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# Sampling of French cervid populations for genetic analysis of susceptibility towards chronic wasting disease

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Roe deer (*Capreolus capreolus*)



Red deer (*Cervus elaphus elaphus*)

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## Background

- Chronic wasting disease (CWD) is a highly transmissible prion disease in cervids known since 1967 in North America, where white-tailed deer (*Odocoileus virginianus*) and other cervids have been impacted with population-level consequences<sup>a</sup>.
- In 2016 CWD was found in wild Eurasian tundra reindeer (*Rangifer tarandus tarandus*) herds in Norway, and subsequently identified in moose (*Alces alces*) and red deer (*Cervus elaphus elaphus*). Since, CWD-infected animals were identified in two additional European countries: Sweden and Finland<sup>b</sup> (Figure 1).

➔ Might weaken the European cervid populations<sup>c, d</sup>.

- Roe deer and red deer account for the vast majority of wild cervids in France.
- Symptom-based event monitoring established in France.
- Experimental transmissions of North American CWD isolates to sheep, bovine and porcine species have confirmed the **potential for these agents to propagate in major farmed animal species<sup>a</sup>**, and the risk to human health requires new investigation criteria<sup>e</sup>.



Figure 1. Cases of affected cervids recorded in Europe.

## The study

We started to investigate the polymorphism of the *PRNP* gene in French red deer and roe deer populations, as part of the EU-CWD project (2021-2025) funded by the ANR (French National Research Agency).

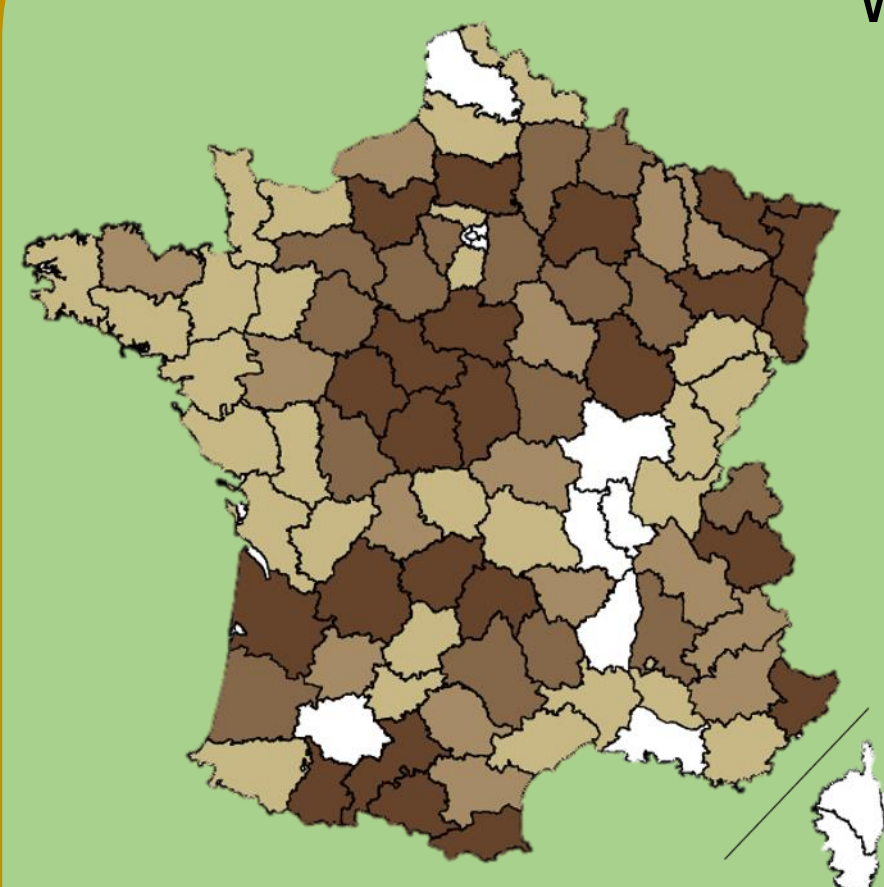


Figure 2. Departmental red deer hunting bag in 2020-2021 (total: 53 181 red deers)

Species absent or not hunted  
1 – 250  
251 – 500  
501 – 1 000  
1 001 – 3 000  
© Wild ungulates network (OFB) & National and departmental hunting federations



The aim of this study is to obtain a reliable picture of *PRNP* polymorphisms distribution within French red deer and roe deer populations (see Figures 2 and 3 for national distribution of deer populations from hunting bags) and to estimate their susceptibility towards CWD.

