Molecular analysis of the nucleoprotein gene of canine distemper virus isolated from clinical cases of the disease in foxes, minks and dogs

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Abstract

In this study, we used RT-PCR to detect and characterize canine distemper virus isolated from 9 naturally infected foxes, 3 minks and 3 dogs in Poland by amplifying and sequencing a portion of the NP gene. A 293-bp fragment of the CDV NP gene was amplified by RT-PCR. Sequencing of the PCR products from the isolates led to the identification of 3 sequence variants. The mostly representative polymorphic variant No. 1 showed high homology with Chinese isolate of CDV with a accession number EF 375619. The sequences of all isolates from this polymorphic variants compared with the sequences of other polymorphic variants obtained in the study and with European and American isolates sequences from GenBank showed the conservative nucleotides changes in positions 57, 132, 143, 159 and 237. These mutations can indicate that in this part of Europe there are new variants of CDV.

Key words: CDV, RT-PCR, NP-gene, sequencing

Introduction

Canine distemper (lat. *febris catarrhalis infectiosa canum*) is a highly infectious, systemic viral disease, with high fever and signs of catarrhal inflammation of the alimentary and respiratory mucosa, accompanied by neurological complications and secondary respiratory infections (Appel 1987). The aetiological factor of the disease is canine distemper virus (CDV) of *Morbilivirus* genus belonging to the family *Paramyxoviridae*. It is highly infectious to many species of carnivores and may contribute to a significant depopulation of some of them (Myers et al. 1997). The genetic material of CDV is a single strand of RNA consisting of approximately 15,616 nucleotides. Within the genome six protein-coding genes were identified: membrane protein (M), two glycoproteins (hemagglutinin – H and fusion protein), two viral replication proteins (phosphoprotein P and protein L) and nucleocapsid protein -N (Sidhu et al. 1993). Comparing the sequences of particular protein-coding genes of CDV, it was demonstrated that the most frequent differences between the reference strains and CDV isolates occur in the following genes: hema-