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(ACMCIP Abstract)



VIRTUAL ABSTRACT

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Abstract details



The genus *Culicoides* (Fam. Ceratopogonidae), commonly named biting midges, are the smallest hematophagous dipterans with public health importance worldwide. *Culicoides* transmit multiple pathogens to humans and animals, but as vectors of arboviruses, they achieve their principal importance; more than 50 viruses have been isolated from *Culicoides* species. From the almost 1400 morphospecies identified, Mexico has 84 morphospecies. However, some regions of Mexico are still scantily studied. This is the case of Chihuahua, located in Northwest Mexico, where does not have any record for *Culicoides* species. In the present study, DNA barcode, bionomic parameters, and arboviral diagnosis of *Culicoides* from San Buenaventura, Chihuahua, Mexico were estimated. Here, collections of *Culicoides* were carried out from April through September 2020 in San Buenaventura, Chihuahua, by using the human-landing-collection (HLC) method, CDC, and mosquito magnet traps. Morphological keys and corroborated by DNA barcoding were performed to *Culicoides* identification. The daily pattern of total landing activity of *Culicoides* was estimated. Also, pools of *Culicoides* were achieved for the screening of viruses by metagenomic analyses. In this research, *Culicoides furens* was identified as unique species. DNA barcode reveals a possible complex compared with those in DNA databases. Host-seeking females of *C. furens* showed a unimodal human-landing activity pattern between 4-8 pm. The human daily landing rate was directly proportional to temperature and solar radiation, but there was a significant negative association with wind speed. Overall, a daily landing rate (DLR) of 88 lands/person/day was estimated. Several sequences of possible arbovirus associated with *C. furens* were detected. We conclude that *Culicoides furens* is the first species reported in Chihuahua, northwest Mexico. Also, this is the first study of metagenomics analyses in *Culicoides* in Mexico. The data offer insights into the ecology of *C. furens*, a potential vector of arbovirus in Mexico.

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First record of the genus *Culicoides* (Diptera: Ceratopogonidae) in Chihuahua, Northwest Mexico: A study of DNA barcode, human-landing rate, arbovirus detection, and public health importance of *Culicoides furens*



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BACKGROUND

The genus *Culicoides* (Fam. Ceratopogonidae), commonly named biting midges, are the smallest hematophagous dipterans with public health importance worldwide. *Culicoides* transmit multiple pathogens to humans and animals, but as vectors of arboviruses, they achieve their principal importance; more than 50 viruses have been isolated from *Culicoides* species. From the almost 1400 morphospecies identified, Mexico has 84 morphospecies. However, some regions of Mexico are still scantily studied. This is the case of Chihuahua, located in Northwest Mexico, where does not have any record for *Culicoides* species. In the present study, DNA barcode, bionomic parameters, and arboviral diagnosis of *Culicoides* from San Buenaventura, Chihuahua, Mexico were estimated.

METHODS

Collection of biting midges: The sampling plot was 5 m from the riverbanks of the Santa María river (29°51'09"N, 107°29'20"W, 1540 masl; Fig. 1). It is a semi-naturalized area, 3 km downstream from a small dam that marks the end of the urbanized area of the city. The banks of the river are partially vegetated with typical species of riverside groves such as *Populus* spp., *Salix* spp. and *Quercus* spp. and other shrub species such as *Tamarix* spp., and mainly surrounded by irrigated lands in the San Buenaventura, such as walnut and corn. Collection were carried out from April through September 2020 in San Buenaventura, Chihuahua, by using the human-landing-collection (HLC) method, CDC, and mosquito magnet traps (Figure 1).

Identification of biting midges: Morphological keys were used to identify the biting midges. Then, the species were corroborated by DNA barcoding using specific primers (LCO1490 and HCO2198) to amplify the cytochrome oxidase subunit I (Folmer et al., 1994). PCR reactions were performed in a total volume of

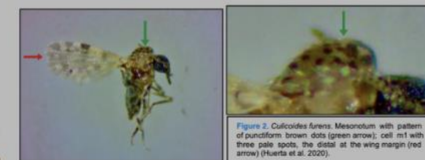
Human-landing-collection: Four collectors of flies were situated 10 meters apart, collectors were under the shadow of a tree to catch wild host-seeking females of biting midges and mosquito species (Fig. 1). The fly collectors were not smokers and did not wear cologne or any lotion that could influence the host-seeking behavior of biting midges. The biting midges were collected when they were exposed on skin. Host-seeking females were captured while they were landing or attempting to feed on the human collector by using a manual aspirator (Bloquip cat. 1135A). Then were killed and maintained at -80°C until identification or molecular analysis. Sampling was carried out between 7:00 am to 8:00 pm for 10 consecutive days. To determine the daily patterns of human-landing activity, the human-landing rate per hour was calculated as the total number of flies caught during each sampling period divided by the number of fly collectors, and it was expressed as the number of lands/person/hour. A GLIMMIX model was used to fit the human-landing rate during the 12 days to a negative binomial distribution, and the least square means (LSM) of the sampling periods were compared (Ruiz-Arondo et al. 2017). Also, climatic variables were register to find which of them are correlated with human-landing-collection.



Metagenomic analysis: Pools of *Culicoides* were achieved for the screening of viruses by metagenomic analyses. Firstly, Qiagen RNA mini kit was used to perform the RNA extraction. Then, RNA concentration was quantified. RNA samples with >100 ng/μL were sent to new generation sequencing at DNA facility Iowa State University (Ames, Iowa, USA).

RESULTS

***Culicoides* species:** *Culicoides furens* (Fig. 2) was the specie identified. This is the first record in Chihuahua state.



Human-landing-collection: Host-seeking females of *C. furens* showed a unimodal human-landing activity pattern between 4-8 pm. The human daily landing rate was directly proportional with temperature ($P < 0.001$) and solar radiation ($P < 0.001$), but there was a significant negative association with wind speed ($P < 0.001$). Overall, a daily landing rate (DLR) of 88 lands/person/day was estimated.

DNA barcode and Metagenomic analysis: Unfortunately, due to the covid

Chat

