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SCIENTIFIC NOTE

FIRST RECORD OF *MANSONIA DYARI* FROM SAINT CROIX, UNITED STATES VIRGIN ISLANDS

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ABSTRACT. The first report of *Mansonia dyari* on Saint Croix, United States Virgin Islands (USVI), is confirmed. Adult and larval specimens were collected in 2018 and 2019 through adult surveillance and larval collections. Specimens were identified by microscopic methods, and a representative specimen was confirmed by DNA sequencing (mitochondrial cytochrome *c* oxidase subunit I). Morphological features are reviewed and compared with *Mansonia flaveola*, a species previously reported in the USVI. Notes are provided on the locations, collection methods, and mosquito associates found with *Ma. dyari* in the USVI.

KEY WORDS Caribbean, distribution, *Mansonia dyari*, surveillance

The paucity of recent studies documenting the Culicidae fauna in the United States Virgin Islands (USVI) limits the ability of public health officials to prepare for and address emerging mosquito-borne diseases. Natural disasters (e.g., Hurricanes Irma and Maria) and outbreaks of dengue, chikungunya, and Zika viruses within the USVI clearly underscore the need for robust integrated mosquito surveillance and management efforts (Feldstein et al. 2016, Rice et al. 2018, Schnall et al. 2019). Recently initiated mosquito surveillance and focused surveys within the islands are expected to improve the accuracy of the valid species records for the islands. Here we report the first records of *Mansonia dyari* (Belkin, Heinemann, and Page) on the island of St. Croix, identified during ongoing adult surveillance (2018–19) and a larval survey conducted in 2019 (Table 1).

Adult females were collected by BG-Sentinel traps (Biogents USA, Moorefield, WV) baited with the BG artificial human skin scent lure (Biogents USA), and larvae were predominantly collected in an inland freshwater pond (Fig. 1**)** by rinsing *Pistia* sp. roots into a bucket and examining the water for immature specimens. The mosquitoes were identified using morphological characters described in Belkin et al. (1970) and Darsie and Ward (2005). Previously published records for the USVI only report the presence of *Ma. flaveola* (Coquillett) (Flemings and Walsh 1966, Porter 1967). However, the adult females we collected (Table 1) had palpi that were less than 0.35 the length of the proboscis and lacked spiniform setae on the posterior margin of abdominal tergum VII; *Ma. flaveola* has palpi about 0.5 the length of the proboscis, and *Ma. titillans* (Walker) has spiniform setae on the posterior margin of abdominal tergum VII. Larval collections were obtained in January and May 2019 from a single location (Table 1). The ventral brush (seta 4-X) possessed 3 pairs of setae on the grid and seta 1-S was multibranched, thus morphologically differentiating the specimens from both *Ma. flaveola* and *Ma. titillans*. Immature *Culex erraticus* (Dyar and Knab) and *Anopheles albimanus* Wiedemann were collected contemporaneously with the *Ma. dyari* specimens obtained as larvae from a freshwater pond (site coordinates: 17.74548, –64.68660).

To confirm the identity by molecular methods, genomic DNA was extracted from a single larva collected on January 29, 2019, using a DNeasy blood and tissue kit (Qiagen, Inc., Germantown, MD) with a 24-h proteinase-K incubation. The anchored hybrid enrichment probe set from Young et al. (2016) was used to capture genomic and mitochondrial loci; resulting libraries were then sequenced on a HiSeq 2500 (Illumina, Inc., San Diego, CA). Raw sequence reads were quality filtered and mapped to the *Aedes aegypti* (L.) mitochondrion genome (RefSeq: NC_035159.1) using the MITObim pipeline (Hahn et al. 2013). Draft mitochondrial genomes were aligned and annotated in Geneious v11.1.5 (Biomatters, Ltd., Auckland, NZ). The resulting 1,218-bp sequence (GenBank Accession Number: MN129182) is a partial (approximately 80%) read of the complete mitochondrial cytochrome *c* oxidase subunit I (COI); the sequence was subsequently analyzed using the Barcode of Life Database (BOLD) identification tool (Ratnasingham and Hebert 2007). The partial se-

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Table 1. *Mansonia dyari* collections in St. Croix, United States Virgin Islands (2018–19).

Collection method (no. collections)	Collection date	No. *Ma. dyari* collected
2018		
BG-Sentinel trap (2)	Apr. 4, 2018	1
	Apr. 11, 2018	1
2019		
BG-Sentinel trap (3)	Feb. 2, 2019	1
	Feb. 27, 2019	2
	Apr. 3, 2019	1
Larval collections (2)	Jan. 29, 2019	1
	May 24, 2019	35

quence was found to match deposited COI sequences reported as *Ma. dyari* (range 100–97.4%, $n = 99$); the sequence did not match the *Ma. flaveola* sequences available in the BOLD. A BOLD TaxonID tree–based approach (Kimura-2 parameter) revealed that our submitted sequence aligns within a clade containing *Ma. dyari* from Puerto Rico; a pairwise analysis comparing our sequence with *Ma. dyari* from Puerto Rico (BOLD: MOSN659-18.COI-5P) demonstrated a 100% match of a 658-bp region.

