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Molecular evidence of canine parvovirus type 2 (Protoparvovirus carnivoran1) circulation before the 1978 panzootic

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Canine parvovirus type 2 (CPV-2) caused a global panzootic in dogs in 1978 after emerging from a feline panleukopenia virus (FPV)-like ancestor. Although serological studies have suggested earlier circulation, direct pathological and molecular evidence has been lacking.
To investigate the early history of CPV-2, we screened 10 archival canine pathology specimens collected in 1977 and 1978 in Berlin, Germany, using shotgun high-throughput sequencing. We recovered a near-complete CPV-2 genome (99% genome coverage) from a dog that died in 1977. Histopathological findings were consistent with classical parvoviral disease. In addition, the reconstructed viral genome differed from the previous most ancient genome of CPV-2 (derived from a dog sampled in the USA in 1978) at only 2 noncoding positions. These findings therefore show that CPV-2 circulated in dogs before its first recognition and already cause a similar disease. They also demonstrate that CPV-2 did not evolve measurably at the amino acid level in the first months of the panzootic. Together, these results support earlier serological observations and highlight the value of archival pathology collections for reconstructing pathogen emergence and early spread.

Keywords

Canine parvovirus type 2 (CPV-2); pathogen emergence; archival pathology collections; high-throughput sequ

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Professional Status of the Speaker

Senior Scientist

Junior Scientist Status

No, I am not a Junior Scientist.

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