



LITHUANIA

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Rabies situation in Lithuania in the last few years (2015-2018)

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The aim of this study was to present the current epidemiological data regarding rabies cases in Lithuania. Also to evaluate efficiency of oral vaccination (ORV) campaigns by measuring antibody response and tetracycline biomarker from the target animals.

MATERIALS AND METHODS : all suspected animals, animals found dead, road killed animals, which bite or scratch humans, or animals for rabies diagnosis, also as a separate group red foxes and racoon dogs shot for the efficiency of ORV are sent to the National Food and Veterinary Risk Assessment Institute (NFVRAI).

The methods were used within the frame of rabies eradication programme : FAT, RTCIT (on N2a cells), RT-PCR, ELISA. For rabies diagnosis confirmation and sequence analysis the samples were sent to the ANSES – Nancy Laboratory for Rabies and Wildlife.

RESULTS : during the last few years (2015-2018), three cases of rabies have been identified in wild animals: in 2015 were detected 2 cases (red fox and racoon dog) in Ignalina district and in the last two years since 2016, no case of rabies was found. However, in the end of 2018, one positive rabies case in red fox near Bielorussian border zone (Šaščininkai district, Pagaujėnų village) was detected. The brain tissue of the fox was shown positive by FAT and RTCIT on (N2a cells) for the presence of rabies antigen and infectious virus. Rabies RNA was also detected by molecular biology techniques hnRT PCR PCR as described by « P/R Heaton et al. 1997 AND Orlovska et al 2008 » and RT-PCR by SYBR®Green. The presence of tetracycline in jaw and tooth samples showed high level of bait uptake, from 90% in 2013 to 77% in 2018. Decrease of seroconversion from 53% in 2015 to 34% in 2018 of animals from the vaccination area.

CONCLUSION : During 2015-2018, three rabies cases have been detected in the border area with Belarus. The phylogenetic analysis based on the comparison of the partial N gene sequence with representative RABV sequences showed that the isolate (2018 DR-1790) corresponds to a field rabies virus isolate. The genetic analysis showed that the sample belonging to the group C1a/CA1 was assigned to Russian samples and two Lithuanian samples isolated in 2015. Based on the nucleotide comparison of partial N gene, 99% of nucleotide identities were shown between the sequence (2018 DR-1790) and sequences within the group CA1/C1a, previously identified in the steppe and the forest steppe ecological regions of the European part of Russia, in the western part of Kazakhstan and in central and eastern regions of Ukraine. This finding support the hypothesis of movement of rabies-infected hosts from the Belarus or Russia.