

# Canine distemper virus epidemic in Swiss wildlife: epidemiological investigations and assessment of the risk of infection for domestic dogs

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## Key words

Canine Distemper, Morbillivirus, wildlife, domestic dog, Switzerland, spillover, virology, epidemiology

## Aim of the study

- (1) To confirm the role of canine distemper virus (CDV) as etiological agent;
- (2) To describe the lesions associated with CVD infections in different hosts;
- (3) To document the spatio-temporal evolution of the outbreak and identify possible risk factors for infection;
- (4) To characterize the virus in order to document his relatedness to known strains already described in wildlife and dogs, and assess the potential for a spillover from wild to sympatric domestic carnivores.

## Material and methods

A selection of 136 CDV-infected wild carnivores sampled at the FIWI in 2009-2011 and few lagomorphs, rodents and domestic carnivores, were used for this study. Histopathological, virological and serological investigations were carried out on a subsample of 50-70 animals, and both descriptive and molecular epidemiological data were collected.

## Results and significance

The CDV distemper outbreak 2009-2011 in Switzerland was characterized by an unusually high morbidity and mortality among wild carnivores and an increasing range of host taxa including non-carnivore species. It spread from east to west, affecting mainly foxes and badgers in the eastern Swiss cantons. The identified virus strains showed similarities with wild and domestic isolates from Hungary, Austria, south Germany and north Italy, supporting the hypothesis of a virus migrating from eastern European countries with fox movements. However, similarities with a former Swiss strain indicated that a re-emergence of a local stain may also have occurred. Wild carnivores appeared to be highly susceptible to the virus but no particular predisposing factors were identified. In contrast, we have shown that the novel CDV strains which emerged during the 2009-2010 were characterized by an increased virulence associated with a novel molecular signature present in their H protein, and with a Snyder-Hill-like pathology. The novel strains showed a remarkable plasticity, being able to infect a large number of wild carnivores including large free-ranging and domestic felids, rodents, lagomorphs, and vaccinated dogs. The in-depth H protein investigation revealed the existence of a previously unknown compensatory system that is likely to be relevant for CDV infectivity and immune-escape.

## Publications, posters and presentations

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**Project 1.11.17**

**Project duration 2010-2014**