

Mapping the KDR mutation in *Culex pipiens* throughout Alameda County

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INTRODUCTION

The development of resistance to insecticides that target adult mosquitoes can hinder a District's ability to successfully kill mosquitoes that are infected with arboviruses, making insecticide resistance a public health threat. *Culex pipiens* mosquitoes represent a heightened risk of arboviruses transmission to humans, because their preferred larval habitats are often located within urban centers and near to people. Their proximity to people and the propensity of *Cx. pipiens* to take blood meals from people makes it crucial to eliminate arbovirus-carrying *Cx. pipiens* when they are detected. Knowing the status of genetic resistance of these mosquitoes to the pyrethroid class of insecticides would help vector control workers select the most effective pesticide for adulticide operations. Genetic resistance to pyrethroids can be evaluated in *Cx. pipiens* using an assay that detects the mutant knockdown resistance (*kdr*) single nucleotide polymorphism (SNP) in the voltage-gated sodium channel gene that confers resistance to pyrethroid insecticides.

METHODS AND MATERIALS

The mosquitoes were collected throughout Alameda County, California during 2018 for the purpose of determining mosquito abundance and arbovirus prevalence. Up to five females from each collection were saved individually and later tested by the *kdr* SNP test using standard quantitative polymerase chain reaction (qPCR) methods. Nucleic acids were extracted using the MagMAX – 96 Viral RNA Isolation Kit (ThermoFisher Scientific) and the *kdr* SNP evaluated using qPCR. All genotyping calls were determined automatically using the QuantStudio Design &

Analysis Software (ThermoFisher Scientific). In some cases, the *kdr* genotype was evaluated at the same site on multiple occasions during 2018.

RESULTS DISCUSSION

A total of 390 *Cx. pipiens* were analyzed for the *kdr* SNP. When combined into a single group, 33.3% were homozygous susceptible, 38.5% were heterozygous susceptible/resistant, and 28.2% were homozygous resistant. To test whether the location of mosquito collection affected the proportion of mosquitoes with the mutant *kdr* SNP, the collections sites were combined into three regions of Alameda County based upon natural and anthropogenic barriers: north (north of Interstate 238 and west of the East Bay Hills), south (south of Interstate 238 and west of the East Bay Hills), and east (east of the East Bay Hills). The northern region of the county lacks extensive agriculture and pyrethroids have not been applied by vector control agencies. In agreement, the northern region had the lowest proportion of homozygous resistant mosquitoes (Table 1). In contrast, the eastern region of Alameda County, home to several vineyards, farms and pastures, had the highest proportion of *Cx. pipiens* with the homozygous resistant *kdr* SNP (Table 1). *Culex pipiens* that were collected from the southern region of the county displayed an intermediate proportion of specimens that contained the mutant *kdr* SNP (Table 1), which may result from the dispersal of resistant mosquitoes from the eastern region of the county via highway corridors that follow natural valleys in the East Bay Hills to the southern region of the county (e.g. State Route 84 and Interstate 680). These data are useful for determining the most suitable pesticide to use, by region, for controlling adult mosquitoes.

Table 1.—Geographic Distribution of the *kdr* SNP in Alameda County, CA

County Region	Homozygous Susceptible	Heterozygous Susceptible/Resistant	Homozygous Resistant	Total Number of Mosquitoes
North	50.8%	38.5%	10.7%	123
South	38.7%	40.9%	20.4%	137
East	11.5%	35.9%	52.7%	130