

PRESS RELEASE

New study reveals the microbiota composition of *Culex perexiguus* mosquito, the main West Nile Virus

- The role of the microbiota could determine the capacity of mosquitoes to transmit the disease.



Picture taken during the process of identification of the captured mosquitoes. Photo: Josué Martínez de la Puente

Seville, 5 March 2025. A scientific team led by the Doñana Biological Station – CSIC has conducted the first characterization of the microbiota of *Culex perexiguus*, the primary vector of the West Nile virus in Andalusia. The study also explores the potential link between the composition of these mosquitoes' microbiota and West Nile virus infection. The work was carried out in collaboration with researchers from the Biomedical Research Institute of Málaga, the University of Granada, the CIBER for Epidemiology and Public Health, and the CIBER for Obesity and Nutrition Pathophysiology, among other institutions.

The microbiota of mosquitoes—the community of microorganisms present in these insects—plays a key role in their biology and capacity to transmit pathogens. The bacteria within this microbiota can modulate the mosquito's immune response, compete with pathogens for resources, or even release compounds that affect pathogen development. Identifying the natural composition of mosquito microbiota is essential for understanding the epidemiology of pathogen transmission in the region and potentially developing innovative strategies for controlling vector-borne diseases.

The mosquitoes analyzed in this study were collected in the province of Seville, in southwestern Spain, during the West Nile virus outbreak in 2020. Using molecular techniques, the research team identified that the predominant bacteria in the *Culex perexiguus* microbiota belonged to the families *Burkholderiaceae* and *Erwiniaceae*. In contrast, bacteria of the genus *Wolbachia*, known to block virus replication in other mosquito species, were rare in *Culex perexiguus*.

“The differences in the *Culex perexiguus* microbiota compared to those identified in other mosquito species could help us understand the key role of *Culex perexiguus* in the transmission of West Nile virus,” says Marta Garrigós, lead author of the study and a predoctoral researcher at the Doñana Biological Station-CSIC.

Despite the microbiota's relevance in vector competence, the study found no significant differences in bacterial diversity between infected and non-infected mosquitoes. “Among other possibilities, this could be due to the fact that we analyzed pooled mosquito samples, which might obscure individual-level differences,” explains Josué Martínez de la Puente, a scientist at the Doñana Biological Station and principal investigator of the project. However, he also emphasizes that “these findings highlight the importance of conducting future studies under controlled laboratory conditions to better understand the relationship between mosquito microbiota and their ability to transmit pathogens.”

Reference:

Marta Garrigós, Mario Garrido, María José Ruiz-López, María José García-López, Jesús Veiga, Sergio Magallanes, Ramón Soriguer, Isabel Moreno Indias, Jordi Figuerola, Josué Martínez-de la Puente. **Microbiota composition of *Culex perexiguus* mosquitoes during the West Nile virus outbreak in southern Spain.** *PLoS One*. <https://doi.org/10.1371/journal.pone.0314001>