

## The Pigeon Circovirus Evolution and Epidemiology under Conditions of One Loft Race Rearing System: The Preliminary Results

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**Abstract :** Viral diseases, especially those leading to impairment of the immune system, are among the most important problems in avian pathology. However, there is not much data available on this subject other than commercial poultry bird species. Recently, increasing attention has been paid to racing pigeons, which have been refined for many years in terms of their ability to return to their place of origin. Currently, these birds are used for races at distances from 100 to 1000 km, and winning pigeons are highly valuable. The rearing system of racing pigeons contradicts the principles of biosecurity, as birds originating from various breeding facilities are commonly transported and reared in "One Loft Race" (OLR) facilities. This favors the spread of multiple infections and provides conditions for the development of novel variants of various pathogens through recombination. One of the most significant viruses occurring in this avian species is the pigeon circovirus (PiCV), which is detected in ca. 70% of pigeons. Circoviruses are characterized by vast genetic diversity which is due to, among other things, the recombination phenomenon. It consists of an exchange of fragments of genetic material among various strains of the virus during the infection of one organism. The rate and intensity of the development of PiCV recombinants have not been determined so far. For this reason, an experiment was performed to investigate the frequency of development of novel PiCV recombinants in racing pigeons kept in OLR-type conditions. 15 racing pigeons originating from 5 different breeding facilities, subclinically infected with various PiCV strains, were housed in one room for eight weeks, which was supposed to mimic the conditions of OLR rearing. Blood and swab samples were collected from birds every seven days to recover complete PiCV genomes that were amplified through Rolling Circle Amplification (RCA), cloned, sequenced, and subjected to bioinformatic analyses aimed at determining the genetic diversity and the dynamics of recombination phenomenon among the viruses. In addition, virus shedding rate/level of viremia, expression of the IFN- $\gamma$  and interferon-related genes, and anti-PiCV antibodies were determined to enable the complete analysis of the course of infection in the flock. Initial results have shown that 336 full PiCV genomes were obtained, exhibiting nucleotide similarity ranging from 86.6 to 100%, and 8 of those were recombinants originating from viruses of different lofts of origin. The first recombinant appeared after seven days of experiment, but most of the recombinants appeared after 14 and 21 days of joint housing. The level of viremia and virus shedding was the highest in the 2nd week of the experiment and gradually decreased to the end of the experiment, which partially corresponded with Mx 1 gene expression and antibody dynamics. The results have shown that the OLR pigeon-rearing system could play a significant role in spreading infectious agents such as circoviruses and contributing to PiCV evolution through recombination. Therefore, it is worth considering whether a popular gambling game such as pigeon racing is sensible from both animal welfare and epidemiological point of view.

**Keywords :** pigeon circovirus, recombination, evolution, one loft race

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