



# Frequency of the Val1016Ile mutation on the *kdr* gene in *Aedes aegypti* (Diptera: Culicidae) in south Brazil

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**ABSTRACT.** Recently, the number of *Aedes aegypti* foci has increased in west of Santa Catarina, south Brazil, which has increased concern regarding mosquito-borne disease outbreaks such as dengue fever, Zika virus, and chikungunya. Therefore, it is important to monitor genetic resistance to insecticides through “knockdown resistance”. Homozygosity (Ile/Ile) at position 1016 in

the coding region of a voltage-dependent sodium channel gene ( $Na_v$ ) may induce resistance to pyrethroid insecticides. We evaluated the frequency of these alleles in *A. aegypti* in west Santa Catarina. In total, 349 specimens were obtained from the microregions of Joaçaba (31), Concórdia (35), Chapecó (154), and São Miguel do Oeste (129). We found that 109 individuals (31.0%) were homozygous for Val/Val, 102 (29.0%) were heterozygous for Val/Ile, and 138 (40.0%) were homozygous for Ile/Ile. The allele frequencies were similar for Val (0.455) and Ile (0.545). Joaçaba and Concórdia had the highest mutant allele frequencies (0.825 and 0.685, respectively). Therefore, these populations should be monitored for increases in pyrethroid resistance. The São Miguel do Oeste and Chapecó populations had similar frequencies of Val and Ile and were not in Hardy-Weinberg equilibrium, suggesting that a selection pressure or other evolutionary force has occurred. In conclusion, the observed frequency of Ile/Ile homozygous individuals in the region studied requires attention, because the implementation of controls using pyrethroid may increase the frequency of the mutant allele through the selection of resistant populations.

**Key words:** Mechanism of resistance; Mosquito; kdr; Genetic diversity