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**Asymptomatic carriers of equine piroplasmosis:
prevalence differences between 4 French regions and low
genetic diversity of Theileria equi and Babesia caballi**

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Asymptomatic carriers of equine piroplasmosis

Prevalence differences between 4 French regions

Low genetic diversity of *Theileria equi* and *Babesia caballi*



INRAE



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- 2 Oniris, Cisco, Nantes
- 3 VetAgro Sup, Lyon
- 4 ENVT, Toulouse
- 5 ENVA, Maisons Alfort

Equine piroplasmosis

- tick-borne disease
- worldwide distribution with few indemn countries imposing import restrictions
- clinical, subclinical or asymptomatic with long term carriers (4 years to life long)
- two etiological blood parasites: *Babesia caballi* and *Theileria equi*
- great genetic diversity of both species: several cryptic species?

Objectives

- to evaluate the prevalence of piroplasmosis carriers in different regions of France
- to genotype french isolates

The study

- piroplasmosis asymptomatic equids in 4 geographical regions around the veterinary school focal points
- blood samples, consents and questionnaires – 2019 to 2022
- nPCR specific for each parasite species, partial 18S rRNA sequencing and phylogenetic analysis

Prevalence of piroplasmosis asymptomatic carriers

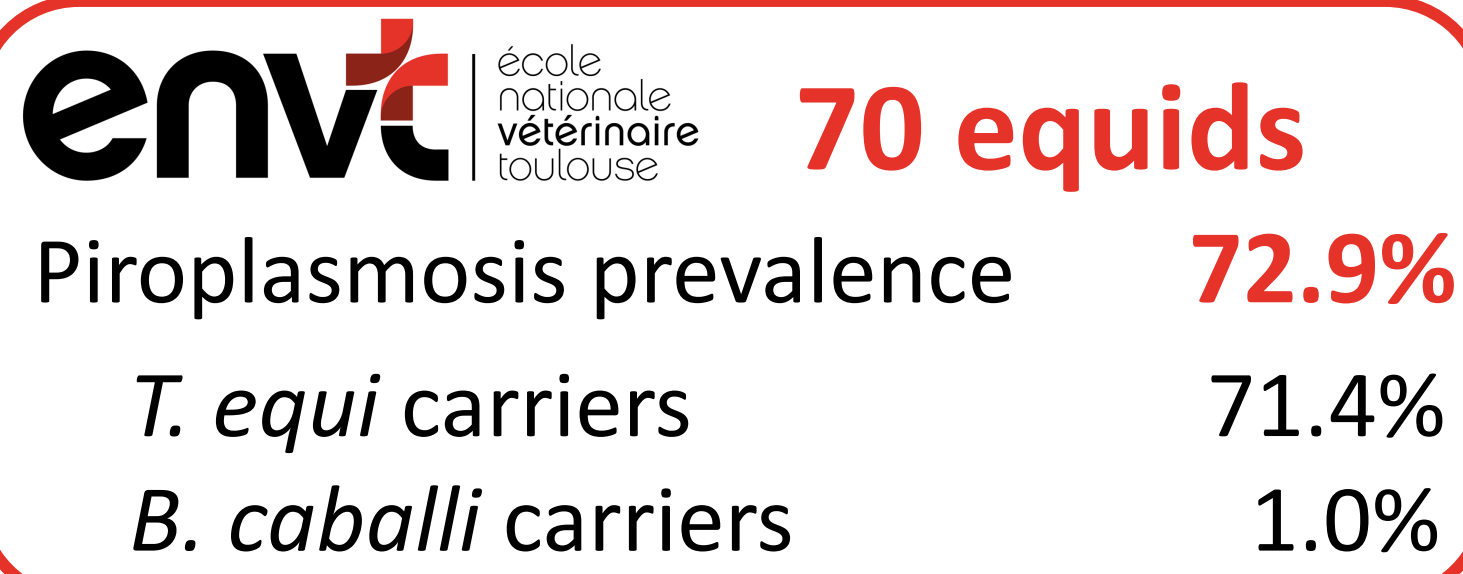
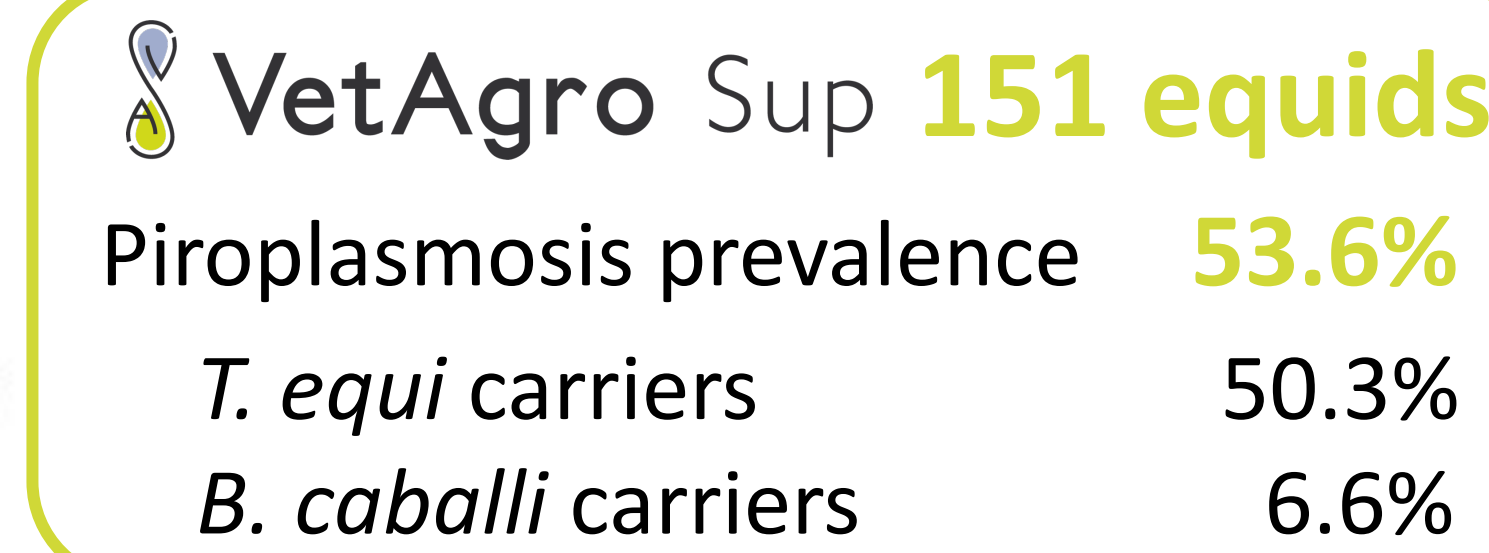


High prevalence of *T. equi* carriers and low prevalence of *B. caballi* carriers

Abundance vs rarity of competent vectors?
High vs low prevalence of infected ticks?
Persistence vs elimination by the equids' immune system?

A north to south carrier prevalence gradient

geographic distribution and abundance of competent tick vectors?



