

West Nile virus in Germany: vector competence of native *Culex pipiens* and *Aedes albopictus*

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Being a question of time, West Nile virus (WNV, Flavivirus, Flaviviridae) eventually emerged in Germany, with the first antigen detection in September 2018 in a great grey owl in the federal state of Saxony-Anhalt. Once established, WNV, like many arthropod-borne viruses, poses a continuous threat to wild and captive animal species as well as to human health. The virus is maintained in an enzootic cycle between ornithophilic mosquitoes as vectors and birds as amplifying hosts. Humans and horses are considered dead-end hosts, where an infection generally progresses asymptotically and only in rare cases leads to neuroinvasive disease.

Multiple virus genome detections, obtained from the north to the south of Germany, raise the question of how WNV spreads throughout Germany and which vectors possibly play a key role in its transmission. Infection experiments were performed with three native mosquito colonies (*Culex pipiens* biotype *pipiens*, *Culex pipiens* biotype *molestus*, *Aedes albopictus*) and the WNV lineage 2 strain isolated from the first infected owl in Germany. The mosquitoes were fed with a virus-spiked blood meal and incubated for two to three weeks at 25°C, representing average summer temperatures in Germany. To assess the vector competence of a colony, mosquito saliva, bodies and extremities were tested for the presence of viable virus or viral RNA. All tested species were susceptible to a WNV infection, with individual specimens transmitting virus in their saliva