Polish Journal of Veterinary Sciences Vol. 14, No. 1 (2011), 141-143

DOI 10.2478/v10181-011-0021-z

Short communication

Isolation of an atypical pigeon paramyxovirus type 1 in Poland

K. Śmietanka, Z. Minta

National Veterinary Research Institute, Department of Poultry diseases,
Al. Partyzantów 57, 24-100 Pulawy, Poland

Abstract

In this study, a pigeon paramyxovirus type 1 (PPMV-1) isolated from a flock of ornamental pigeons in Poland in 2010 is described. The PPMV-1/Poland/H2/10 isolate showed the amino acid sequence at the cleavage site of F2/F1 ^{112}KRQKRF^{117} i.e. typical of virulent strains. Despite having the monoclonal antibody binding pattern typical of pigeon variants PPMV-1 (antigenic group "P"), the Polish isolate clustered into genetic sublineage 4a, which is usually associated with PMV-1 isolated from poultry.

Key words: paramyxovirus type 1, pigeons, sublineage 4a

Introduction

Newcastle disease, which is caused by an antigenic "pigeon variant" of the avian paramyxovirus type 1 (PPMV-1), was first described in the early 1980s in Italy (Biancifiori and Fioroni 1983), but its origin appears to be in the Middle East in the 1970s (Kaleta et al. 1985). The disease spread rapidly throughout the world, becoming panzootic in racing, ornamental and feral pigeons (Alexander and Senne 2008). The clinical signs are mainly associated with nervous disorders accompanied by watery green diarrhoea. The PPMV-1 differs antigenically and genetically from PMV-1, which is usually detected in poultry (Alexander et al. 1997, Aldous et al. 2003).

In our study we performed a partial sequencing of the F gene from the isolate PPMV-1/PL/H2/10, detected in a hobby flock of ornamental pigeons (English carrier) in Poland in 2010.

Materials and Methods

The virus, isolated in SPF embryonated eggs, was identified by using a haemagglutination inhibition (HI) test with NDV-specific polyclonal antiserum and with the monoclonal antibody (mAb) 161/617, which specifically recognises antigenic variants of PPMV-1 (kindly provided by Dr. Ruth Manvell, VLA Weybridge). The RNA was extracted from infected allantoic fluid using a Qiagen RNeasy Kit according to the manufacturer's instructions. Reverse transcription and PCR reaction were performed using a Qiagen RT-PCR kit (primer sequences and RT-PCR conditions available upon request). The nucleotide sequence analysis of the PCR product (512 bp, sequenced in Genomed, Warsaw) were conducted using LaserGene sequence analysis software (DNASTAR, Inc., Madison, WI). For phylogenetic analysis, the variable region of the F gene (nucleotides from 47 to 420) was used and

