

PHYLOGENETIC ANALYSIS OF RABIES VIRUS IN LITHUANIAN RED FOX AND RACCOON DOG POPULATIONS

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Summary. The aim of present work was to determine nucleoprotein region sequences and characterize the rabies virus (RV) isolates in order to know which virus group (biotype) is circulating in Lithuanian population of red foxes and raccoon dogs. A panel of 22 rabies isolates from red foxes (8) and raccoon dogs (14) were collected and studied, originated mainly from the central, eastern and northern regions of Lithuania. The nucleoprotein gene of rabies viruses were amplified from the brains samples and the 400 b nucleotide sequences were compared with those of others selected rabies virus sequences from Latvia, Estonia, Russia, Poland and other West European countries available in the GenBank. All rabies isolates from Lithuania demonstrated a high degree of genetic similarity in nucleoprotein region with nucleotide identity from 97.7% to 100%. Phylogenetic analysis of nucleoprotein gene suggested that all Lithuanian strains were from the North East Europe (NEE) group of the first rabies virus genotype and were closely associated with the rabies isolates from Poland, Latvia, Estonia, Finland, and North-Eastern part of Russia.

Keywords: rabies, phylogenetic analyses, Lithuania.