

P2334

Abstract (poster session)

Cross-sectional flavivirus surveillance reveals West Nile virus lineage 1 strains in *Culex pipiens sensu lato* and *Ochleratatus caspius* mosquitoes (Diptera: Culicidae) from Eastern Thrace region, Turkey

K. Ergünay, F. Günay, K. Öter, Ö. Erisöz Kasa, S. Örsten*, H. Erdem, A. Özkul, B. Alten (Ankara, Istanbul, TR)

Objectives: West Nile virus (WNV), a mosquito-borne Flavivirus has caused outbreaks of severe neuroinvasive disease in humans and horses in Europe, the Mediterranean Basin and emerged in the American continent. Serosurveillance reports have revealed human WNV exposure in various regions in Turkey; however, clinical cases have been reported after 2009-2010 and mosquito species responsible for virus transmission have not yet been characterized. This study presents the preliminary findings of the first mosquito field survey for WNV and other Flaviviruses in Eastern Thrace region, northwestern Anatolia, a region neighboring Greece and Bulgaria and the site of the recent identification of *Aedes albopictus* (*Stegomyia albopicta*) in Turkey. **Methods:** Mosquito sampling was performed during July 2012 in 10 peri-domestic sites at 3 locations with CDC miniature light traps. Captured mosquitoes were sorted according to species using standard keys, pooled as 30-40 individuals and homogenized via established procedures. Nucleic acids were extracted from homogenates of each pool via commercial assays and investigated for WNV RNA via a nested Polymerase Chain Reaction (PCR) targeting viral envelope glycoprotein and a pan-Flavivirus nested PCR as described previously. Amplicons from positive WNV-specific PCR were sequenced and analyzed. **Results:** A total of 2017 specimens in 51 pools were evaluated that include *Culex pipiens sensu lato* (11 pools, 21.6%) and *Ochleratatus caspius* (40 pools, 21.6%) species. WNV and pan-flavivirus PCR were positive in 4 pools (4/51, 7.8%) that include 3 (3/11, 27.3%) *Cx.pipiens* s.l. and 1(1/40, 2.5%) *Oc.caspius* pool. Remaining pools were negative in pan-Flavivirus PCR. Sequences obtained from WNV-specific amplicons were characterized as Lineage 1 Clade 1a and similar or identical with patient-derived sequences from the region, identified during August, 2012. **Conclusion:** Activity of WNV Lineage 1 strains were detected in Eastern Thrace region, Turkey in *Cx.pipiens* s.l. and *Oc. caspius* mosquitoes, possibly involved in human transmission.