

VIROLOGY, INFECTIOUS DISEASES AND COVID-19

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Phylogenetic analysis and geographical distribution of torquetenovirus in the Romanian population

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Torquetenovirus (TTV) has a high prevalence in humans, yet there is limited information on its circulation in the human population. This study aimed to estimate the geographical distribution and phylogenetic relationships between TTV isolates found in the Romanian general population. A number of 200 volunteers aged 51.6 ± 17.1 were tested for TTV DNA presence in blood using PCR techniques targeting the untranslated region of the viral genome. A region of approximately 400 bp of 3'UTR was sequenced by Sanger technology in 40 volunteers residing in all seven development regions of Romania, in order to determine the geographical distribution of TTV and to describe the phylogenetic relationships between isolates. The prevalence of TTV DNA was 66%. Most of Romanian sequences clustered with isolates from genogroup 1, currently assigned to TTV1 and TTV3 species, while two other sequences clustered closest with TTV19-SANBAN and TTV22-svi-1 (genogroup 3). Phylogenetic analysis showed segregation between isolates from north-east and center-west Romania. In order to better characterize certain isolates (e.g. seasonality, pathogenic potential), further phylogenetic studies should focus on distinguishing between genogroups/genotypes

Keywords: phylogeny, phylogeography, DNA virus infection

Biography:

Sonia received her Ph.D. degree in biology from the University of Bucharest in 2016 and she nurtures a keen interest in molecular virology, multifactorial disorders and population genetics. She is currently a member of the Human Genome and Molecular Diagnostics laboratory and her study focuses on human anelloviruses as environmental factors in multifactorial diseases.