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Invasion and Expansion of Aedes vittatus in the Americas: A Potential Bridge Vector Between Sylvatic and Urban Arboviral Cycles

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The first record of *Aedes vittatus* (Diptera: Culicidae) in the Americas was published five years ago, specifically from the Dominican Republic[1]. This landmark discovery marked a significant advancement in the study of invasive mosquito species within the region, owing to its potential role as a vector for yellow fever, Zika, chikungunya, and dengue viruses in the Old World[2]. The aforementioned study had already flagged the potential invasiveness of this species and its threat to other Caribbean islands and broader American regions, anticipating a scenario of progressive geographic expansion facilitated by regional connectivity and trade.

After five years, its presence has not only been confirmed within the Dominican Republic[3], but also across other parts of the Caribbean. Indeed, soon after the initial findings in the Dominican Republic, this species was also reported in the neighboring island of Cuba, initially in Guantánamo[4], followed by Camagüey[5], and Santiago de Cuba[6]. More recently, the species' range has further expanded with its discovery in Jamaica[7], and notably, its first appearance in continental North America, specifically in Mexico's Yucatán Peninsula[8,9]. These emerging detections across another Caribbean island and, more significantly, in North America, underscore the species' ecological adaptability and highlight the urgent necessity to investigate its introduction pathways and its potential impact on arboviral transmission, particularly under conditions of accelerating climate change and increasing human mobility.

Initial analyses of the mitochondrial COI gene have suggested that *Ae. vittatus* underwent multiple introductions to the continent. Molecular studies have demonstrated that the genetic sequence of the mosquitoes collected from Cuba closely matches that of specimens from India[4], while those from the Dominican Republic align genetically with *Ae. vittatus* from Pakistan[1]. Furthermore, the genetic profile of the Jamaican specimens shows similarities with specimens from Cuba, India, and Nepal[7], supporting the hypothesis of repeated, independent introduction events rather than a single founder population spreading regionally.

Aedes vittatus displays an opportunistic oviposition strategy, laying eggs in transient, sunlit containers, and rock pools where embryos enter dormancy until inundation[10]. These eggs tolerate prolonged desiccation, remaining viable through high temperatures and dry periods, a trait implicated in the species′ recent long-distance spread to Caribbean islands[11]. Desiccation resistance is a shared ecological trait among synanthropic *Aedes* (e.g., *Aedes aegypti* and *Aedes albopictus*), facilitating stealthy, human-mediated transport and establishment, particularly via the movement of goods capable of retaining small volumes of water. Understanding egg tolerance and oviposition microhabitats is therefore essential for surveillance and biosecurity to prevent further incursions, as these early life stages represent the most cryptic and transportable phase of the invasion process.

The situation is concerning because the role of this new invasive mosquito species in arbovirus transmission remains unclear within this new geographical scenario. At present, the Americas are grappling with significant chikungunya and dengue epidemics, impacting several Caribbean nations, including Cuba[12]. Consequently, the introduction of this new vector could subtly reshape the epidemiological landscape, as *Ae. vittatus*, unlike the main vectors such as *Ae. aegypti* and *Ae. albopictus*, which mainly breed in domestic and peri-domestic environments[13], can readily colonize natural bodies of water, thereby expanding the ecological interface between sylvatic and urban transmission cycles.

This situation underscores the need to reassess vector surveillance and control strategies across the Americas, particularly in countries where *Ae. vittatus* is already established. Unlike other medically important *Aedes* species, this invasive mosquito displays distinct bioecological traits that may influence its population dynamics, dispersal, and interaction with human environments[2], thereby requiring tailored management approaches. Strengthening entomological monitoring through integrated molecular, ecological, and epidemiological frameworks is therefore essential, especially given that the current distribution of this species is likely underestimated in ecologically suitable yet insufficiently surveyed regions.

Key uncertainties remain regarding the introduction, spread, and public health implications of this invasive mosquito species in the Americas. Considering the molecular origins revealed by genetic studies, what pathways facilitated its introduction into the region? Could these mosquitoes have been transported via specific goods, analogous to the documented spread of *Ae. albopictus* through used tires[14]? Are countries where *Ae. vittatus* has been detected implementing adequate surveillance and control responses? Will this species expand beyond its current range and colonize additional nations? From a bioecological perspective, how might this species interact competitively with sympatric mosquitoes such as *Ae. aegypti* and *Ae. albopictus* that exploit overlapping breeding habitats? From an epidemiological standpoint, although this species is already known to be a competent arbovirus vector in certain countries of its native range, could it have the capacity to transmit these viruses in the Americas? If so, could it act as a bridge vector, thereby modifying the transmission dynamics between sylvatic and urban cycles and among different hosts?

Addressing these critical research gaps is essential to strengthen regional vector control and reduce emerging public health risks in a rapidly changing, interconnected world. It is time to truly put One Health into practice.

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