

## Temporal and spatial pattern of canine distemper virus emergence globally

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### Background

Emerging viral diseases shared between wild and domestic animals are spreading to new geographical locations. The spread of cosmopolitan viruses at the human-domestic-wild interface is influenced by human action in the wild and by climate change. Canine distemper RNA virus (CDV) causes an acute, highly contagious disease with high mortality. It is a globally distributed virus, affecting a wide range of wild and domestic species belonging to the order Carnivora.

### OBJECTIVES

1. To understand its global distribution, using temporal detection and molecular sequencing.
2. To assess detection in wild and domestic hosts.
3. To detect spillover phenomena at the wild-domestic interface.

### PCR quality criteria

- PCR protocol
- Type of PCR
- Target gene and primers used
- Positive and negative controls used
- Method of detection of PCR products

### Data analysed

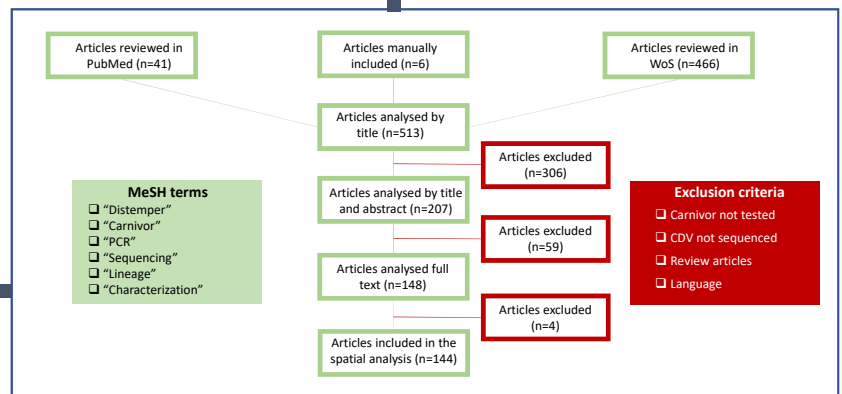
Bibliometric

Geographical

Analytical

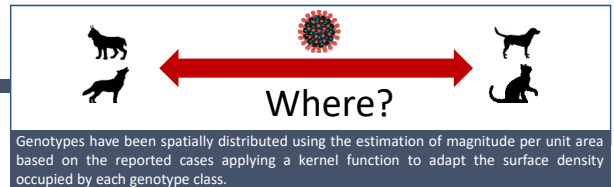
### Materials and Methods

A systematic review restricted to PubMed and WOS databases from 1988 to the present was carried out. MeSH terms and exclusion criteria are represented in the following diagrama.

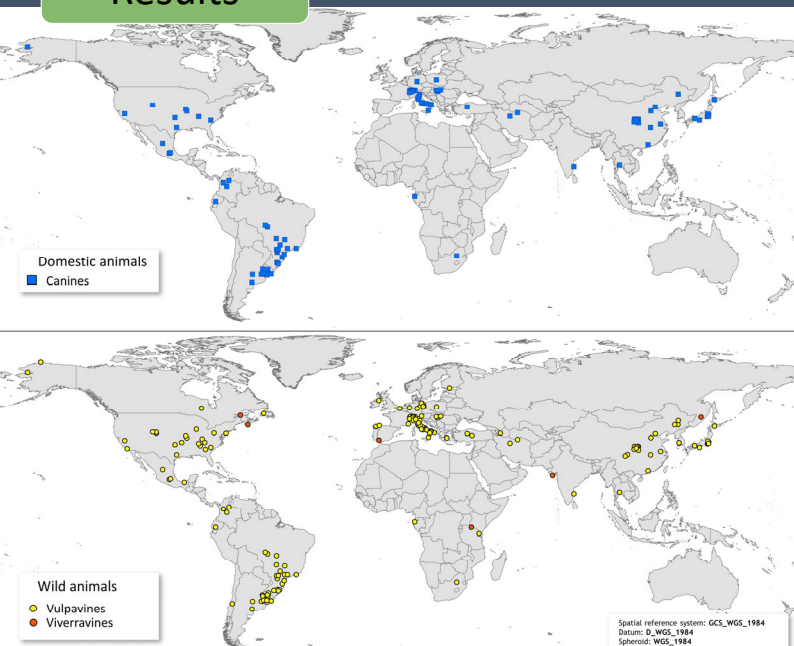


### Spatial analysis

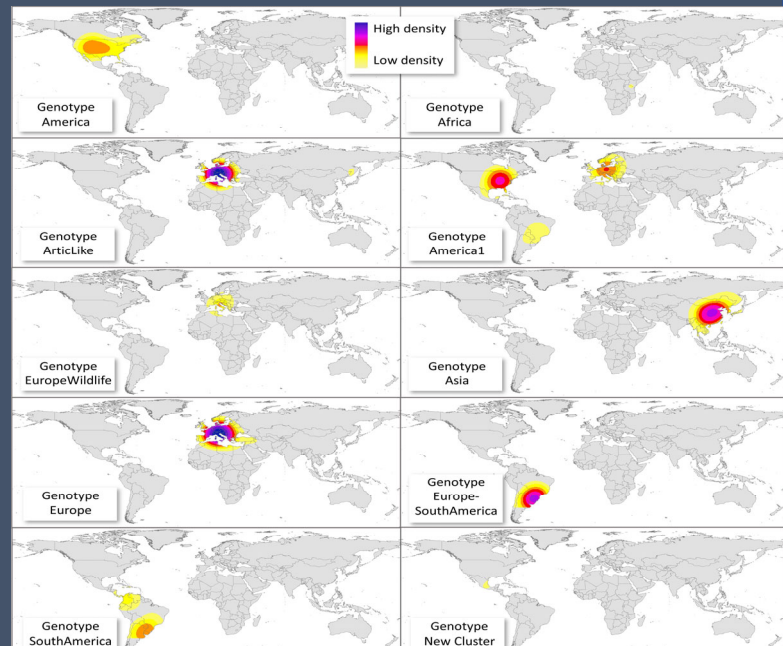
Allows cartographically detecting where identical lineages overlap in different hosts



### Results



Spatial location of all CDV positive carnivores classified according to domestic animals and two classes of wild animals: viverravines and vulpavines.



Spatial representation of the CDV genotypes obtained in the review according to the density of occupied area.