Species absent or not hunted  
1 – 2 500  
2 501 – 5 000  
5 001 – 7 500  
7 501 – 10 000  
10 001 – 22 000  
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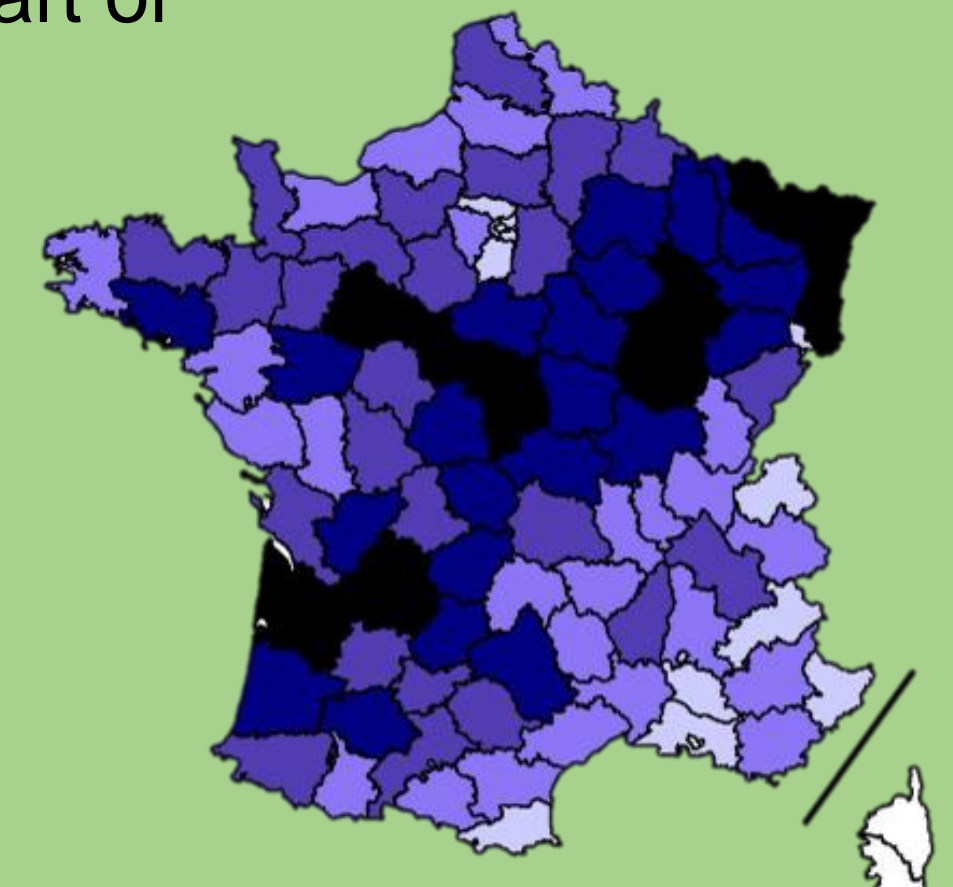


Figure 3. Departmental roe deer hunting bag in 2020-2021 (total: 530 805 roe deers)

## Methodology and Results

- A national sampling of red deer and roe deer populations was carried out during the 2020-2021 and 2021-2022 winters, using the cervid population/health monitoring program of the OFB (French Biodiversity Agency) with the collaboration of local hunters' associations.
- To be representative of the French cervid populations, the collection scheme integrated selection criteria such as **historical origin**, **geographical distance** between animals, **landscape organization** and **sex ratio**.
- Muscle samples were taken from the cervid, preserved in alcohol (70°) before DNA extraction. Amplification of the open reading frame of the *PRNP* gene by PCR was followed by direct sequencing analysis.
- Our French-Set consisted of 1319 samples belonging to **609 roe deer and 710 red deer** (Figure 4).
- Currently 1/3 of the French-Set were analyzed.



**Roe deer:** no polymorphism detected yet. This lack of diversity has also been observed in other European roe deer populations<sup>f</sup>.



**Red deer:** Five nucleotide variants (three synonymous substitutions and two non-synonymous substitutions) at positions previously identified in European red deer<sup>a</sup> were observed so far.

