BORDER DISEASE EVOLUTION IN PYRENEAN CHAMOIS POPULATIONS

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Introduction

Border disease is caused by border disease virus (BDV), a widely distributed pestivirus among wildlife. However, Pyrenean chamois is the only free-ranging species on which BDV has had a great impact, being responsible for recent declines of chamois populations due to the emergence of several high mortality outbreaks. Since 2001, when chamois BDV was first described, ruminant pestiviruses have been relevant in wildlife health surveillance.

Objectives

To perform a complete review of border disease evolution in Pyrenean chamois populations since its presence was first detected.

Ethiology and epidemiology

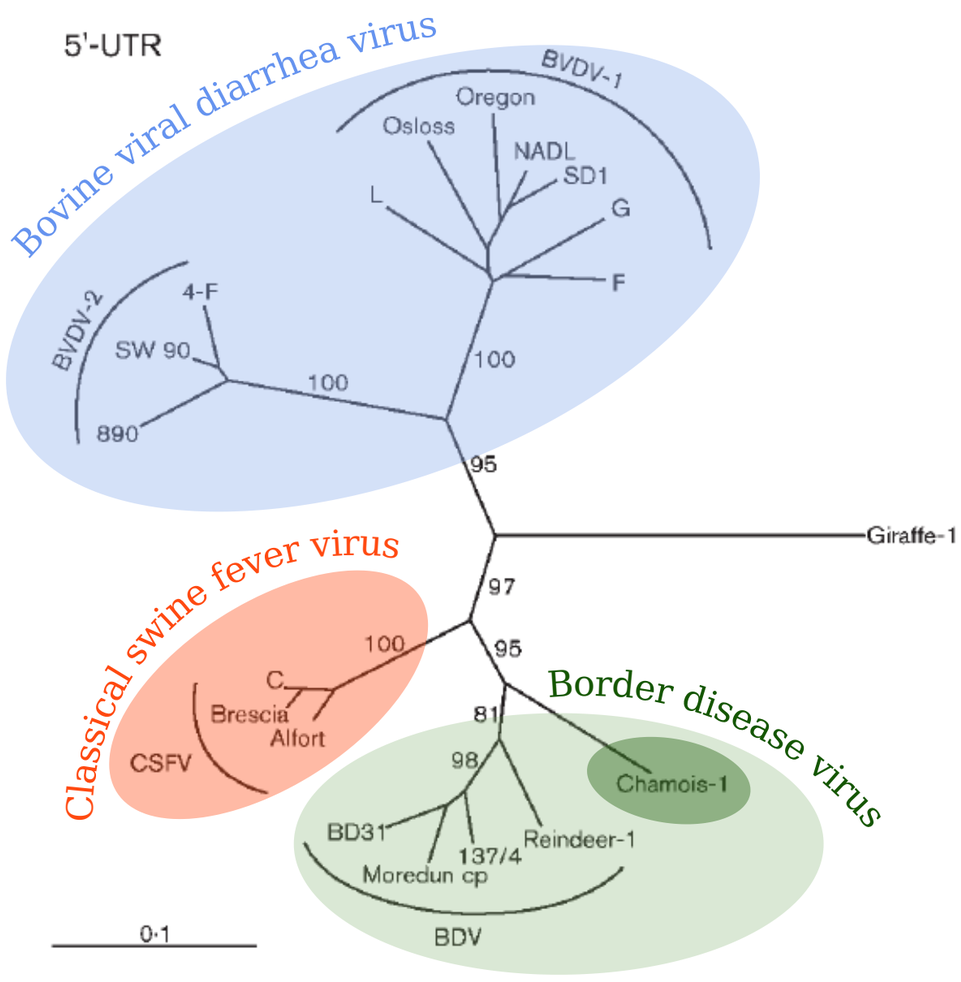

Figure 1. Phylogenetic tree showing the genetic relationship between pestivirus strains (modified from Arnal et al. 2004).

