

P0450

Poster Session I

Emerging viruses / viral infections

MOLECULAR DETECTION OF SALEHABAD / ADRIA VIRUS IN SANDFLIES AND WEST NILE VIRUS IN MOSQUITOES FROM EASTERN THRACE, TURKEY

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Objectives: Activity of West Nile virus (WNV) and Toscana virus (TOSV) have been revealed in Eastern Thrace region, northwestern Anatolia in 2012; during investigation of clinical cases of febrile disease and central nervous system infections of unknown etiology. Moreover, WNV lineage 1 viruses were detected in mosquitoes from the region. In this study, preliminary findings of the field survey for WNV and Phlebovirus vectors performed during 2013 in Eastern Thrace region were represented.

Methods: Sampling was performed during July-August 2013 in 10 peri-domestic sites at 3 locations with miniature light traps. Mosquito specimens, sorted according to species using standard keys, and sandfly specimens were pooled as 1-40 individuals according to the capture site and date. Nucleic acid extraction and cDNA synthesis were performed in homogenates of each pool via commercial assays and further investigated for WNV RNA via a nested Polymerase Chain Reaction (PCR) in mosquito and via pan-phlebovirus nested PCR in sandfly pools. Species distribution in reactive sandfly pools were determined by biological barcoding via cytochrome c oxidase sequence analyses. Target amplicons were cloned in plasmids using commercial assays and characterized by sequencing.

Results: A total of 1353 mosquitoes that comprise *Ochlerotatus caspius* (90.6%), *Culex pipiens sensu lato* (4.3%), *Anopheles maculipennis sensu lato* (3.4%), *Culex theileri* (1.6%) and *Anopheles claviger* (0.1%) species were evaluated in 47 pools. Collected sandflies include 246 specimens, identified as *Phlebotomus* spp., grouped in 26 pools. WNV RNA was detected in an *Oc. caspius* pool (2.1%) that include specimens collected at a location where WNV was previously identified in *Oc. caspius* mosquitoes in 2012. The sequence was characterized as lineage 1 clade 1a that demonstrated 1-3% diversity with the sequences identified in mosquitoes in the region during 2012. One sandfly pool (3.8%) was positive in pan-phlebovirus PCR and the sequence of the amplicons revealed 77.1% and 76.3% similarity to Salehabad and Adria viruses, respectively. Molecular barcoding results demonstrated the positive pool to include *Phlebotomus perfiliewi sensu lato* species.

Conclusion: Ongoing activity of WNV lineage 1 strains were observed in Eastern Thrace region. Phlebovirus sequences suggesting the circulation of Salehabad or Adria viruses were identified in *P. perfiliewi s.l.* sandflies, comprising the first report of these strains from Turkey.