

NorVect Conference 2015 – poster session

SPECTRUM OF TICK-BORNE DISEASES PATHOGENS IN KAZAKHSTAN

¹Ravilya Yegemberdiyeva, ²Zhanna Shapiyeva, ¹Andrey Dmitrovskiy, ³Aitmagambet Turebekov

¹Kazakh National Medical University, Almaty, Kazakhstan

²SPC of Sanitary and Epidemiological Expertise and Monitoring, Almaty

³West-Kazakhstan Medical Academy, Aktobe

Background. The number of tick-borne diseases (TBD), such as Crimean-Congo hemorrhagic fever (CCHF), tick-borne encephalitis virus (TBEV), tick-borne typhus of North Asia (tick-borne typhus), tularemia are officially registered in Kazakhstan. However, it is known that ticks can be reservoirs for significant specter of the different pathogens. In this connection, it became necessary to expand the range of laboratory methods for diagnosis of TBD and to improve the epidemiological surveillance of TBD in Kazakhstan.

The aim of study was the evaluation of infectiousness of *Ixodid* ticks by TBEV, *B.burgdorferi* sl, *B.miyamotoi*, *A. phagocytophillum*, *E. chaffeensis* and *E.muris* in some regions of Kazakhstan.

Materials and methods. In 2008 281 samples of *I.persulcatus* ticks from the East Kazakhstan region and 212 samples of *I.persulcatus* from Almaty region were tested. In 2014 33 ticks of *D.marginatus* from Aktobe region, 7 samples of *H.asiaticum* , *H.anatolicum*, *R.pumilo* from Atyrau region, 30 ticks *D.niveus* from Kyzyl-Orda region and 30 samples of *D.daghestanicus* from Zhambyl region were also tested.

The identification of pathogen microorganisms was done by using RT-PCR with "AmpliSens - TBEV, *B.burgdorferi* sl, *A. phagocytophillum*, *E. chaffeensis* / *E.muris*» - FRT (Central Research Institute of Epidemiology, Russia, Moscow). It was developed on the basis of RT-PCR technique specific for *B.miyamotoi*.

Results. Studies of the ticks from the East Kazakhstan region demonstrated 2.8% (8 of 281 ticks) infected ticks with TBEV. The genotyping of all isolates were assigned to the Siberian subtype of TBEV. The DNA of *B.burgdorferi* sl was found in 40.6% of samples (in 114 of 281 ticks), *B.miyamotoi* - 2.1% (6 of 281 ticks), *A. phagocytophillum* - 2.1% (6 of 281 ticks), *E.chaffeensis* / *E.muris* - 7.8% (22 of 281 ticks). The genotyping of pathogenic *Ehrlichia* determine *E.muris*.

In Almaty region, TBEV was found in 3.3% of ticks (7 of 212 ticks). The DNA of *B.burgdorferi* sl – in 36.8% of the samples (78 of 212 ticks), *B.miyamotoi* - 5,7% (12 of 212 ticks), *A.phagocytophillum* - 1,4% (3 of 212 ticks), *E.muris* - 6.1% (12 of 212 ticks). In Aktobe region, TBE virus was in 3.0% of samples (1 of 33 ticks), *E.muris* – 72.7% (24 of 33 ticks), *A.phagocytophillum* – 6.1% (2 of 33 ticks). The results for Lyme borreliosis were negative. In Atyrau oblast, *E.muris* detected in 100% of samples. Pathogens of TBE, Lyme borreliosis and anaplasmosis were not found. In Kyzyl-Orda region, *B.miyamotoi* was in 5.3% of samples (5 of 19 ticks), *E.muris* - 6,7% (2 of 19 ticks). Pathogens of TBEV, Lyme borreliosis and anaplasmosis also were not found. In Zhambyl region, the results of the above 4 pathogens were negative.

CONCLUSIONS: For the first time, new TBD pathogens in *Ixodid* ticks (*B.burgdorferi* sl, *B.miyamotoi*, *A. phagocytophillum*, *E. chaffeensis* / *E.muris*) were obtained in Kazakhstan. The results show the need for further in-depth study of TBD in Kazakhstan.