

Technical University of Denmark



## Genetic characterization of canine distemper virus involved in outbreaks in farmed mink in Denmark 2012

Trebbien, Ramona; Struve, T.; Hjulsager, Charlotte Kristiane; Chriél, Mariann; Larsen, Lars Erik

*Publication date:*  
2013

[Link back to DTU Orbit](#)

*Citation (APA):*

Trebbien, R., Struve, T., Hjulsager, C. K., Chriél, M., & Larsen, L. E. (2013). Genetic characterization of canine distemper virus involved in outbreaks in farmed mink in Denmark 2012. Abstract from NJF Seminar 464 : Autumn Meeting in Fur Animal Research 2013, Reykjavik, Iceland.

## DTU Library

Technical Information Center of Denmark

---

### General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

## **Genetic characterization of canine distemper virus involved in outbreaks in farmed mink in Denmark 2012**

<sup>1</sup>Trebbien, R., <sup>2</sup>Struve, T. <sup>1</sup>Hjulsager, C.K., <sup>1</sup>Chriel, M., <sup>1</sup>Larsen, L.E.

<sup>1</sup>*National Veterinary Institute, Technical University of Denmark, Bülowsvej 27, DK-1870 Frederiksberg C, Denmark.*

<sup>2</sup>*Kopenhagen Diagnostik, Kopenhagen Fur, Langagervej 60, DK-2600 Glostrup, Denmark.*

Danish farmed mink herds experienced a large outbreak of canine distemper virus in 2012. Full-length sequence analysis (1824 nucleotides) of the variable hemagglutinin (H) gene were performed on 27 viruses collected from mink and on 7 viruses collected from wild foxes. Results of the study showed that the farmed mink and wild fox population were infected by identical viruses which strongly indicate an epidemiological link between these populations. Accordingly, diseased and dead foxes were observed in some of the mink herds in connection to the outbreak. The Danish virus strain clustered phylogenetically with other European canine distemper viruses and showed the highest level of similarity (99.3 - 99.6 %) to viruses isolated from wild foxes in Germany. The fox should therefore be considered as an important wild life reservoir of canine distemper virus and may also contribute to the transmission of the virus between mink farms during outbreaks.