Correspondence to: K. Śmietanka, e-mail: ksmiet@piwet.pulawy.pl

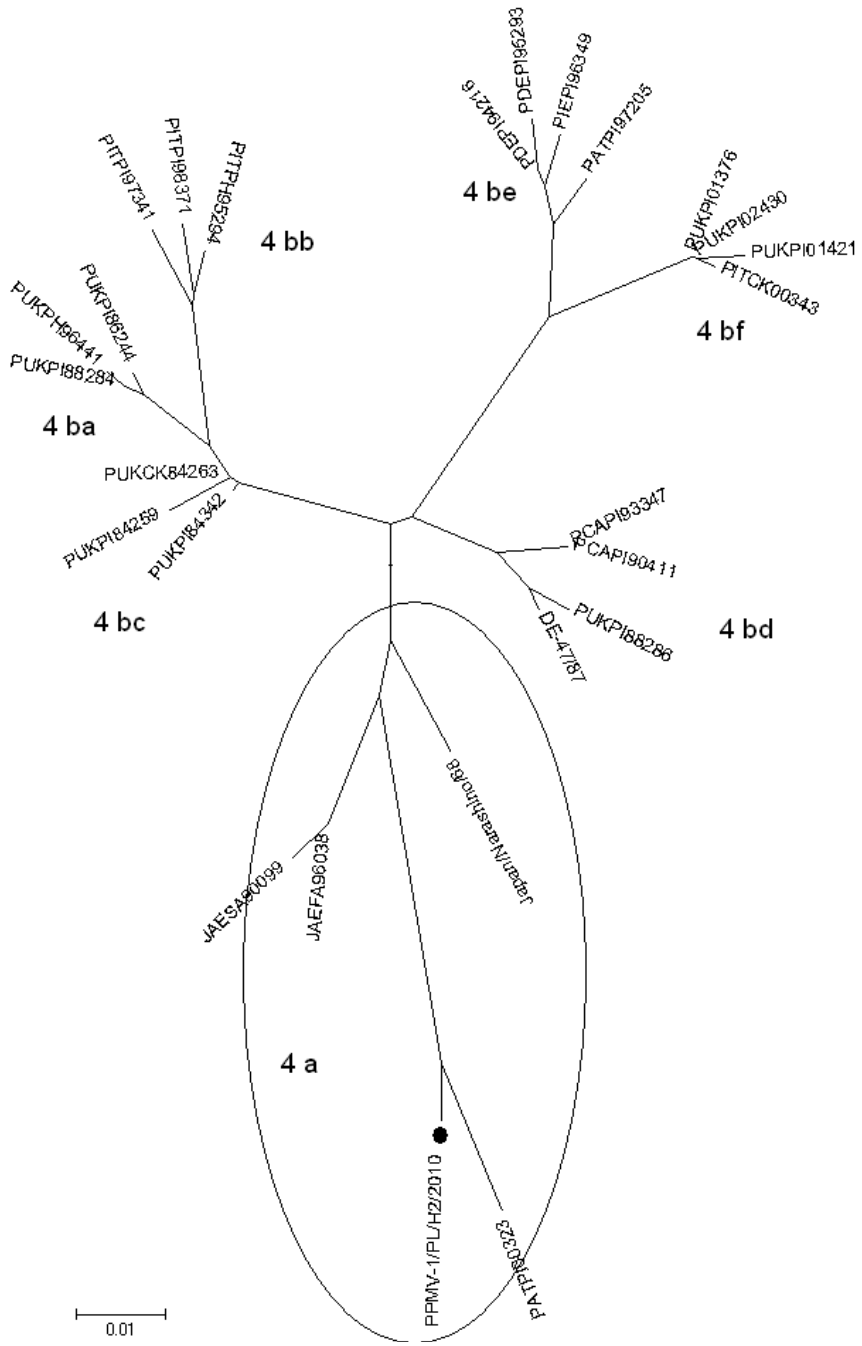

Fig. 1. Comparison of the nucleotide sequences of the F gene (nucleotides 47 to 420) of PPMV-1 isolate detected in pigeons in Poland (PPMV-1/PL/H2/10) and other sequences of PMV-1 of sublineages 4a and 4b obtained from the GenBank database. The tree was constructed using the neighbor-joining method in MEGA 4 software. Branch lengths represent the predicted number of substitutions and are proportional to the differences between the isolates. The nucleotide sequence of PPMV-1/PL/H2/10 was submitted to the GenBank with accession number HM627541.

phylogenetic trees were constructed with MEGA 4 software (Tamura et al. 2007).

Results and Discussion

The virus was identified in the HI test as avian paramyxovirus type 1, and based on its reactivity with the 161/617 mAb it was classified into antigenic group "P" ("pigeon variants") (Alexander et al. 1997). The results of molecular assessment of pathogenicity indicated high virulence of the tested isolate (amino acid motif at the cleavage site of F2/F1 protein ^{112}KRQKRF^{117}). The results of phylogenetic investigations indicate that, despite antigenic similarity to

"pigeon variants", which usually represent sublineage 4b (Aldous et al. 2004), the PPMV-1/PL/H2/10 isolate represents sublineage 4a. To our knowledge there have been very few reports on PPMV-1 belonging to this genetic sublineage: Aldous et al. (2003, 2004) described two "4a" PPMV-1 isolated from pigeons in Turkey in 1995 and in Austria in 2000. The PPMV-1/PL/H2/10 shared the highest nucleotide sequence homology (97.8%) with the Austrian isolate PATPI00323 (GenBank: AY471789). The nucleotide sequence similarity of the Polish isolate to the sequences of typical "4b" PPMV-1 used for comparison was lower and ranged from 89.9 to 92.3% (Fig. 1). This finding is significant since it indicates that viruses of sublineage 4a have been circulating in pigeons in Europe and possibly in the Middle East since at least the mid 1990s without being totally replaced by the predominant group 4b of PPMV-1. The origin of viruses from sublineage 4a in pigeons is unknown. This group contains mostly "ancient" PMV-1, isolated since 1968 mainly in domestic fowl from the Middle East, Europe and Africa (Aldous et al. 2003). Presumably a small fraction of PMV-1 naturally existing in fowl established itself in the pigeon population. Similarly to "4b" PPMV-1, the virus has undergone some adaptive changes to the new host expressed by the antigenic profile in the F protein typical of "pigeon variants". More extensive surveillance is necessary to establish how widespread the representatives of sublineage 4a in pigeons are.

Acknowledgements

We thank Elżbieta Juszczuk and Monika Olszewska for excellent technical assistance. This study has been funded by European Network of Excellence (EPIZONE) WP6.2 "Molecular epidemiology and surveillance of AI and APMV".

References

Aldous EW, Mynn JK, Banks J, Alexander DJ (**2003**) A molecular epidemiological study of avian paramyxovirus type 1 (Newcastle disease virus) isolates by phylogenetic analysis of a partial nucleotide sequence of the fusion protein gene. Avian Pathol 32: 239-256.

Aldous EW, Fuller CM, Mynn JK, Alexander DJ (**2004**) A molecular epidemiological investigation of isolates of the variant avian paramyxovirus type 1 virus (PPMV-1) responsible for the 1978 to present panzootic in pigeons. Avian Pathol 33: 258-269.

Alexander DJ, Manvell RJ, Lowings JP, Frost KM, Collins MS, Russell PH, Smith JE (**1997**) Antigenic diversity and similarities detected in avian paramyxovirus type 1 (Newcastle disease virus) isolates using monoclonal antibodies. Avian Pathol 26: 399-418.

Alexander DJ, Senne DA (**2008**) Newcastle disease, other avian paramyxoviruses, and pneumoviruses infections. In: Saif YM (ed) Diseases of Poultry, 12th ed, Blackwell Publishing, Ames, pp 75-116.

Biancifiori F, Fioroni A (**1983**) An occurrence of Newcastle disease in pigeons: virological and serological studies on the isolates. Comp Immunol Microbiol Infect Dis 6: 247--252.

Kaleta EF, Alexander DJ, Russell PH (**1985**) The first isolation of the avian PMV-1 virus responsible for the current panzootic in pigeons? Avian Pathol 14: 553-557.

Tamura K, Dudley J, Nei M, Kumar S (**2007**) MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. Mol Biol Evol 24: 1596-1599.