

AN INDICATOR FRAMEWORK FOR THE MONITORING OF VECTOR-BORNE DISEASE: A STUDY IN ITALY AND GREECE

Falcinelli M.*^[1], Damiani C.^[2], Cappelli A.^[2], Gavaudan S.^[3], Canonico C.^[3], Currà C.^[4], Mavridis K.^[5], Vontas J.^[5], Ricci I.^[2], Favia G.^[2]

^[1]School of Biosciences and Veterinary Medicine, University of Camerino, Camerino, Italy; ^[2]School of Biosciences and Veterinary Medicine, University of Camerino, CIRM Italian Malaria Network, Camerino, Italy; ^[3]Istituto Zooprofilattico Sperimentale dell'Umbria e delle Marche "Togo Rosati", Perugia, Italy; ^[4]Department of Infectious Diseases, Istituto Superiore di Sanità, Rome, Italy; ^[5]Institute of Molecular Biology and Biotechnology, Foundation for Research and Technology-Hellas, Heraklion, Greece

Keywords: Mosquito, Vector-borne diseases, Arbovirosis

INTRODUCTION: In the last decades, we are experiencing a rapid warming of the Earth and a deterioration of natural environments that are leading to disequilibrium and biodiversity loss of unprecedented proportions (Rocklöv et al., 2020. *Nat Immuno*, 21:479-83). This scenario is impacting human and animal health, as vector-borne diseases (VBDs) are (re-)emerging in several countries as shown by recent outbreaks in Italy (De Carli et al., 2023. *Euro Surveill*, 28(44): 2300552). Thus, a multifaceted surveillance approach is crucial to understand the levels of risk that countries face and to define the necessary counteractions. This study aims to understand which biotic and abiotic factors affect the (re-)emergence of VBDs transmitted in selected Italian and Greek areas and their related ecological contexts through a coordinated approach of vector surveillance, pathogens screening, and environmental monitoring.

MATERIALS AND METHODS: Entomological surveillance was conducted in 67 sampling sites in the Marche and Umbria regions (Italy), and in 14 sampling sites in central Crete (Greece). Adult mosquitoes were collected over two years (2022-2023) from May to October. Each site was georeferenced. Date and onsite meteorological variables were recorded. Human population density, vegetation covering, and human land use were retrieved by remote sensing data. Specimens were morphologically and molecularly identified. Screening of USUTU (USUV) and West Nile viruses (WNV) was performed by RT-PCR on pooled *Culex pipiens*. *Aedes albopictus* and *Cx. pipiens* were analysed to detect filariae and both V1016G and L1014F kdr mutations by PCR.

RESULTS AND CONCLUSIONS: In the three studied areas several mosquito species have been identified, most of them were *Cx. pipiens* and *Ae. albopictus*. In Italy, we detected USUV and *Setaria* spp in *Cx. pipiens*. Studying the abundance of the USUV reservoir (wild birds), we observed a correlation between host frequency and the positivity of *Cx. pipiens* across months. Additionally, we identified two land cover variables (rural area and urbanization) that can affect the distribution of *Cx. pipiens* and *Ae. albopictus* in the Marche region. In Crete, for the first time, we found pools of *Cx. pipiens* positive for the WNV. Moreover, we observed an increasing frequency of hybrids of *Cx. p. pipiens/Cx. p. molestus* that could be considered a risk factor for the perpetuation of viral transmission among animals and humans since they are opportunistic feeders. The pathogen screening also revealed a pool of *Ae. albopictus* positive for *Dirofilaria repens*. Regarding the L1014F mutation implied in the insecticide resistance, we registered an increasing frequency of the resistant genotype in *Cx. pipiens* in both Italy and Greece. This approach repeated over time will provide a detailed map of the risks associated with mosquitoes and a large amount of data accessible to all the scientific community, offering an opportunity to optimize control strategies.