar, R., Liscia, A., 1999. Factors modulating the blood feeding behavior and the electrophysiological responses of labral apical chemoreceptors to adenine nucleotides in the mosquito *Aedes aegypti* (Culicidae). J. Insect Physiol. 45, 801–808. https://doi.org/10.1016/s0022-1910(98)00153-x.

Wilke, A.B.B., Chase, C., Vasquez, C., Carvajal, A., Medina, J., Petrie, W.D., et al., 2019. Urbanization creates diverse aquatic habitats for immature mosquitoes in urban areas. Sci. Rep. 9, 15335. https://doi.org/10.1038/s41598-019-51787-5.

Wisely, S.M., Torhorst, C.W., Botero-Cañola, S., Atsma, H., Burkett-Cadena, N.D., Reeves, L.E., 2025. Evaluation of mosquito blood meals as a tool for wildlife pathogen surveillance. Pathogens 14, 792. https://doi.org/10.3390/pathogens14080792.

Wolff, G.H., Riffell, J.A., 2018. Olfaction, experience and neural mechanisms underlying mosquito host preference. J. Exp. Biol. 221, jeb157131. https://doi.org/10.1242/jeb.157131.

Wu, Y., Wu, J., Wu, Q., Cai, H., Hu, J., Lin, Z., et al., 2025. The making of a dangerous vector: factors shaping the vector competence of *Aedes* mosquitoes. Front. Cell. Infect. Microbiol. 15, 1718737. https://doi.org/10.3389/fcimb.2025.1718737.

Yan, J., Gangoso, L., Ruiz, S., Soriguer, R., Figuerola, J., Puente, J.M. la, 2021. Understanding host utilization by mosquitoes: determinants, challenges and future directions. Biol. Rev. 96, 1367–1385. https://doi.org/10.1111/brv.12706.

Zhan, Y., Alberto, D.A.S., Rusch, C., Riffell, J.A., Montell, C., 2021. Elimination of vision-guided target attraction in *Aedes aegypti* using CRISPR. Curr. Biol. 31, 4180–4187.e6. https://doi.org/10.1016/j.cub.2021.07.003.

Zhao, Z., McBride, C.S., 2020. Evolution of olfactory circuits in insects. J. Comp. Physiol. A 206, 353–367. https://doi.org/10.1007/s00359-020-01399-6.

Zhao, Z., Zung, J.L., Hinze, A., Kriete, A.L., Iqbal, A., Younger, M.A., et al., 2022. Mosquito brains encode unique features of human odour to drive host seeking. Nature 605, 706–712. https://doi.org/10.1038/s41586-022-04675-4.

Zung, J.L., McBride, C.S., 2025. Sebaceous origins of human odor. Curr. Biol. 35, R303–R313. https://doi.org/10.1016/j.cub.2025.03.031.