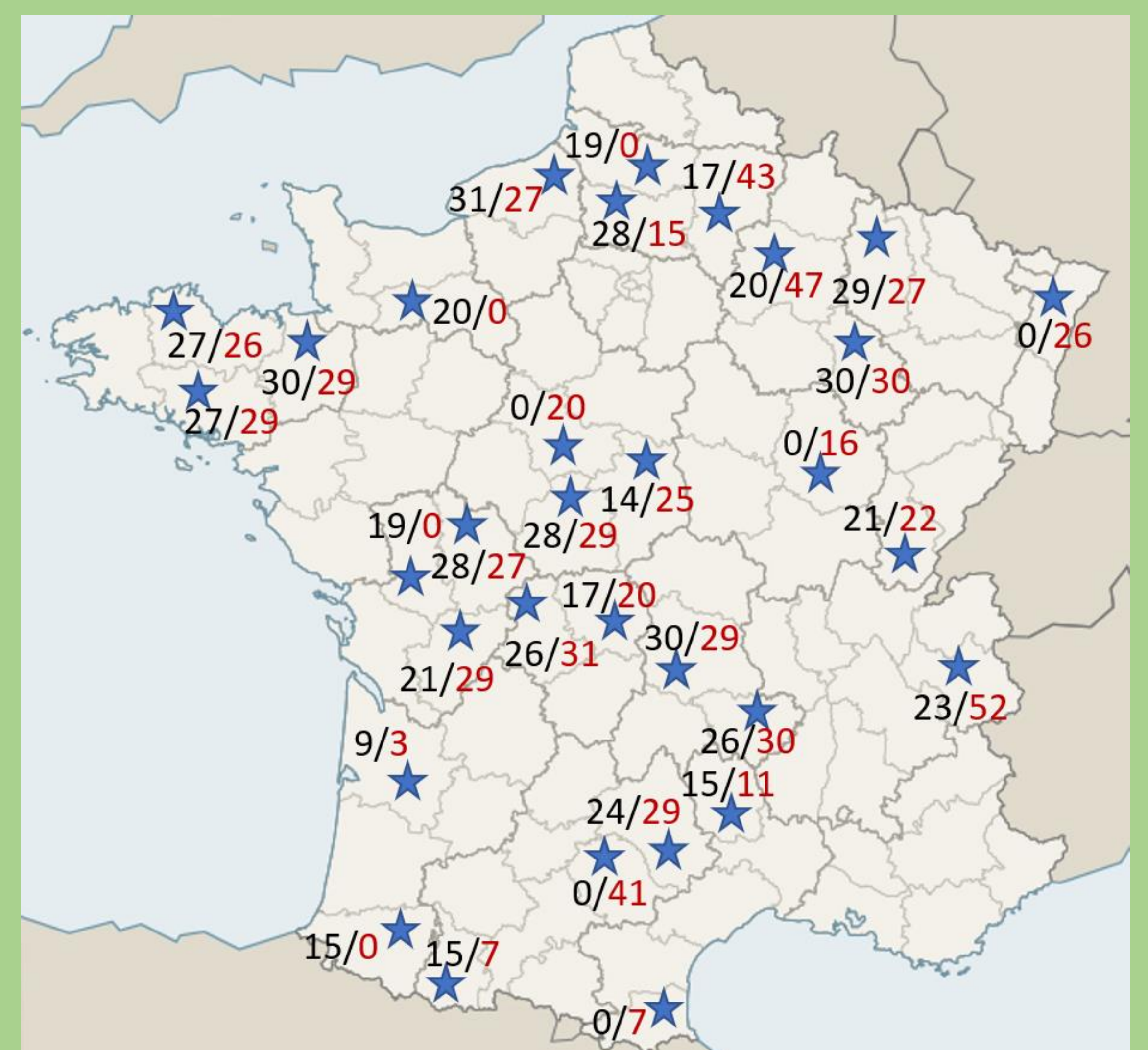


Figure 4. Geographical distribution of the samples collected (black numbers = roe deer; red numbers = red deer).

This study will allow us to **compare regional/national differences in *PRNP* genotype frequencies among deer populations** and to potentially **identify novel *PRNP* polymorphisms**. Their association with susceptibility or resistance towards CWD will then be investigated.



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