



# Genetic diversity of Bovine Viral Diarrhea (BVD) virus: does it matter?

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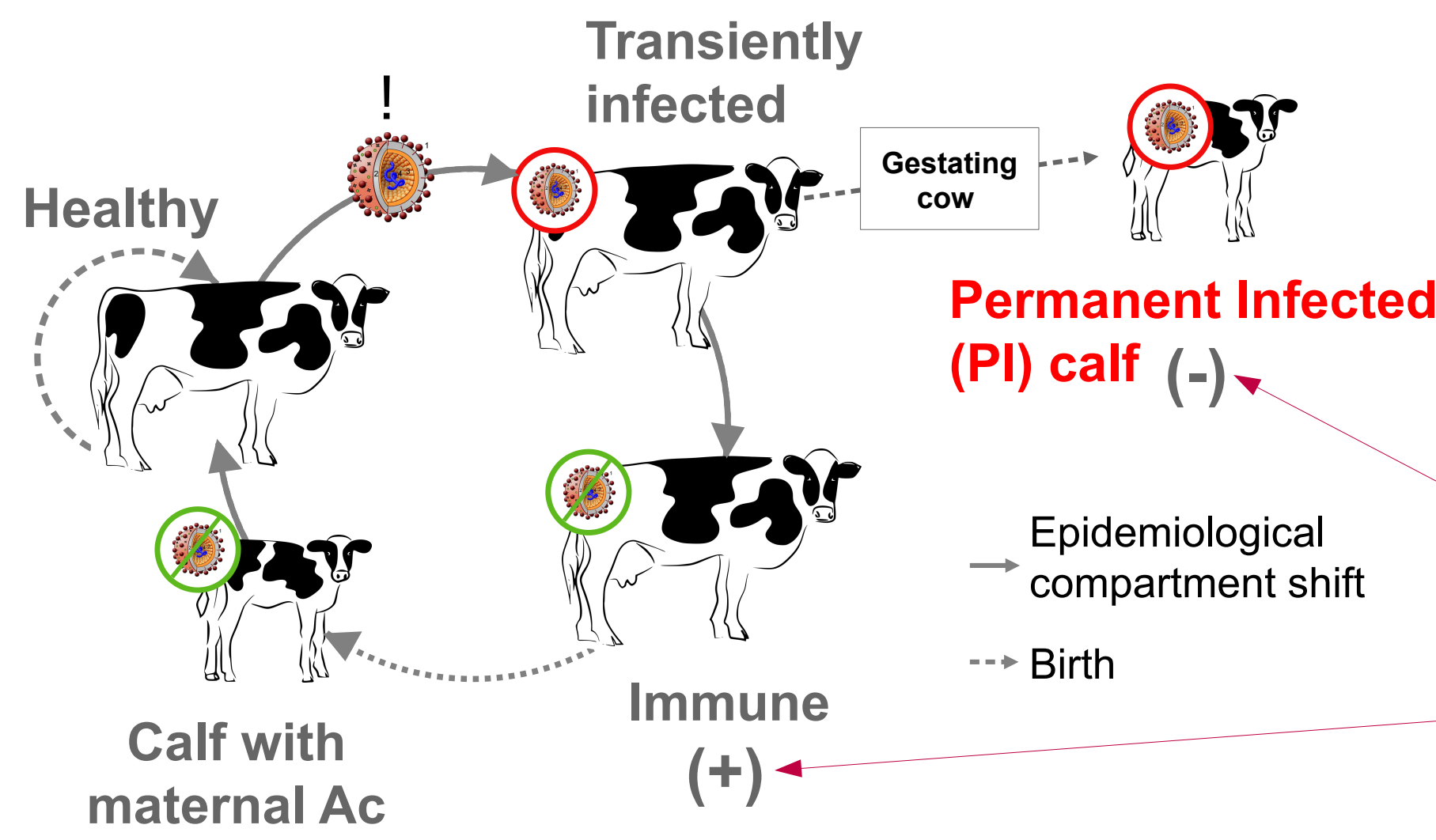
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## BVD disease

