Veterinary Microbiology 150 (2011) 63–69

Contents lists available at ScienceDirect

Veterinary Microbiology

journal homepage: www.elsevier.com/locate/vetmic

A distinct CDV genotype causing a major epidemic in Alpine wildlife

Isabella Monne [a,*], Alice Fusaro [a], Viviana Valastro [a], Carlo Citterio [a], Manuela Dalla Pozza [a], Federica Obber [a], Karin Trevisiol [a], Mariapia Cova [b], Paola De Benedictis [a], Marco Bregoli [a], Ilaria Capua [a], Giovanni Cattoli [a]

[a] *Istituto Zooprofilattico Sperimentale delle Venezie, Viale dell'Università, 10, 35020 Legnaro (PD), Italy*
[b] *Istituto Zooprofilattico Sperimentale della Lombardia e dell' Emilia Romagna, Via P. Rovelli, 53, 24100 Bergamo (BG), Italy*

ARTICLE INFO

Article history:
Received 29 June 2010
Received in revised form 28 December 2010
Accepted 10 January 2011

Keywords:
Canine distemper virus
Wildlife
Wild carnivores
Evolutionary dynamics
Haemagglutinin gene (H)

ABSTRACT

Canine distemper virus (CDV) infection represents an important conservation threat to many carnivore species and has contributed to the population decline of several wild terrestrial and aquatic mammalian species. Since 2006, the Alpine region of North-Eastern (NE) Italy has been experiencing a severe and widespread outbreak of CDV affecting the wild carnivore population. In this study we performed an extensive phylogenetic and molecular evolutionary analysis of CDV identified during the recent wildlife epidemic in the Alpine region. Our analysis yielded data on the evolutionary dynamics of the Alpine wildlife CDV epidemic and revealed the emergence and spread of a single genetic cluster of CDV. The wide distribution of the novel cluster combined with the identification of a specific amino acid mutation, which is believed to increase the ability of the virus to replicate in a wider host range, raises concerns over the possible implications of the spread of this virus on the conservation of endangered wildlife species.

1. Introduction

Canine Distemper virus (CDV) belongs to genus Morbillivirus, family Paramyxoviridae and is the causative agent of a severe infectious disease affecting a broad range of wild and domestic carnivores. This virus possesses a non-segmented single stranded negative RNA genome encoding six proteins. Among them, the haemagglutinin (H) protein is a key component of the virus, being responsible for the first virus-host cell interaction and initial virus entry (Appel, 1987; Martella et al., 2008). The H protein binds to the signalling lymphocyte activation molecule (SLAM) on the membrane of the host target cells resulting in cellular infection. Mapping of the distribution of mutations at sites under positive selection pressure has shown that key amino acid substitutions associated with host specificity fall into the SLAM-binding region of the H protein (McCarthy et al., 2007).

The H gene and its encoded protein are subject to a higher genetic and antigenic variation respectively than other viral genes. For this reason it has been the primary focus of previous molecular epidemiological studies of CDV. Seven clusters have been identified based on the genetic relationship between complete H gene sequences of distinct CDV strains, namely America-1, America-2, Arctic-Like, Asia-1, Asia-2, Europe-1 and Wildlife (Martella et al., 2006; McCarthy et al., 2007).

CDV infection represents an important conservation threat to many carnivore species and has contributed to the population decline of several wild terrestrial and aquatic mammalian species (Murray et al., 1999; Kennedy et al., 2000). The mountainous region located in South Central Europe (the Alps) is home to several large endangered carnivore species such as the Eurasian lynx (*Lynx lynx*), the wolf (*Canis lupus*) and the brown bear (*Ursus arctos*), all susceptible to CDV infection (Daoust

---

* Corresponding author at: Research and Development department, Istituto Zooprofilattico Sperimentale delle Venezie, Viale dell'Università, 10, 35020, Legnaro, Padova, Italy. Tel.: +39 0498084381, fax: +39 0498084360.
E-mail address: imonne@izsvenezie.it (I. Monne).

0378-1135/$ – see front matter © 2011 Elsevier B.V. All rights reserved.
doi:10.1016/j.vetmic.2011.01.009

