Occurrence of *Bordetella bronchiseptica* in domestic cats with upper respiratory tract infections

M. Garbal¹, Ł. Adaszek¹, P. Łyp¹, J. Frymus², M. Winiarczyk³, S. Winiarczyk¹

¹ Department of Epizootiology and Infectious Diseases, Faculty of Veterinary Medicine, University of Life Sciences Lublin, Głęboka 30, 20-612 Lublin, Poland
² Division of Surgery and Anaesthesiology of Small Animals, Faculty of Veterinary Medicine, Warsaw University of Life Sciences, Nowoursynowska 159 C Warsaw, Poland
³ Department of Vitreoretinal Surgery, Medical University of Lublin, Chmielna 1, 20-079 Lublin, Poland

Abstract

*Bordetella bronchiseptica* is a widespread Gram-negative pathogen occurring in different mammal species. It is known to play a role in the etiology of infectious atrophic rhinitis of swine, canine kennel cough, respiratory syndromes of cats, rabbits and guinea pigs, and sporadic human cases have also been reported. The aim of this article is to present the occurrence of infections caused by these bacteria in domestic cats with respiratory symptoms, as well as to conduct a molecular analysis of the flaA gene *B. bronchiseptica* for the purpose of ascertaining whether cats become infected with one or more bacteria strains. *B. bronchiseptica* was isolated from the respiratory system of 16 out of 35 domestic cats with symptoms of respiratory tract infections. Polymorphism analysis of polymerase chain reaction products of *B. bronchiseptica* flaA was performed to reveal the possible differences in nucleotide sequences of the flagellin gene.

The phylogenetic analysis of nucleotide sequences obtained during PCR indicated that the isolates of bacteria from our own studies are characterised by 100% homology of the analysed fragment of the flaA gene, which suggests maintenance of a single genotype of these microorganisms in the cat population. Moreover, the bacteria revealed full homology with reference strain *B. bronchiseptica* ATCC 4617, and 99.4% homology with strain *B. parapertussis* ATCC 15311. This indicates that the PCR optimised for the *Bordetella* spp. flaA gene, combined with sequencing of amplicons obtained in PCR, is an effective diagnostic method allowing differentiation of *Bordetella* spp. type microorganisms.

Key words: *Bordetella bronchiseptica*, PCR, microbiological examination, domestic cat

Correspondence to: Ł. Adaszek, e-mail: ukaszek0@wp.pl, tel.: +48 814 456 192