- Complex epidemiological cycle
- Endemic disease with local and regional spread due to trade

### Etiological agent: BVD virus

- RNA virus
- Genetic diversity ++: > 22 genotypes



## Disease control

National eradication since 2019 in France; implementation differs from region to region

## Disease monitoring

- Serology**  
(-) negative  
(+) positive
- Genetic data**  
Is BVDV present?  
No assessment of genotype

→ Serology: complex interpretation, time lag  
 → Genetic diversity not taken into account

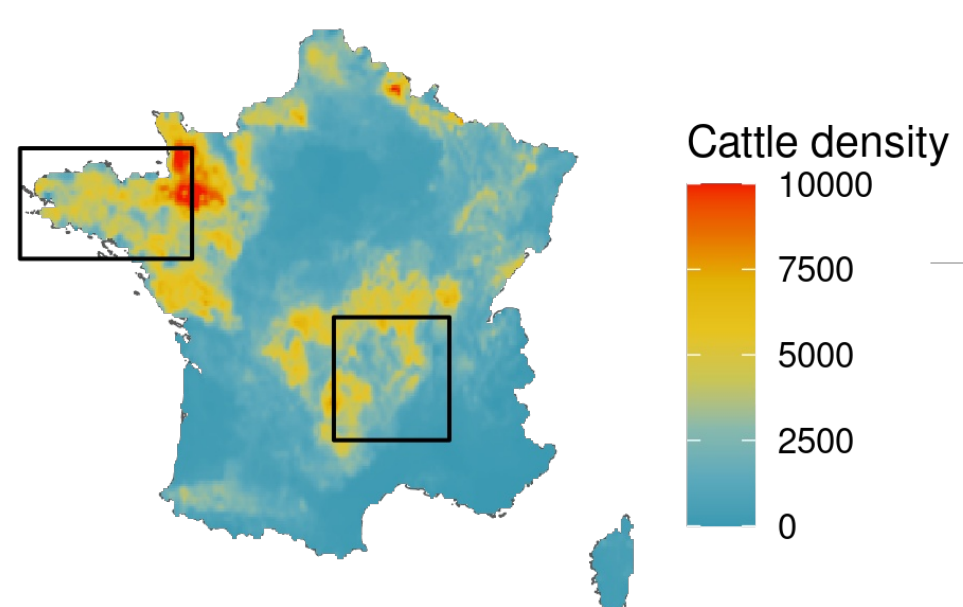
## QUESTIONS

⇒ Are there different circulation dynamics between genotypes that could have an impact on the effectiveness of disease surveillance and control measures?