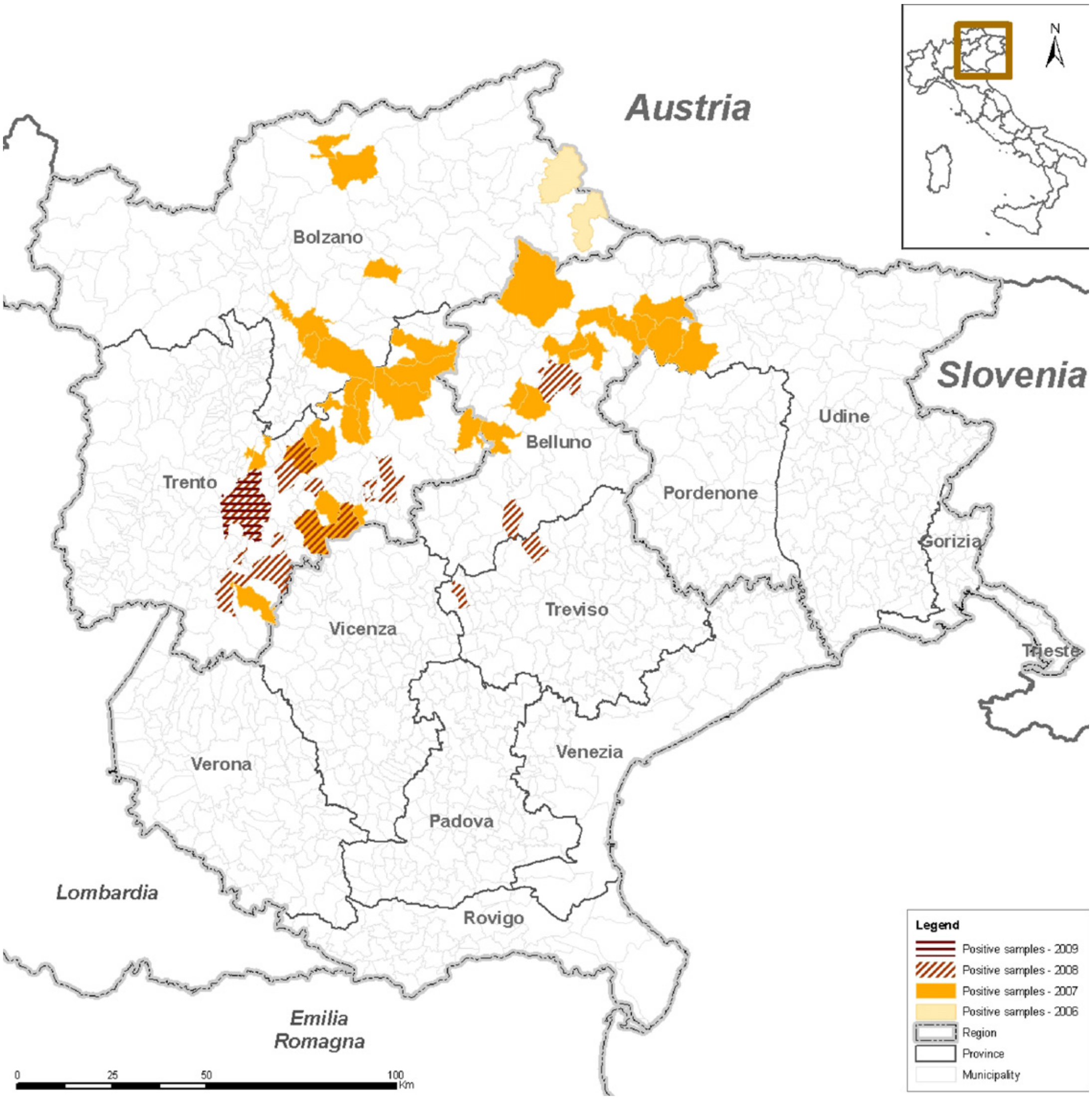

Fig. 1. Geographical distribution of the 96 CDV strains from wildlife species analyzed in the present study.

et al., 2009; Marsilio et al., 1997; Martella et al., 2008). Since 2006, the Alpine region of North-Eastern Italy has been experiencing CDV outbreaks affecting the wild carnivore population. Several foxes, badgers and a stone marten, which were found dead or showed neurological and respiratory signs, tested positive for CDV infection. The early CDV cases were identified only in the North-Eastern part of the Italian Alps, but since 2007 infections have spread southwest reaching the Pre-Alps and urbanized areas of the region, thus posing a risk to other wild carnivores and susceptible pets (Fig. 1). To date it is unclear how CDV reached these regions, propagated and evolved and whether multiple viral strains of the virus have been involved in this epidemic.

This study describes the dynamics of the recent CDV wildlife epidemic through an extensive molecular and phylogenetic analysis of the Italian CDVs identified between 2006 and 2009.

2. Materials and methods

2.1. Samples

The 96 CDV positive samples analyzed in this study were collected between October 2006 and March 2009 from three regions namely Veneto, Friuli Venezia Giulia and Trentino Alto Adige located in the north-eastern part of Italy (Fig. 1). All the samples were collected from wild animals, in particular foxes ($n = 66$) (*Vulpes vulpes*), badgers ($n = 29$) (*Meles meles*) and one stone marten (*Martes foina*). 75 out of 96 animals testing positive for CDV were found dead. The remaining animals displayed one or more of the following clinical signs: myoclonus, ataxia, ocular–nasal discharge and dyspnea. In addition, 23 CDVs detected in domestic dogs from the same regions between 2000 and 2007 were included in this study. Information regarding the wildlife CDVs viruses analyzed