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First genetic characterization of *Usutu virus* from *Culex pipiens* mosquitoes Serbia, 2014

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Since its first appearance in Europe, *Usutu virus* (USUV) diverged to several different genetic lineages. The virus was reported to date from multiple countries across Europe (Hungary, Italy, Switzerland, Spain, Germany, Czech Republic and Belgium). Considering the more frequently published impact of the virus on humans it is crucial to investigate locally circulating genetic variants and trace its evolution. We retrospectively analyzed mosquito samples from Serbia Vojvodina region, collected during 2014. In this study, we report the results of the screening of 23753 female mosquitoes (753 pools) for USUV-specific nucleic-acid. Based on phylogenetic analysis the Serbian USUV sequence was most closely related to the virus that emerged in Austria in 2001, in Hungary in 2005 and was circulating until 2015 in Hungary. This data presents a wider geographic distribution of this genetic variant and provides the first genetic data from this region.

Recent Publications

1. Zana B (2016) Genomic characterization of West Nile virus strains derived from mosquito samples obtained during 2013 Serbian outbreak. *Journal of Vector Borne Diseases* 53:379.
2. Zana B (2017) Molecular traces of a putative novel insect flavivirus from *Anopheles hyrcanus* mosquito species in Hungary. *Acta Virologica* 61:127-129.
3. Bányai K (2017) Candidate new rotavirus species in Schreiber's bats, Serbia. *Infection, Genetics and Evolution* 48:19-26.
4. Kemenesi G (2017) Highly divergent cyclo-like virus in a great round leaf bat (*Hipposideros armiger*) in Vietnam. *Archives of Virology* 162:2403-2407.
5. Kurucz K (2017) Ecological preferences of the putative West Nile virus vector *Uranotaenia unguiculata* mosquito with description of an original larval habitat. *North-Western Journal of Zoology* 13(2):193-199.

Biography

Brigitta Zana is a PhD student at University of Pécs, Hungary. Her PhD program is focusing on the description and genetic characterization of viral pathogens distributed by different vector organisms such as bats, mosquitoes and ticks. Her findings give detailed genetic characterization and phylo-geographic information about human pathogenic viruses circulating in Central Europe and Asia.

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