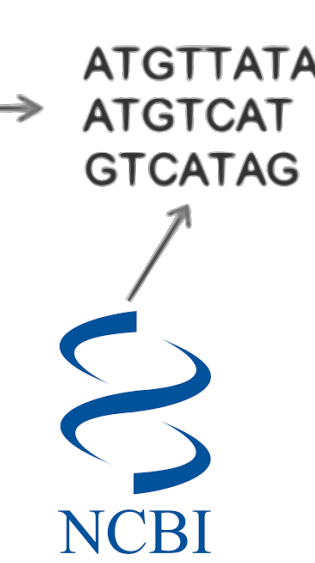
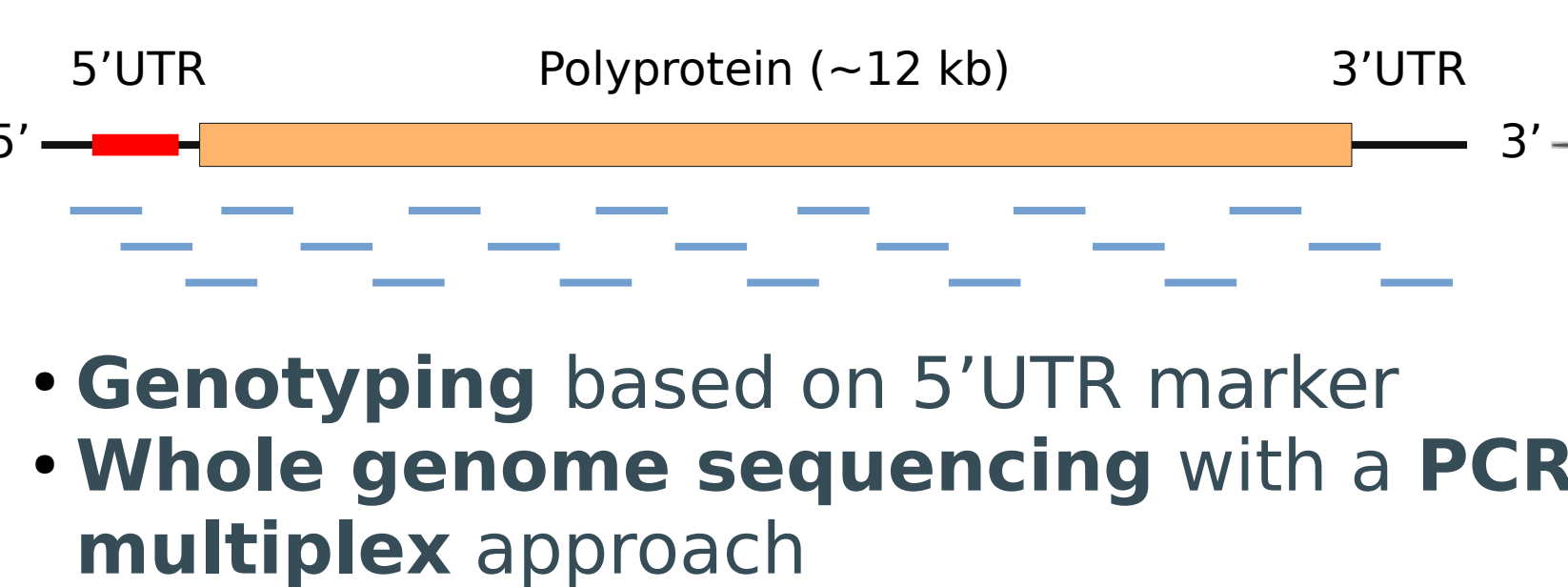
## METHODS



