### Accepted Manuscript

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

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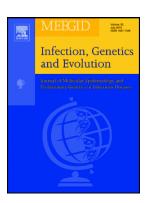
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## ACCEPTED MANUSCRIPT

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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