



V 14 Isolation and preliminary characterization of a tick-borne encephalitis virus strain in ticks from Mongolia

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Tick-borne encephalitis virus (TBEV), a member of the family Flaviviridae, causes one of the most important inflammatory diseases of the central nervous system (CNS), namely severe encephalitis in Europe and Asia. In Mongolia, TBE is known since the 1980s. The numbers of human cases have been increasing during the last years. Endemic areas of TBE associated with severe CNS diseases have been reported mainly in the provinces (Aimak) Selenge and Bulgan in northern Mongolia close to the Russian border. We report the first isolation and preliminary genetic characterization of a TBE virus strain from ticks collected in Mongolia.

Sixty-eight ticks (*Ixodes persulcatus*) were collected by flagging in the Bulgan district near Khylganatt in the north of Mongolia in July 2010. Ticks were homogenized individually and supernatants were used for nucleic acid extraction (QIAGEN Viral RNA Extraction Kit). Extracted RNA was screened for TBEV-specific sequences by real-time RT-PCR. In 2 out of 68 (3%) tested ticks, RNAs were reactive. The real-time RT-PCR-positive tick supernatants were inoculated into Vero cells. A TBEV strain (MucAr M14/10) could be recovered from one of the 2 positive tick supernatants. The second positive tick supernatant with a lower TBEV RNA content proofed negative in cell culture.

By conventional RT-PCR targeting the E gene, the entire E gene could be amplified. By direct sequencing, the 1488-nt-long E gene sequence was obtained. Sequence comparison of the E gene revealed the highest homology on the nucleotide level (96.7%) and on the amino acid level (99.5–99.7%) to 3 strains of a subclade of the Siberian subtype of TBE virus, the strains Zausaev (AF527415), IR99-2m7 (AB049351), and Lesopark (GU121966), respectively.