Ear loops from the national eradication plan

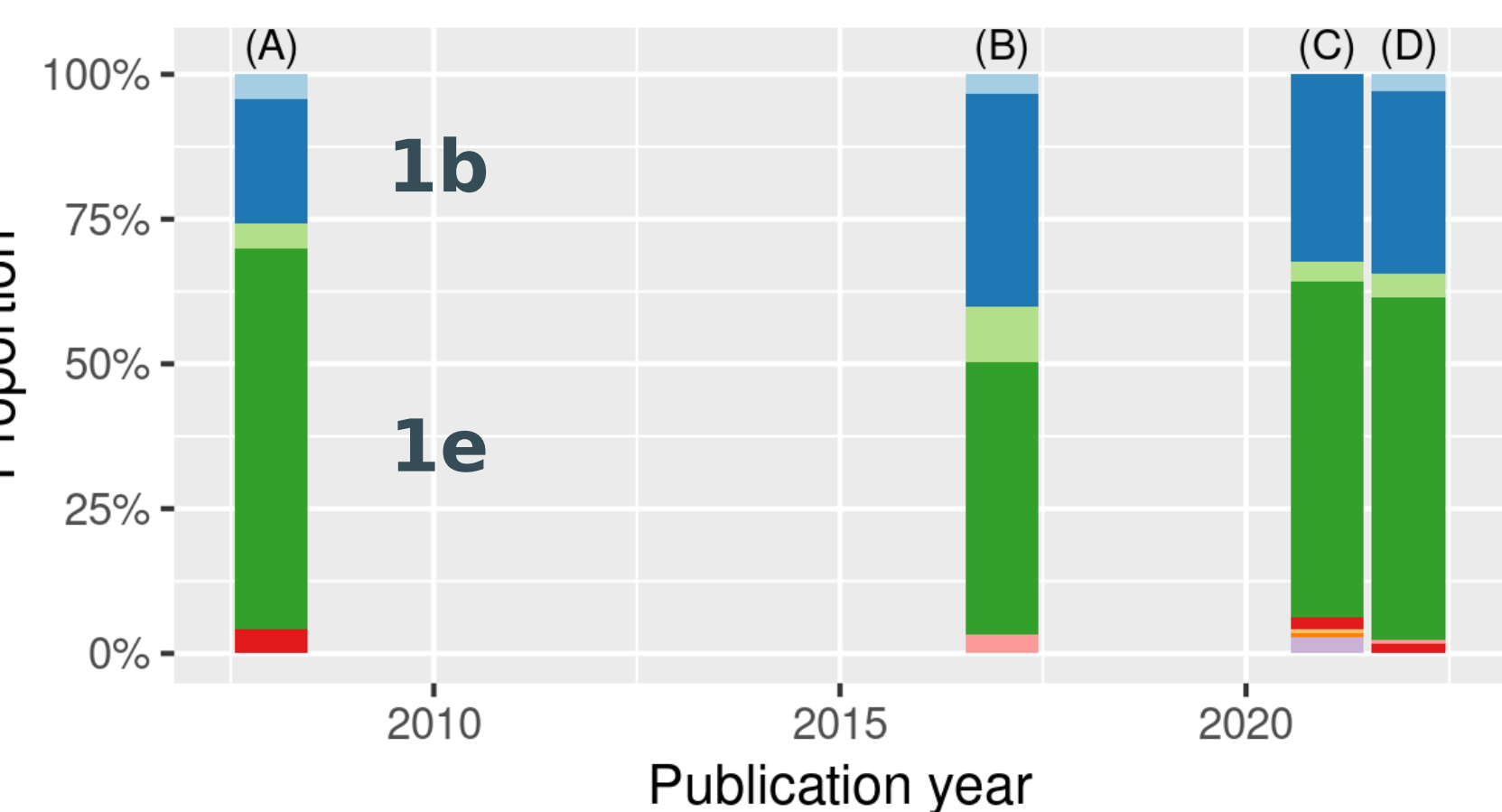


### BVDV genome structure



Phylogenetic & Phylodynamic analyses  
**BEAST v1**

## RESULTS



(A) Vilcek et al., 2008  
 (B) Private labs  
 (C) Rivas et al., 2022  
 (D) Lescoat et al., unpublished

### Stable proportion of genotypes in France

Main genotypes: 1e & 1b

BUT...