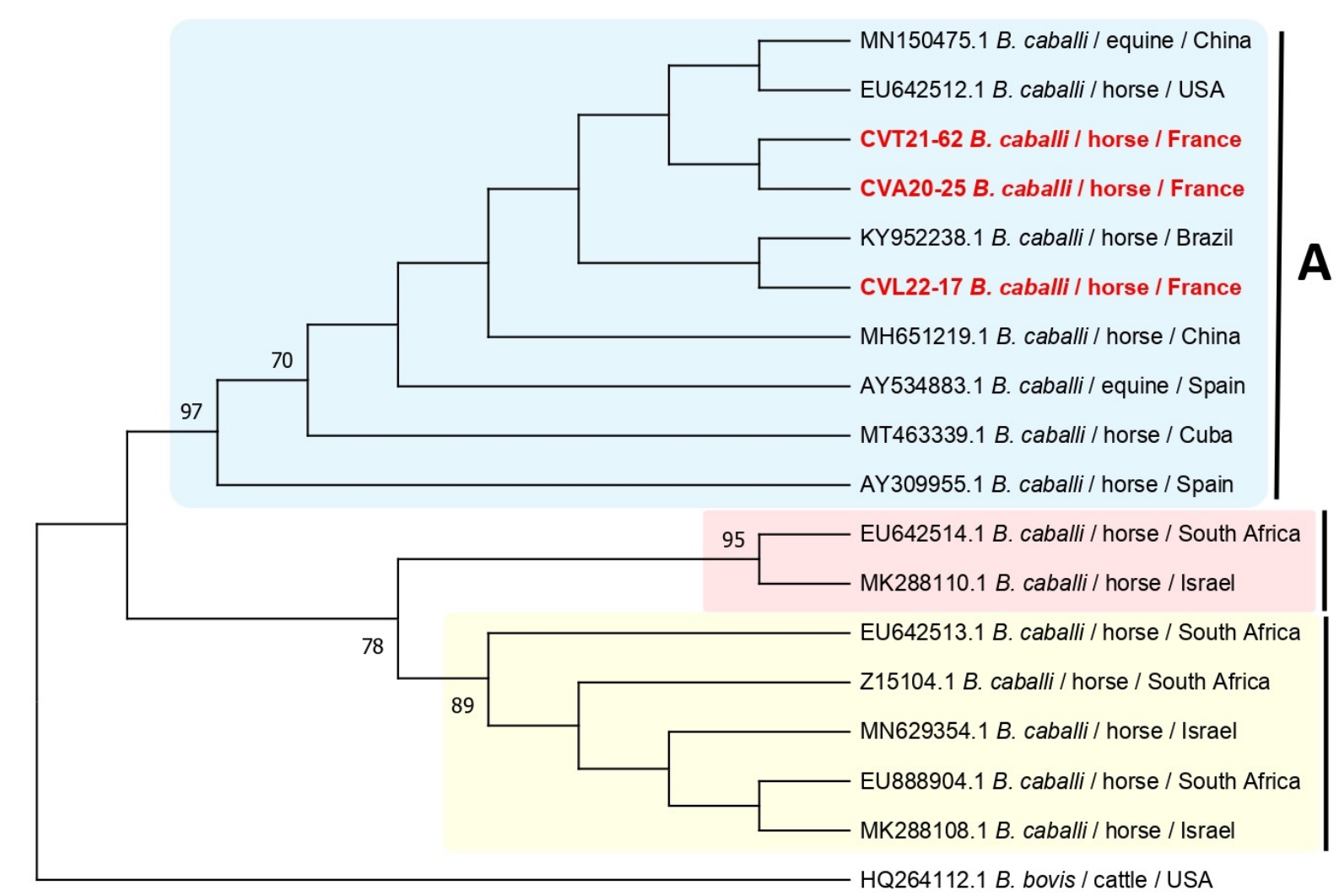
Genotyping and phylogenetic analysis

All sequenced isolates of *B. caballi* from France belong to the genotype A

A great majority of *T. equi* isolates from France cluster within the genotype E, with a few isolates (4/194) belonging to the genotype A

B. caballi

18 partial 18S rRNA sequences (651-958 bp)