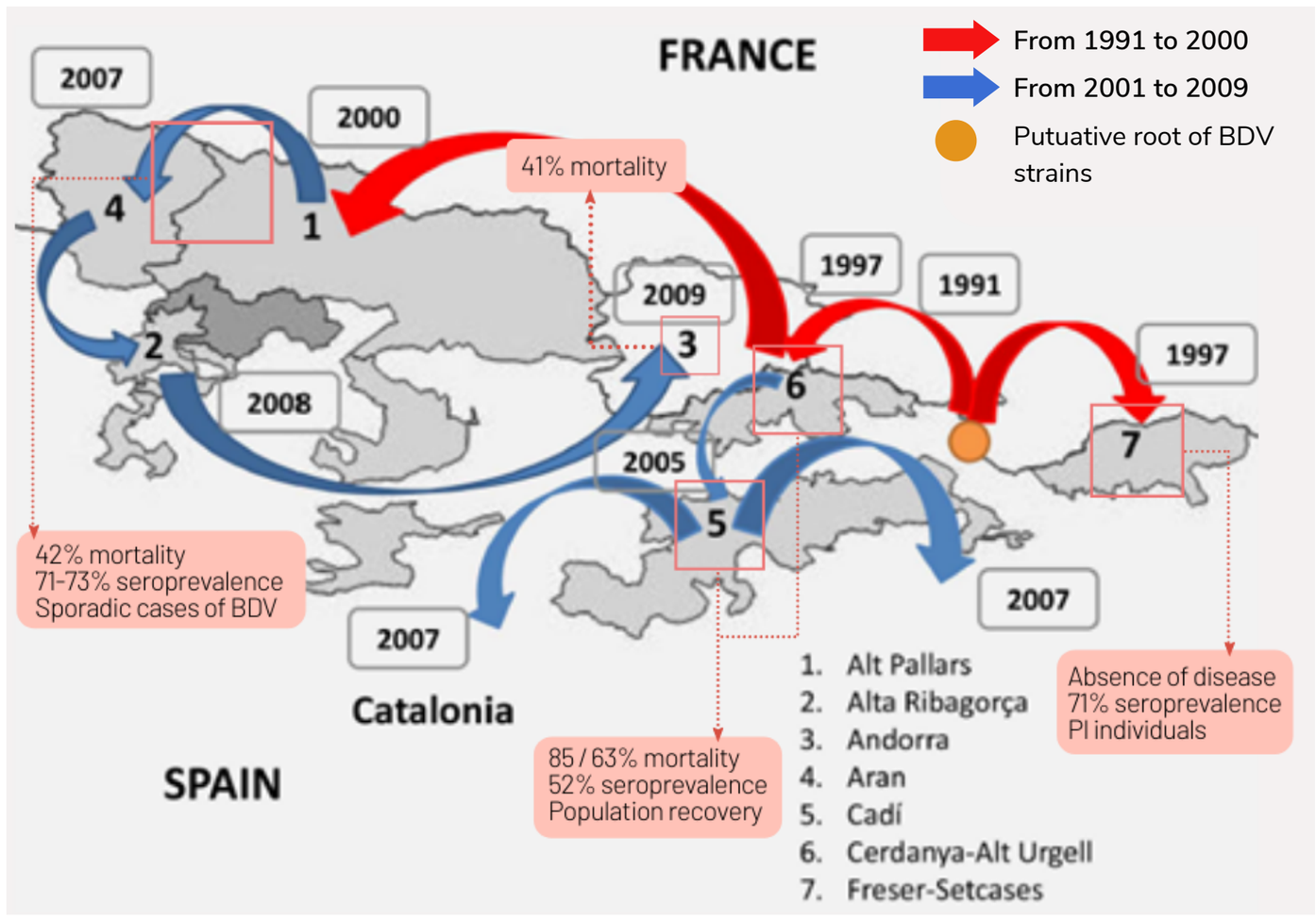

Figure 2. Spatiotemporal dynamics of BDV in Pyrenean chamois (modified from Luzzago et al. 2016).

Clinical signs and lesions

Figure 3. Pyrenean chamois with extensive alopecia and skin hyperpigmentation (provided by Ignasi Marco)

- Caquexia, weakness
- Alopecia, skin hyperpigmentation
- Difficulty in locomotion
- Absence of flight reaction

- Bacterial purulent broncopneumonia
- Non-supurative meningoencephalitis
- Cerebral oedema and neurodegeneration

Diagnosis

RT-PCR → virus isolation

ELISA → VNT [1]

IPMA [2]

[1] Virus neutralization test (VNT)
[2] Indirect immunoperoxidase monolayer assay (IPMA)

Conclusions

- Since the emergence of the first outbreak in 2001, chamois BDV has shown a rapid evolution with high transmission and mortality rates.
- Epidemiological variability within different outbreaks is mostly associated with strain virulence and immunity of the population affected.
- The presence of BDV in chamois populations that have recovered after a high mortality outbreak and do not show clinical signs of disease requires further investigation. Moreover, it is important to determine if these populations have reached an equilibrium between the host and virus.

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