### Clade topology

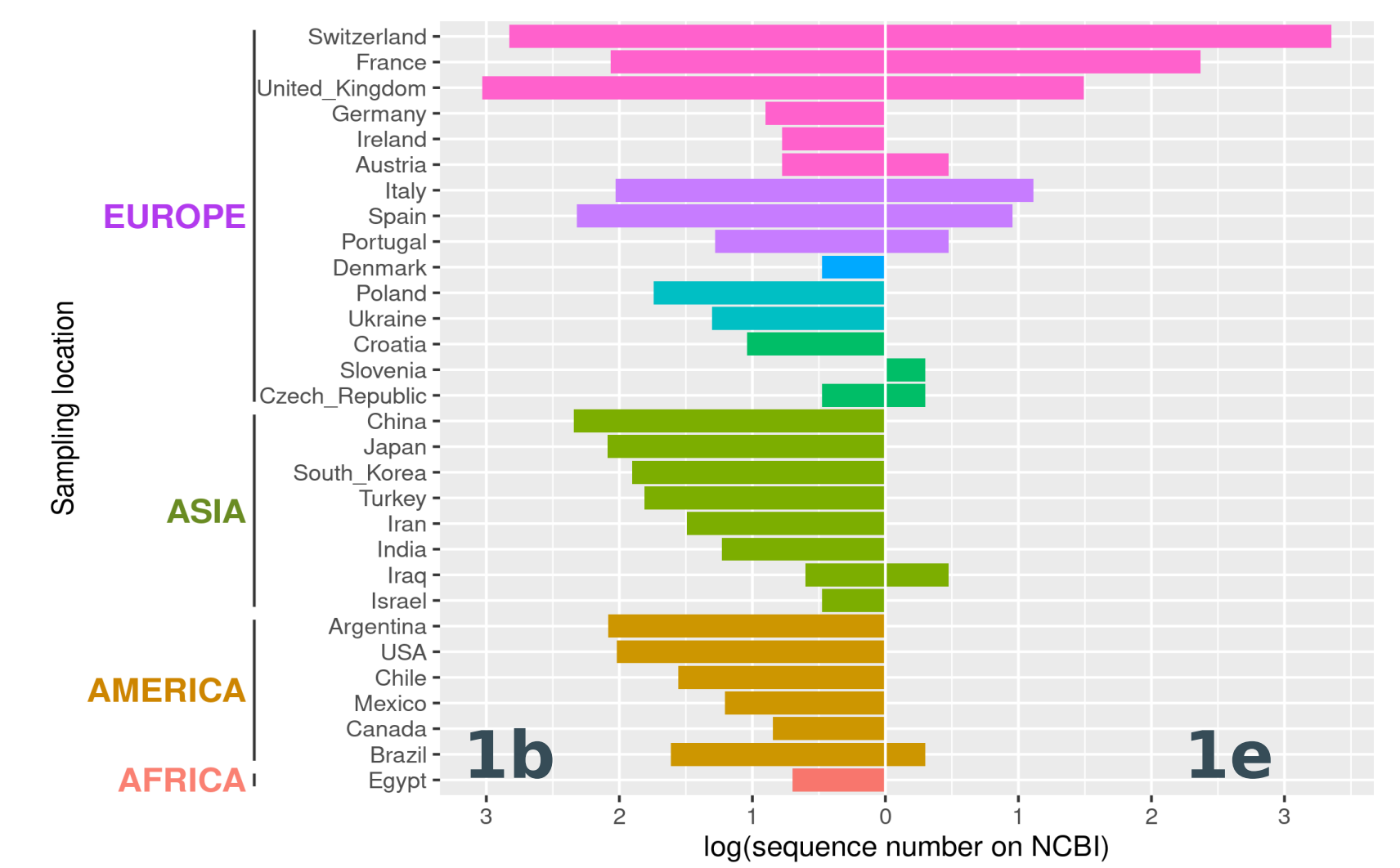
**1e:** multiple clades, main one = closely related genotypes