Mansonia dyari is a well-known pestiferous species and has been implicated in the transmission of Venezuelan equine encephalitis and St. Louis encephalitis viruses (Gilyard 1944, Anonymous 1978, Lounibos et al. 1990). Studies by Turell et al. (2013) also report *Ma. dyari* as a competent vector of Rift Valley fever virus. Although limited in number and scope, studies on the host-feeding behaviors of this species suggest a broad feeding range to include mammals, reptiles (alligator), and avian hosts (Anonymous 1978, Lounibos et al. 1990, Rodrigues and Maruniak 2006). Thus, there remains a clear need to assess the potential for *Ma. dyari* to serve as an arbovirus vector in the Caribbean.

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Fig. 1. Freshwater pond containing a large mat of *Pistia* sp. where larval *Mansonia dyari* were collected in St. Croix, United States Virgin Islands (2019).

REFERENCES CITED

Anonymous. 1978. *Gorgas Medical Laboratory annual report. 1977*. Washington, DC: US Government Printing Office.

Belkin JN, Heinemann SJ, Page WA. 1970. The Culicidae of Jamaica (Mosquito Studies. XXI). *Contrib Am Entomol Inst* 6:1–458.

Darsie RF Jr, Ward RA. 2005. *Identification and geographic distribution of the mosquitoes of North America, north of Mexico*. Gainesville, FL: Univ. Press of Florida.

Feldstein LR, Ellis EM, Rowhani-Rahbar A, Halloran ME, Ellis BR. 2016. The first reported outbreak of chikungunya in the U.S. Virgin Islands, 2014–2015. *Am J Trop Med Hyg* 95:885–889.

Flemings MB, Walsh RD. 1966. Mosquitoes of the American Virgin Islands. *Mosq News* 26:424–426.

Gilyard RT. 1944. Mosquito transmission of Venezuelan encephalomyelitis virus in Trinidad. *Bull US Army Med Dept* 75:96–107.

Hahn C, Bachmann L, Chevreux B. 2013. Reconstructing mitochondrial genomes directly from genomic next-generation sequencing reads—a baiting and iterative mapping approach. *Nucleic Acids Res* 41:e129.

Lounibos LP, Larson VL, Morris CD. 1990. Parity, fecundity and body size of *Mansonia dyari* in Florida. *J Am Mosq Control Assoc* 6:121–126.

Porter JE. 1967. A checklist of the mosquitoes of the Greater Antilles and the Bahama and Virgin Islands. *Mosq News* 27:35–41.

Ratnasingham S, Hebert PD. 2007. BOLD: The Barcode of Life Data System (http://www.barcodinglife.org). *Mol Ecol Notes* 7:355–364.

Rice ME, Galang RR, Roth NM, Ellington SR, Moore CA, Valencia-Prado M, Ellis EM, Tufa AJ, Taulung LA, Alfred JM, Perez-Padilla J, Delgado-Lopez CA, Zaki SR, Reagan-Steiner S, Bhatnagar J, Nahabedian JF 3rd, Reynolds MR, Yeargin-Allsopp M, Viens LJ, Olson SM, Jones AM, Baez-Santiago MA, Oppong-Twene P, Van-Maldeghem K, Simon EL, Moore JT, Polen KD, Hillman B, Ropeti R, Nieves-Ferrer L, Marcano-Huertas M, Masao CA, Anzures EJ, Hansen RL Jr, Perez-Gonzalez SI, Espinet-Crespo CP, Luciano-Roman M, Shapiro-Mendoza CK, Gilboa SM, Honein MA. 2018. Vital Signs: Zika-associated birth defects and neurodevelopmental abnormalities possibly associated with congenital Zika virus infection—U.S. territories and freely associated states, 2018. *MMWR Morb Mortal Wkly Rep* 67:858–867.

Rodrigues SC, Maruniak JE. 2006. Blood meal identification from mosquitoes collected at a commercial alligator farm. *J Am Mosq Control Assoc* 22: 557–560.

Schnall AH, Roth JJ, Ekpo LL, Guendel I, Davis M, Ellis EM. 2019. Disaster-related surveillance among US Virgin Islands (USVI) shelters during the Hurricanes Irma and Maria response. *Disaster Med Public Health Prep* 13:38–43.

Turell MJ, Britch SC, Aldridge RL, Kline DL, Boohene C, Linthicum KJ. 2013. Potential for mosquitoes (Diptera: Culicidae) from Florida to transmit Rift Valley fever virus. *J Med Entomol* 50:1111–1117.

Young AD, Lemmon AR, Skevington JH, Mengual X, Ståhls G, Reemer M, Jordaens K, Kelso S, Lemmon EM, Hauser M, De Meyer M, Misof B, Wiegmann BM. 2016. Anchored enrichment dataset for true flies (Order Diptera) reveals insights into the phylogeny of flower flies (family Syrphidae). *BMC Evol Biol* 16:143.