



Article

# Identification of Mosquito Bloodmeals Collected in Diverse Habitats in Malaysian Borneo Using COI Barcoding

Katherine I. Young <sup>1,\*</sup>, Joseph T. Medwid <sup>1</sup>, Sasha R. Azar <sup>2,3,4</sup> , Robert M. Huff <sup>5</sup>, Hannah Drumm <sup>6</sup>, Lark L. Coffey <sup>6,7</sup> , R. Jason Pitts <sup>5</sup>, Michaela Buenemann <sup>8</sup> , Nikos Vasilakis <sup>2,3,9,10,11</sup> , David Perera <sup>12</sup> and Kathryn A. Hanley <sup>1</sup>

<sup>1</sup> Department of Biology, New Mexico State University, Las Cruces NM 88003, USA; jtmedwid@nmsu.edu (J.T.M.); khanley@nmsu.edu (K.A.H.)

<sup>2</sup> Department of Pathology, University of Texas Medical Branch, Galveston, TX 77555, USA; srazar@utmb.edu (S.R.A.); nivasila@utmb.edu (N.V.)

<sup>3</sup> Department of Microbiology and Immunology, University of Texas Medical Branch, Galveston, TX 77555, USA

<sup>4</sup> Institute for Translational Sciences, University of Texas Medical Branch, Galveston, TX 77555, USA

<sup>5</sup> Department of Biology, Baylor University, Waco, TX 76706, USA; Robert\_Huff1@baylor.edu (R.M.H.); Jason\_Pitts@baylor.edu (R.J.P.)

<sup>6</sup> School of Veterinary Medicine, University of California Davis, Davis, CA 95616, USA; hdrumm@ucdavis.edu (H.D.); lcoffey@ucdavis.edu (L.L.C.)

<sup>7</sup> Department of Pathology, Microbiology & Immunology, University of California Davis, Davis, CA 95616, USA

<sup>8</sup> Department of Geography, New Mexico State University, Las Cruces, NM 88003, USA; elabuen@nmsu.edu

<sup>9</sup> Center for Biodefense and Emerging Infectious Diseases, University of Texas Medical Branch, Galveston, TX 77555, USA

<sup>10</sup> Center for Tropical Diseases, University of Texas Medical Branch, Galveston, TX 77555, USA

<sup>11</sup> Institute for Human Infection and Immunity, University of Texas Medical Branch, Galveston, TX 77555, USA

<sup>12</sup> Institute of Health and Community Medicine, Universiti of Malaysia Sarawak, Sarawak 94300, Malaysia; dperera@unimas.my

\* Correspondence: kiy761@nmsu.edu

Received: 7 January 2020; Accepted: 24 March 2020; Published: 1 April 2020



**Abstract:** Land cover and land use change (LCLUC) acts as a catalyst for spillover of arthropod-borne pathogens into novel hosts by shifting host and vector diversity, abundance, and distribution, ultimately reshaping host–vector interactions. Identification of bloodmeals from wild-caught mosquitoes provides insight into host utilization of particular species in particular land cover types, and hence their potential role in pathogen maintenance and spillover. Here, we collected 134 blood-engorged mosquitoes comprising 10 taxa across 9 land cover types in Sarawak, Malaysian Borneo, a region experiencing intense LCLUC and concomitant spillover of arthropod-borne pathogens. Host sources of blood were successfully identified for 116 (87%) mosquitoes using cytochrome oxidase subunit I (COI) barcoding. A diverse range of hosts were identified, including reptiles, amphibians, birds, and mammals. Sixteen engorged *Aedes albopictus*, a major vector of dengue virus, were collected from seven land cover types and found to feed exclusively on humans (73%) and boar (27%). *Culex tritaeniorhynchus* (n = 2), *Cx. gelidus* (n = 3), and *Cx. quiquefasciatus* (n = 3), vectors of Japanese encephalitis virus, fed on humans and pigs in the rural built-up land cover, creating potential transmission networks between these species. Our data support the use of COI barcoding to characterize mosquito–host networks in a biodiversity hotspot.