

## Blood-meal analysis of *Culex erythrothorax* collected in a marsh habitat

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### INTRODUCTION

*Culex erythrothorax* mosquitoes can transmit arboviruses such as West Nile virus (WNV) and may be highly abundant in marsh habitats that contain tule or bulrush. Knowing the species of animal that infectious mosquitoes take blood from can inform vector control workers of whether there is increased risk of transmitting the virus to humans. For example, if WNV-infected mosquitoes also contain human blood, there may be an increased risk for human infection in the area where the mosquitoes were collected.

### METHODS

Nested PCR was used to amplify the *mitochondrial gene cytochrome c oxidase I (mtCOI)* to identify the species of animal that the mosquito had fed upon. To validate the PCR primers, DNA was extracted from 50 µl of blood collected from rooster, bovine and horse, the *mtCOI* gene amplified using nested PCR, the resulting PCR products separated using gel electrophoresis, the DNA extracted from the gel and sequenced. BLAST queries of

the DNA sequences that were extracted from the blood of known species against the NCBI Nucleotide collection (nr/nt) database returned the *mtCOI* gene of the corresponding species (PCR products were > 500 bp; BLAST Expect values (E) were 0). Of note, as little as 0.5 µl of blood could be amplified using nested PCR and sequenced to determine the species of animal from which the blood was collected DNA was then extracted from blood-engorged *Cx. erythrothorax* that were collected in marsh habitats bordering the San Francisco Bay (California, USA) to determine the species of animal that the mosquitoes had fed upon.

### RESULTS

*Culex erythrothorax* collected at the Hayward Regional Shoreline had fed upon mourning dove, California towhee, Wild Turkey, American crow, and human. The finding that human blood was found in *Cx. erythrothorax* collected at a site that is infrequently visited by people suggests that this WNV vector may disperse from breeding sites to seek blood meals.