

O149

2-hour Oral Session

Emerging viruses: what about "Tick", "Chik" and "Zik"?

**First reporting of Chikungunya virus as well as West Nile virus and mosquito-specific flaviviruses in field-collected mosquitoes from Mediterranean, Aegean, and Thrace regions, Turkey**

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**Background:** Screening of field-collected mosquitoes provides an efficient method to determine the activity of vector-borne viruses within regions with suitable climate and arthropod fauna. Previous reports from Turkey have demonstrated a widespread activity of West Nile virus (WNV), concurrent with the emergence of case clusters. This study was undertaken to investigate mosquito-borne Flavi and Alphaviruses for a cross-sectional view of the activity of these pathogens in regions associated with current residence areas or passage routes of Syrian war refugees.

**Material/methods:** Mosquito sampling was performed during June-August 2015 in several peri-domestic sites with CDC light traps. Captured specimens were sorted according to species, pooled and subjected to nucleic acid purification and cDNA synthesis after homogenization. Generic nested and real-time polymerase chain reaction (PCR) methods were employed for detecting Alpha and Flaviviruses. Positive pools were characterized via sequencing of the amplicons.

**Results:** A total of 4105 specimens that comprise 240 (5.9%) in locations from Aegean, 440 (10.7%) in locations from Mediterranean and 3425 (83.4%) in locations from eastern Thrace region was collected. Morphological identification demonstrated *Aedes caspius* (2511, 61.2%) to be the most abundant species, followed by *Anopheles maculipennis sensu lato* (783, 19.1%), *Culex pipiens sensu lato* (564, 13.7%), *Culex theileri* (134, 3.3%), *Culex tritaeniorhynchus* (48, 1.2%), *Anopheles claviger* (45, 1.1%) and others. The specimens were tested in a total of 188 pools, originating from collection sites in Aegean (32, 17%), Mediterranean (44, 23.4%) and Thrace (112, 59.5%) regions. Generic Alphavirus and Flavivirus PCRs revealed positive results in 2 (1,1%) and 8 (4.3%) pools, respectively. Repeat testing and sequencing revealed Alphavirus positive specimens to be characterized as Chikungunya virus (CHIKV). Positive results originated from *An. maculipennis sensu lato* and *Ae.*

*caspius* pools and displayed 82.9-88.6% sequence homology to several CHIKV strains. In one pool, composed of *Cx. theileri* specimens, WNV lineage 1 clade 1a sequences were detected. Moreover, in 3 *Cx. theileri*, 1 *Uranotenia unguiculata* and 1 *Cx. pipiens* s.l. pools, sequences of Mediterranean Culex Flavivirus strains were identified. Mediterranean Ochleratatus Flavivirus sequences were also characterized in 2 *Ae. caspius* pools.

**Conclusions:** Indigenous activity of CHIKV was identified for the first time in Turkey. Despite detection in mosquito species with limited vector potential, appropriate surveillance and diagnostic measures should be undertaken to monitor virus epidemiology and potential emergence of human cases. Ongoing circulation of WNV lineage 1 strains have further been documented. Presence of several mosquito-specific Flaviviruses have also been initially revealed in Turkey.