



## EVOLUTIONARY TRAITS OF THE BAIKALIAN SUBTYPE OF TBE VIRUS AND GENETIC BOTTLENECK DETECTION IN ZABAİKALSKY KRAI (EASTERN SIBERIA, RUSSIA)

### Background

Last year, an article dedicated to six complete genomes of the relatively new TBEV Baikalian subtype (TBEV-Bkl) was published in *Tick and Tickborne Disease* (TTBD) (Adelshin et al., 2019). All six TBEV-Bkl strains were isolated in the Zabaikalsky Krai territory (Eastern Siberia, Russia). Analysis of 1000 bootstrap replicates (phylogenies) exhibited that the degree of genetic distance of the TBEV-Bkl group from the three established significant subtypes of the TBEV brings it to the same taxonomic level.

Zabaikalsky Krai is a unique place regarding TBEV genetic diversity, where we previously showed circulation of two other TBEV subtypes: Siberian (TBEV-Sib) and Far-Eastern (TBEV-FE) (Sidorova et al., 2012). In total, we had 38 TBEV strains including TBEV-Bkl.

In our last publication (Bondaryuk et al., 2020), we report new E protein partial gene sequences (1308 nt) of 38 TBEV strains, isolated in Zabaikalsky Krai (Eastern Siberia, Russia) in 1960–1963 and 1995–2011. Using this genome data on three TBEV subtypes, we managed to provide a Bayesian phylogenetic analysis (BEAST v.1.10.4) which reveals hidden evolutionary traits of TBEV population from Zabaikalsky Krai.

### Results and discussion

#### *Molecular clock analysis*

Analysis employing the relaxed molecular clock showed that ancestor lineages of all three TBEV subtypes had their own evolutionary rate: the

slowest rate corresponds to a TBEV-Bkl ancestor lineage, the fastest rate belongs to a TBEV-FE ancestor lineage. Difference between them was about 21%. TBEV-Sib ancestor lineage took an intermediate position that probably indicates specific selection pressure impacting on each TBEV subtype during their evolution. It is hard to say now which factors (e.g. ecological factors or immune selection of hosts) have such a strong influence on the evolutionary rate of TBEV.

#### *Population dynamics and possible consequences of large-scale DDT forest dusting*

To reconstruct past population dynamics (changes in effective population size ( $N_e$ )) we used the Bayesian Skyline model (BSL) implemented in BEAST v.1.10.4. BSL. Applying it showed a drastic decline of  $N_e$  in the 1950s that coincides with the date of the beginning of wide dichlorodiphenyltrichloroethane (DDT) forest dusting in Siberia. In Soviet scientific journals, there is a lot of interesting information regarding DDT forest treatment and its efficiency. In particular, Gorchakovskaya reported that studies of DDT against ticks began in 1953. The efficiency of DDT was shown to be high throughout the Siberian territory. Gorchakovskaya also stated that DDT forest dusting led to the extermination of 98–99.9% of adult ticks. Also, DDT significantly reduced numbers of larvae and nymphs (96–98%). In the Kemerovo region (Western Siberia), the forest was dusted by DDT (30 kg/ha) after which no ticks were indicated seven years later, while numbers of field voles and shrews remained high (Gorchakovskaya, 1962). In the Krasno-



Chikoisk district of Chita region (Zabaikalsky Krai now), the efficiency of aerial spraying reached 95–97% (Zlobin and Gorin, 1996). With almost complete tick extermination, Gorchakovskaya also noted the reduction of TBE cases in dusted territories. Thus, we speculate, the drastic decline of Ne can be a sign of large-scale DDT forest dusting.

In the near future, we plan to sequence the complete genomes of 38 TBEV strains from the territory of Zabaikalsky Krai to be able to get more information about inner TBEV population processes.

## Literature

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