**1b:** multiple clades

### Sequence origins

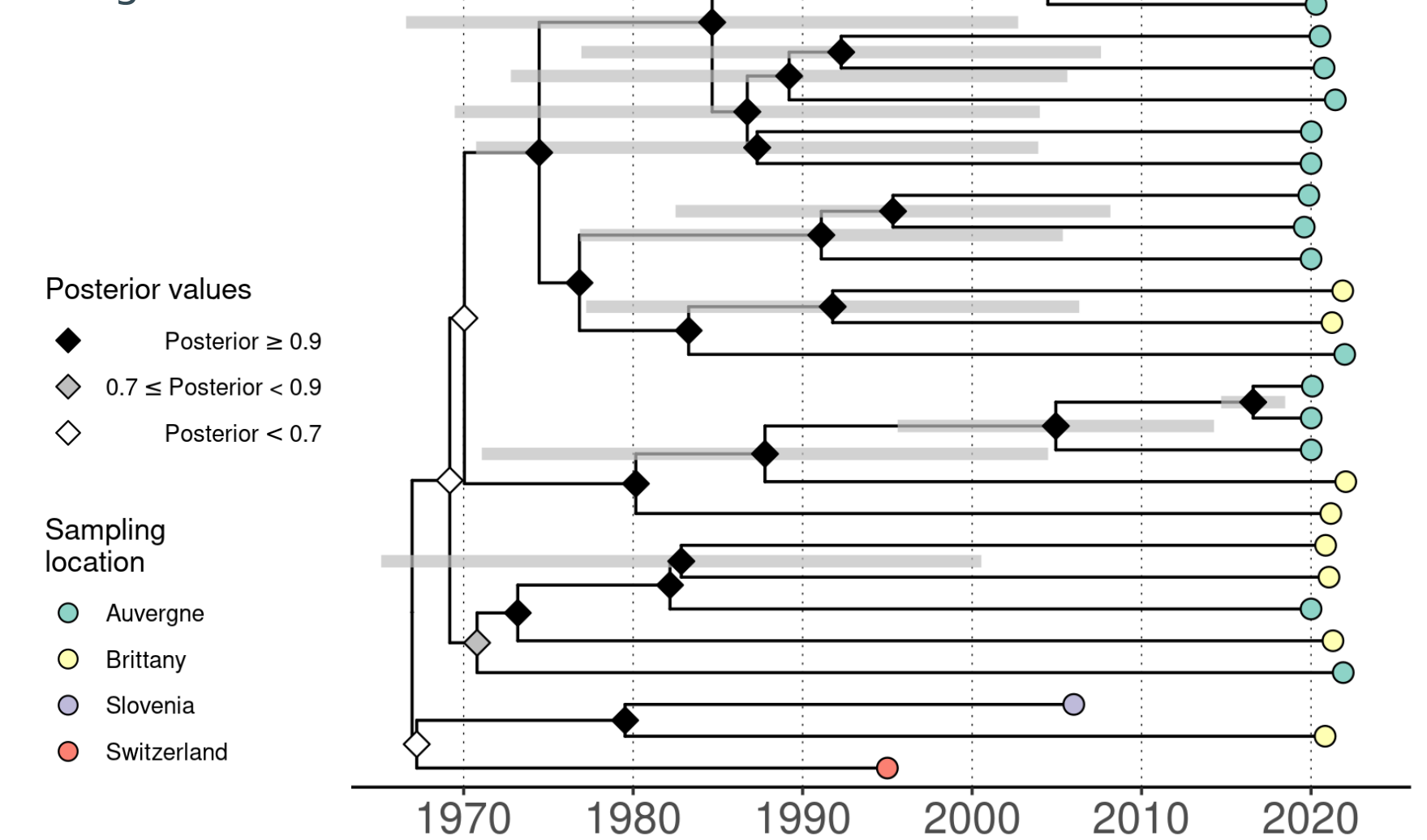
**1e:** majority of the sequences sampled in Western Europe

**1b:** sequences sampled on all continents



### Full genomes

Time-calibrated tree  
 30 genomes



### Hypothesis

**1e:** main clade = demographic (European) explosion

**1b:** multiple international introductions

⇒ **Different epidemic process**  
 How do both genotype persist?  
 What consequences?

