Mosquito breeding site identification in Central Hungary using LIDAR-based microtopography analysis

A. Ahijado[1], R. Bueno-Mari[1,2], M. García-Howlett[1], G. Kemenesi[1,3] and J.P. Orán[1]

[1]*Laboratorios Lokímica, R&D, Calle Meteorito 59, 03006 Alicante, Spain,* [2]*Universitat de Valencia, Parasitology, Avenida Vicent Andrés Estellés s/n, 46100 Burjassot, Spain,* [3]*University of Pécs, Virology, Ifjúság útja 20, 7624 Pécs, Hungary; mgarcia@lokimica.es*

Mosquitoes are a global public health problem. In Hungary, mosquito breeding sites are usually located in depressions near rivers that are temporarily flooded. Climate change and globalisation are causing this pest to become more frequent, as a result of extra flooding events and new invasive species appearance. The aim of this study is to apply LIDAR remote sensing technology to identify these depressions more precisely by taking advantage of its ability to detect the ground surface in areas of abundant vegetation such as the one that characterises the study area. A DTM was generated from the LIDAR data to obtain the depressions through GIS analysis. To determine optimal depressions for mosquito breeding sites, a multi-criteria analysis was carried out using GIS that enabled the integration of various environmental factors (vegetation, altitude, depth, distance to the river, wetlands and floodplains). From the 6,465 depressions that were obtained, 98% had a depth lower than 25 cm. 22% of the depressions turned out to have a high degree of susceptibility to being mosquito breeding sites, 26% medium-high, 27% medium-low, 8% medium and 7% low. Depressions with a high degree of susceptibility are generally located in low areas near the river associated with riparian vegetation. This study demonstrates how integrating remote sensing and environmental data can help approach wetland mosquito problems. The combination of spatial data using GIS and the precision of LIDAR technology has potentially identified the most susceptible areas for mosquito infestations. The methodology developed in this work can be updated and validated in the future with new or more detailed information, particularly mosquito larvae monitoring, in order to improve mosquito vigilance, management and control.

A DNA-based pipeline for species-level identification of Belgian mosquitoes

A. Vanderheyden[1], N. Smitz[2], I. Deblauwe[3], K. De Wolf[3], S. Gombeer[1], K. Meganck[2], A. Schneider[3], J. De Witte[3], A. Vanslembrouck[3], W. Dekoninck[1], T. Backeljau[1,4], M. De Meyer[2], R. Müller[3] and W. Van Bortel[3,5]

[1]*Royal Belgian Institute of Natural Sciences, Taxonomy, Vautierstraat 23, 1000 Brussels, Belgium,* [2]*Royal Museum for Central Africa, BopCo, Leuvensesteenweg 13, 3080 Tervuren, Belgium,* [3]*Institute of tropical medicine, Unit of entomology, Nationalestraat 155, 2000 Antwerp, Belgium,* [4]*University of Antwerp, Evolutionary ecology group, Universiteitsplein 1, 2610 Antwerp, Belgium,* [5]*Institute of tropical medicine, Outbreak research team, Nationalestraat 155, 2000 Antwerp, Belgium; avanderheyden@naturalsciences.be*

Early detection of exotic mosquito species (EMS) is of vital importance to prevent local transmissions of mosquito-borne diseases. From 2017 to 2020, the Belgian federal government and regional authorities funded the MEMO project (Monitoring of Exotic MOsquitoes in Belgium), which aimed at detecting and evaluating the occurrence of EMS in Belgium. During the project 52,478 mosquitoes were collected at 23 points of entry. In order to implement management strategies, especially regarding potential disease vectors, accurate and reliable species-level identification of all mosquito life stages is essential. Therefore, morphological species identifications of a subset of samples, including all EMS, were validated using molecular techniques. About 3,300 specimens were barcoded using multiple markers to obtain an identification at species level (*COI, ITS2, ACE2, CQ11*). To this end, a DNA-based species identification pipeline was established that allowed for the reliable determination of the majority of the native (n=31) and all six EMS of main concern to Europe. To distinguish native species complexes (n_{sp}=6) alternative markers are being investigated. EMS were found to enter Belgium repeatedly through different introduction pathways. The DNA-based pipeline has proven its usefulness to validate the morphological identifications and confirm the presence of EMS, especially in case of damaged specimens or immature stages like eggs.

emca

European Mosquito Control Association

Xth International Conference

3-7 October 2021, Vienna, Austria

New insights in to mosquito and blackfly control

Abstract Book