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Reconsidering the classification of tick-borne encephalitis virus within the Siberian subtype gives new insights into its evolutionary history

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RECONSIDERING THE CLASSIFICATION OF TICK-BORNE ENCEPHALITIS VIRUS  
WITHIN THE SIBERIAN SUBTYPE GIVES NEW INSIGHTS INTO ITS EVOLUTIONARY  
HISTORY

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**Abstract**

Tick-borne encephalitis is widespread in Eurasia and transmitted by *Ixodes* ticks. Classification of its causative agent, tick-borne encephalitis virus (TBEV), includes three subtypes, namely Far-Eastern, European, and Siberian (TBEV-Sib), as well as a group of 886-84-like strains with uncertain taxonomic status. TBEV-Sib is subdivided into three phylogenetic lineages: *Baltic*, *Asian*, and *South-Siberian*. A reason to reconsider TBEV-Sib classification was the analysis of 186 nucleotide sequences of an E gene fragment submitted to GenBank during the last two years. Within the *South-Siberian* lineage, we have identified a distinct group with prototype strains Aina and Vasilchenko as an individual lineage named *East-Siberian*. The analysis of reclassified lineages has promoted a new model of the evolutionary history of TBEV-Sib lineages and TBEV-Sib as a whole. Moreover, we present arguments supporting separation of 886-84-like strains into an individual TBEV subtype, which we propose to name *Baikalian* (TBEV-Bkl).

**Keywords:** *tick-borne encephalitis virus, Siberian subtype, clusteron structure, classification, phylogenetic lineage*

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