### To go further: phylodynamic analyses

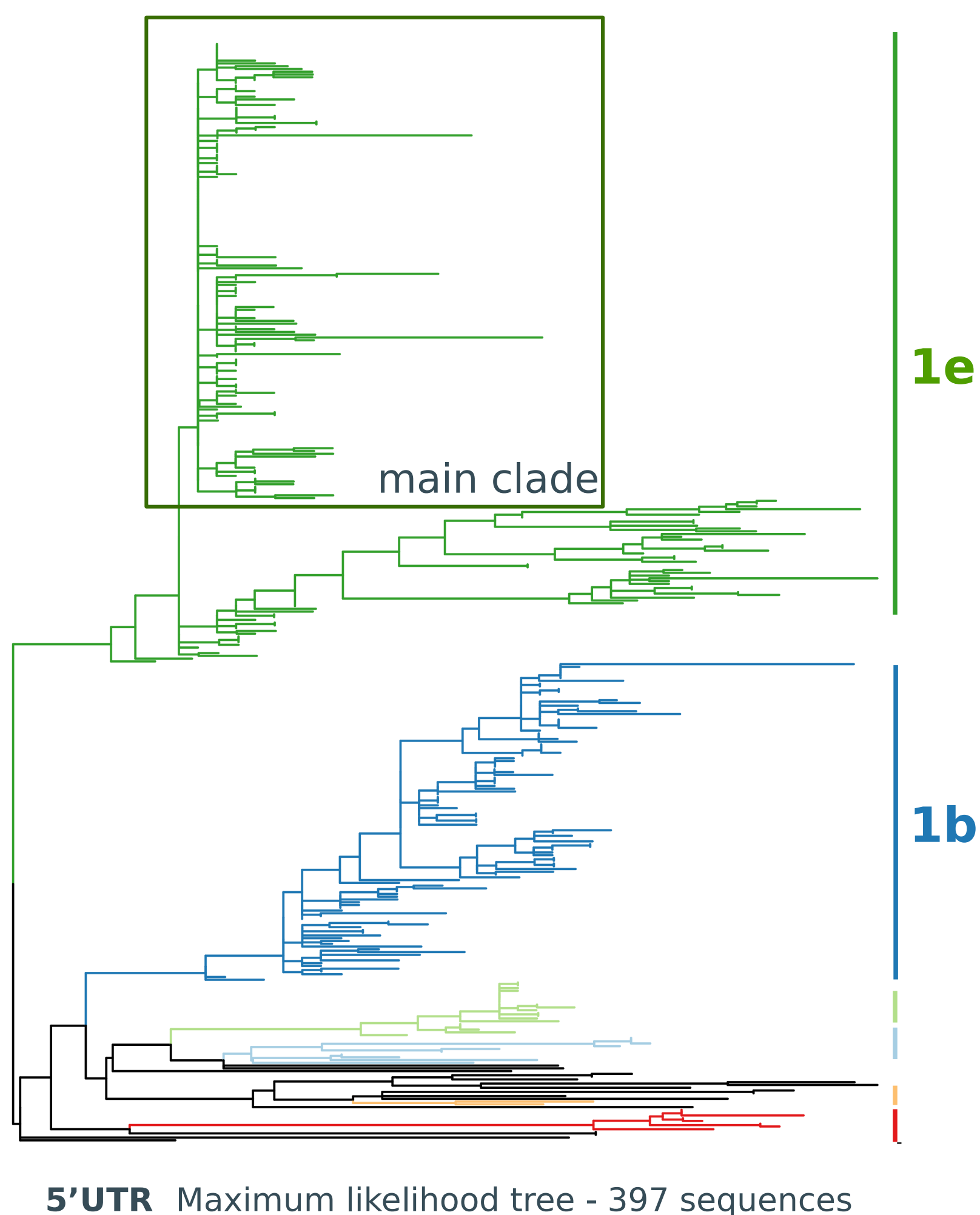
**Problem:** lack of phylogenetic and temporal resolution with 5'UTR marker

**Solution:** successful in-house protocol for full genome sequencing

**First french full BVDV genome sequences**

### Phylodynamics on BVDV-1e (main clade)

- Preliminary analysis
- Demographic explosion circa 1970
- Presumably long-standing divergence within & between BVDV-1e and -1b



## CONCLUSION

- Proportions of BVDV-1e and BVDV-1b are stable despite presumably different introduction mechanisms
- Epidemic history differs between the two genotypes, which could indicate various persistence mechanisms
- Need for more genetic data to uncover finer patterns: full genomes

## PERSPECTIVES

- Obtain **full genomes** for ~500 samples → which samples to include?
  - **Maintenance** and **turn-over** of genotypes at a finer spatio-temporal scales
  - Impact of **anthropic and ecological factors** on genotypes dispersion with phylodynamics analysis
  - Consistency of genomic approach results with **epidemiological surveillance data**
- ⇒ **How to limit BVD resurgences at the end of the national management plan**