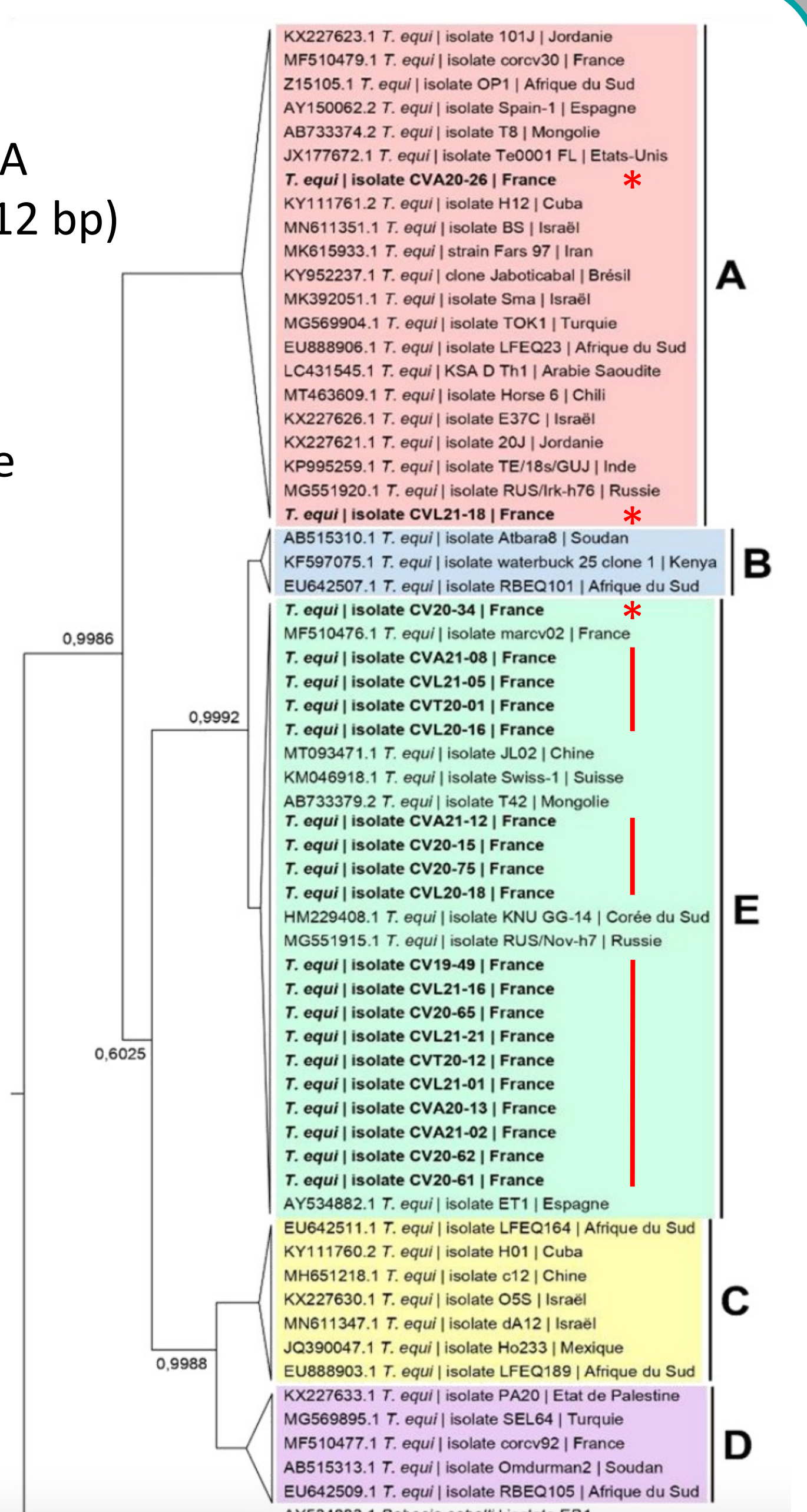
Maximum likelihood phylogeny of partial 18S rRNA sequences of *Babesia caballi* isolates

T. equi

194 partial 18S rRNA sequences (230-1412 bp)

- 17 from Paris
- 50 from Nantes
- 75 from Lyon
- 52 from Toulouse

Genotyping
98 % genotype E
2% genotype A



Evolutionary analysis by bayesian inference method of partial 18S rRNA sequences compared to representative sequences of *T. equi*

Conclusion - Discussion

This study confirms that equine piroplasmosis is endemic in France with an increasing carrier prevalence gradient, from north to south

Link with competent vector species, their abundance and/or geographical distribution?

For each species, most isolates belong to a single genotype (*B. caballi*) or to a dominant genotype (*T. equi*) regardless of their geographical origin.

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