

Aedes aegypti queenslandensis: first geographic occurrence in Brazil and epidemiological implications

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ABSTRACT

Aedes aegypti is the mosquito that has been most successful in adapting to the anthropic environment and transmitting several viruses to humans as well. The species has three subspecies that can be identified by the variations in the color of the abdominal scales. Each subspecies possesses a distinct scale color pattern. Herein, it is described the first register of *Ae. aegypti queenslandensis* in São Paulo State, Brazil. Both the scale color pattern, and factors involved in the emergence of the local population are discussed, as well as possible epidemiological implications.

Aedes (Stegomyia) aegypti (Linnaeus, 1762) is the main hematophagous arthropod vector of several arboviruses in urban areas (Kraemer et al., 2015; Kraemer et al., 2019). It has an extensive record of synonyms, many of which are related to its color variation and are often linked with the species behavior (Hill, 1921; Mattingly, 1957; McClelland, 1974; Rašić et al., 2016). Currently, it is well known that the species exhibit scale color variations that are associated with three distinct subspecies (Mattingly, 1957; McClelland, 1974; Mori et al., 2016). *Aedes (Stegomyia) aegypti formosus* (Walker, 1848) represents the original genetic pool, is sylvatic and has a blackish color speckled with white scales (Soghigian et al. 2020).

Aedes aegypti aegypti (type locality: Kuala Lumpur, Selangor, Malaysia), considered a type form, originated in Africa, whose domestication process began with the exploration of the African continent by Europeans in the 15th century. Its distribution around the world has made it one of the main vectors of arboviruses such as dengue, chikungunya, Zika and urban yellow fever. It currently forms the Aegypti Group along with *Ae. mascarensis* (MacGregor, 1848) and *Ae. pia* (Le Goff & Robert, 2013). It is characterized by having a pale or brownish coloration, with few

whitish scales in the first tergite, and a line of pale scales in the first abdominal tergite (Forattini, 2002; Huang, 2004; Le Goff et al., 2013; Powell & Tabachnick, 2013; Kraemer et al., 2015; Mori et al., 2016; Rašić et al., 2016; Soghigian et al. 2020; WRBU, 2021).

Aedes aegypti formosus is the sylvatic subspecies found across the African continent; it was originally described in Sierra Leone but has been reported in forested regions in eastern and southern sub-Saharan Africa. Abdominal scales are dark-brown to black, covering the tergites (Forattini, 2002; Huang, 2004; Mori et al., 2016; Rašić et al., 2016; WRBU, 2021).

Aedes aegypti queenslandensis (Theobald, 1901) is a variety originally described in Burpengary, Queensland, Australia (type locality), but can be found in Asia, Oceania, Europe and North Africa, Mediterranean region. It has whitish scales covering the abdominal tergites and variation in the color of the scutal scales, which can vary from brown to whitish (Mattingly, 1957; McClelland, 1960; McClelland, 1974; Forattini, 2002; Mori et al., 2016; Rašić et al., 2016; Trari et al. 2017; WRBU, 2021).

Aedes a. aegypti occurs throughout the Pantropical Region and, in the American continent, it is the species with the largest geographical distribution (Brown et al., 2011; Brown et al., 2013; Kraemer et al., 2015). In Brazil, the subspecies was introduced in the period of European colonization, being eliminated in the 1950s, but reintroduced in the

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1960s (Fraiha 1968; Teixeira et al., 1999). After three decades, its presence could already be detected in all Brazilian states (Souza-Santos & Carvalho, 2000). This species has the vectorial capacity to transmit, in addition to dengue viruses, the urban yellow fever virus and chikungunya. Since the arrival of this species in the 16th century, many dengue outbreaks have been recorded in Brazil of endemo-epidemic patterns occurring every three to five years (Dick et al., 2012; Zayed et al., 2012; Kotsakiozi et al., 2017). The state of São Paulo became infested in the early 1980s, due to the influence of neighboring states, with the spreading of the species from the west to the east (Glasser & Gomes 2000). In 2015, the presence of the domestic *Ae. a. aegypti* reached 99.69% of the Brazilian municipalities (Fonseca Júnior et al., 2019).

