

# MOLECULAR EPIDEMIOLOGY OF NEUROINVASIVE FLAVIVIRUS INFECTIONS IN CROATIA

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## INTRODUCTION

(Re-)emerging flavivirus infections represent a public health problem in many parts of the world. Among neuroinvasive flaviviruses, tick-borne encephalitis virus (TBEV), West Nile virus (WNV) and Usutu virus (USUV) are most widely distributed. WNV strains are classified into several genetic lineages of which lineage 1 and 2 are the most widespread. Recent data from the European countries showed that WNV strains detected in humans mainly belong to lineage 2. USUV strains are grouped into 8 lineages: five European (1-5) and three African (1-3). Most human USUV strains belong to European USUV lineages (mainly Europe 2), however African lineages were also documented. The TBEV European subtype is most prevalent in western, northern and eastern Europe and European parts of Russia, with Far East and Siberian subtypes co-circulating in Eastern Europe.

## AIM

The aim of this study was to analyze the molecular epidemiology of neuroinvasive flaviviruses detected in Croatia during the four consecutive transmission seasons (2017-2020).

## MATERIALS AND METHODS

A total of 474 patients with the neuroinvasive disease were included in the study. Viral RNA was detected in cerebrospinal fluid and/or urine samples using a real-time RT-PCR. Samples identified as positive using the real-time RT-PCR assays were subjected to conventional RT-PCR and Sanger sequenced.

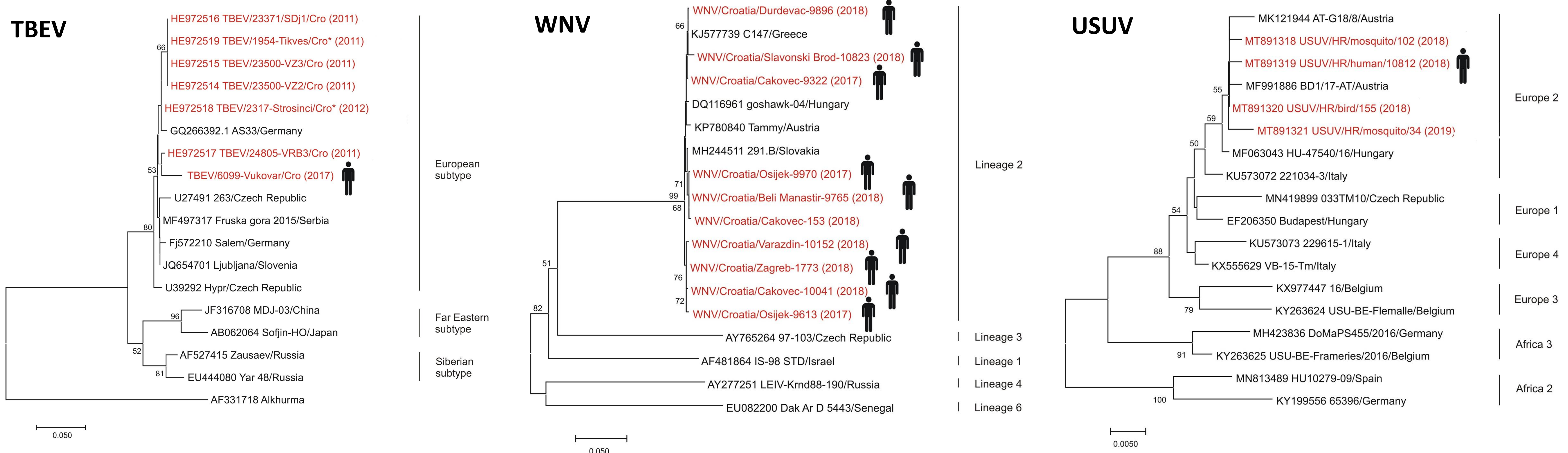


Figure 1. Molecular epidemiology of TBEV, WNV and USUV in Croatia (2017-2018)

## RESULTS

TBEV was confirmed in 43 patients (2017-2020), WNV in 61 (2017-2018) and USUV in three patients (2018). Phylogenetic analysis of detected flaviviruses is presented in figure 1. One TBEV strain detected in the urine sample of a patient with severe neuroinvasive infection (2017) belonged to TBEV European subtype. All 11 sequenced WNV strains (3 from 2017 and 8 from 2018) showed circulation of WNV lineage 2. One USUV strain from a fatal encephalitis case (2018) clustered within Europe 2 lineage.

## CONCLUSION

Molecular epidemiology of flaviviruses detected in Croatian patients showed a similar pattern as in other European countries.



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