

Epidemiology and Public Health

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Phylogenetic analysis of pigeon type paramyxovirus 1 in Germany

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Question: Pigeon type paramyxovirus-1 (PPMV-1), a subgroup of genotype VI avian Paramyxovirus 1 (APMV-1), is endemic in German pigeons since it emerged in the early 1980ies. The current study investigates the epidemiology of PPMV-1 in Germany on the molecular level.

Methods: APMV-1 isolates (n=100) of the past four years between 2008 to 2012 were sequenced and compared to historical PPMV-1 sequences starting from year 1983 and analyzed phylogenetically, focusing on the F2-gene, including the proteolytic cleavage (374 bp) site.

Results: All APMV-1 isolates from pigeons clustered within the genotype VIb, which comprises PPMV-1. The isolates were heterogeneous and grouped within genotype VIb, lineage d and f, that were present already in Germany since 1987 (d) and 2000 (f). Starting in 2009 and dominating isolates since 2011, a distinct group of viruses within lineage f emerged. A re-appearance of in 2012 of strains closely related to viruses last detected in 2009 was noticed.

Conclusions: Outbreaks of paramyxovirus in pigeons were caused by heterogeneous PPMV-1 strains of different lineages which co-circulated. No geographic lineage restriction was observed hinting to a flourish exchange of viruses across Europe. Re-introductions of genetically closely related PPMV-1 strains support the notion of multiple at least partially separated reservoir populations.

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