Because of our finding of specimens of *Ae. a. queenslandensis* in a field work for scientific investigations activity carried out by the Superintendence for the Control of Endemic Diseases (SUCEN), this study aimed to report the presence *Ae. a. queenslandensis* in a Brazilian municipality.

Adults were collected in traps installed in residential properties along the urban perimeter of the city of Taubaté, São Paulo state, using the Adultrap® trap, from July to December 2020, and from January to February 2021. Inspections of the traps were performed twice a week and males and females captured were euthanized with ethyl acetate and stored in entomological boxes, for subsequent identification and photographic records using a Zeiss Stemi 2000-C microscope linked to an Opton 7100 camera and the TCCapture software (Tucsen Photonics®). From the specimens of *Ae. a. queenslandensis* identified, three males (E-15942, E-15943, E-15944) and three females (E-15945, E-15946, E-15947) were deposited in the Entomological Reference Collection, Faculty of Public Health, University of São Paulo, São Paulo, Brazil and the others in the Culicidae Biology and Ecology Laboratory, SUCEN.

Overall, 62 specimens of *Aedes a. queenslandensis* were collected, 57 females and 5 males, categorized into 6 scale color patterns of abdominal tergites (Figure 1). These specimens can be identified by the following characteristics: (A) abdominal tergites I, II and III covered with white scales; (B) abdominal tergites I, II and III with longitudinal line of white scales; (C) abdominal tergite IV-VII with speckled patches of white scales; (D) white scale abdominal tergites, with spots of dark scale laterally; (E) white scaled abdominal tergites with white and black scales covering the lateral areas; (F) completely white scaled tergites and sternites. The patterns described herein correspond to categories 07, 09, 11, 13, 14 and 15 of the classification of McClelland (1974).

Aedes a. queenslandensis and the specimens with the scale color variation described in this study have other morphological similarities (Figure 2), such as: (A) clypeus with silver scales; (B) female maxillary palps, with sparse pale scales; (C) thorax with black and pale scales; (D) scutum with silver scales disposed in lines forming a characteristic “lyre” design.

Currently, it is known that *Ae. a. aegypti* belongs to a monophyletic group with origins in Madagascar, from where it dispersed to the African continent in the last ice age, when the species separated into two distinct populations, with the emergence of lineages of *Ae. a. formosus* and the domestic form, *Ae. a. aegypti* (Fort et al., 2012; Soghigian et al. 2020). The emergence of *Ae. a. queenslandensis* is attributed to the domestication process of *Ae. a. aegypti*, a variation that, despite being genetically indistinguishable from the domestic form, differs in the abdominal scale color patterns. The abdomen of *Ae. a. queenslandensis* is covered with whitish scales more than that of *Ae. a. aegypti*, and its trophic habits are always associated with human populations (Mattingly, 1957; Huang, 1979; Rasić et al., 2016).

The change in scale color pattern in *Ae. aegypti* can be explained by epigenetic regulation, where constant changes in environmental conditions to which the animal is subjected, during its developmental

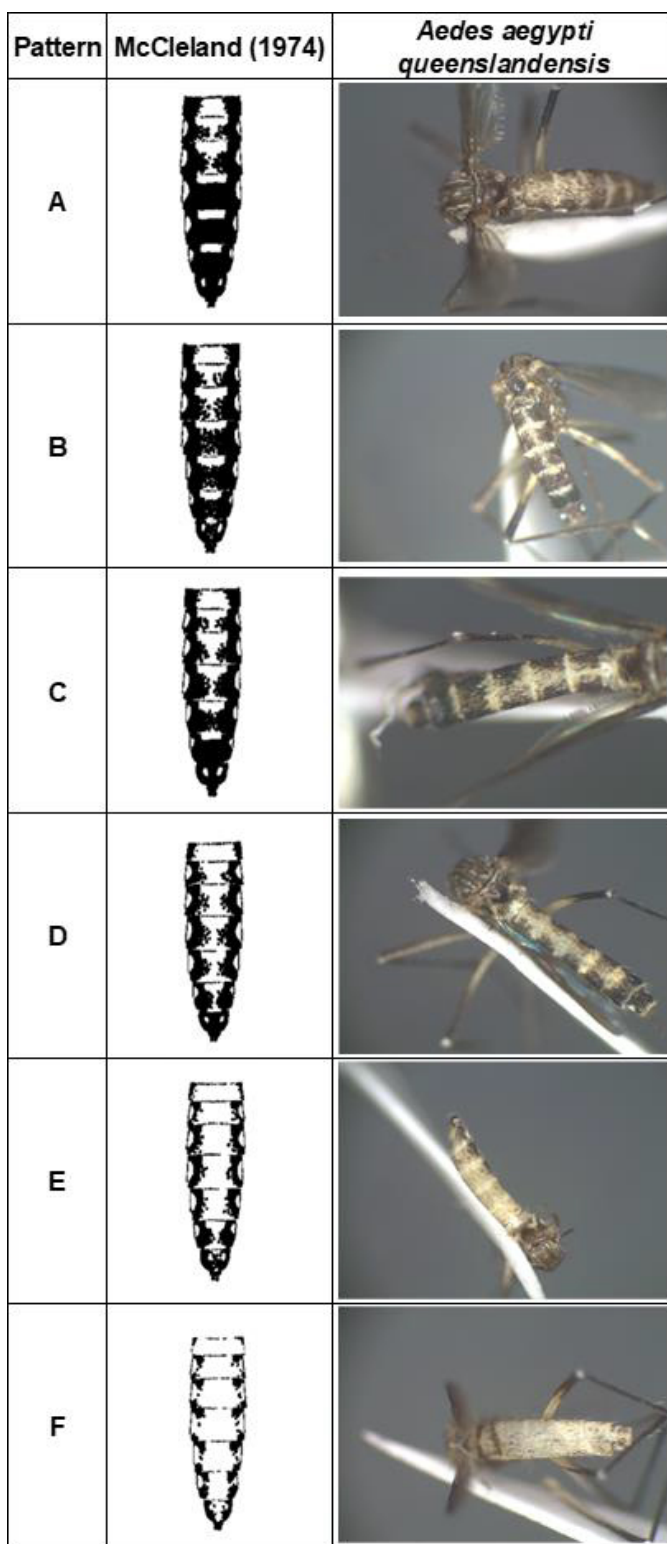


Figure 1 Comparative chart of the scale patterns of the abdomen of *Aedes aegypti queenslandensis* found in the municipality of Taubaté correlated with the patterns described by McClelland (1974).

period, leads to phenotypic mutations, that is, changes in inheritance models that do not involve changes in DNA (Feeney et al., 2014). The manifestation of population variation can be influenced by elements such as the type of breeding site associated with the microclimate and sex-specific response (Paupy et al., 2010; Soghigian et al., 2017);








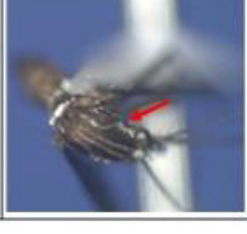
	Structures	<i>Aedes aegypti aegypti</i>	<i>Aedes aegypti queenslandensis</i>
A	Clypeus with silvery white scale spots		
B	Silvery white scales present at apex of maxillary palpus		
C	Thoracic pleura with patches of silvery white scales		
D	Scutum with a conspicuous silvery white, lyre-shaped scale pattern		

Figure 2 Comparative table between females of *Aedes aegypti aegypti* and *Ae. aegypti queenslandensis*.

mutation of the *kdr* nuclear gene (Linss et al., 2014); and climate changes (Tsuda et al., 2003).

The emergence of *Ae. a. queenslandensis* in the Brazilian mosquito population may be related to the occurrence of different genetic lineages. Bracco et al. (2007) suggested that *Ae. aegypti* has two genetic lineages in Brazil. One lineage is closely related to the type form, that contains individuals genetically related to *Ae. a. formosus*. The second lineage clustered with mosquitoes from Asia, like *Ae. a. queenslandensis*. On the other hand, Monteiro et al. (2014) suggested the existence of an *Ae. a. aegypti* strain from the Caribbean, which settled in southern Brazil, and another from Venezuela, which has established and dispersed across the north, both resulting from the reintroduction of the species after its eradication in 1958. Hypothetically, the occurrence of different lineages of *Ae. aegypti* in the municipality of Taubaté can be explained by the introduction of specimens *Ae. a. queenslandensis*. Further investigations will be necessary to verify the presence of *Ae. a. queenslandensis* across the region of Vale do Paraíba, eastern São Paulo state. Scarpassa et al. (2008) suggested that populations of *Ae. aegypti* from the city of Taubaté differ genetically from other populations present in Brazil, which according to the authors is due to the presence of a unique haplotype. The presence of *Ae. a. queenslandensis* corroborates our hypothesis.

Genetic plasticity influences disease transmission, resistance to control measures, reproductive behavior (Craig Junior et al., 1961), and phenotypic plasticity in the heritability of body size (Schneider et al., 2011).

Mattingly (1958) had already mentioned that the presence of subspecies and significant geographic or ecological separation could be associated with differences in the potential vector of the same mosquito species. Research carried out in Bangkok, Thailand, investigated the potential vector of *Ae. aegypti* variations. In this sense, Wasinpiyamongkol et al. (2003), although they found slightly low infection rates for DENV-2 in the *Ae. a. aegypti* and *Ae. a. queenslandensis*, have suggested that the persistence of transovarian transmission by successive generations of mosquitoes is an important mechanism in the maintenance of the dengue virus in interepidemic periods. Therefore, the natural transovarian transmission of dengue virus was verified in the type form (15.6/1,000) and in *Ae. a. queenslandensis* (12.9/1,000), in populations in a residential area of Bangkok, Thailand (Thongrungrat et al., 2011). Despite the finding of a higher frequency of the type form (98.2%), compared to *Ae. a. queenslandensis* (1.8%), they suggested that both morphological variations may act as a facilitator of virus persistence in an area in interepidemic periods. Thongrungrat et al. (2012) corroborated this fact and added data that the phenomenon occurs in both genders of adult mosquitoes, but with a higher rate in males, suggesting its importance in the epidemiology of dengue virus transmission.

Considering the epidemiological importance of *Ae. a. aegypti* in the transmission of several viruses that cause important diseases in humans, in due course, different studies have been carried out to clarify the potential effects that this phenotypic plasticity present in the species

can generate on public health. However, in the literature, so far, there is more information about the biology, behavior, physiology, insecticide resistance, competence and vectoring capacity of the type form and the *Ae. a. formosus*, and little is known about the *Ae. a. queenslandensis*.

Given the above, the meeting reported here highlights the need for detailed systematic studies that include both the morphological and molecular characterization of *Aedes*, as well as competence and vectorial capacity studies.

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Conflicts of interest

The authors declare no conflicts of interest.

Author contribution statement

GVS Conceptualization-Lead, Data curation-Lead, Formal analysis-Lead, Funding acquisition-Lead, Investigation-Lead, Methodology-Lead, Project administration-Lead, Resources-Lead, Software-Lead, Supervision-Lead, Validation-Lead, Visualization-Lead, Writing – original draft-Lead, Writing – review & editing-Lead. MBA Conceptualization-Equal, Data curation-Equal, Formal analysis-Equal, Funding acquisition-Equal, Investigation-Equal, Methodology-Equal, Project administration-Equal, Resources-Equal, Software-Equal, Supervision-Equal, Validation-Equal, Visualization-Equal, Writing – original draft-Equal, Writing – review & editing-Equal. LLNS Data curation-Equal, Investigation-Equal, Methodology-Equal, Supervision-Equal, Writing – original draft-Equal, Writing – review & editing-Equal.

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