

# Bovine tuberculosis and wildlife in France

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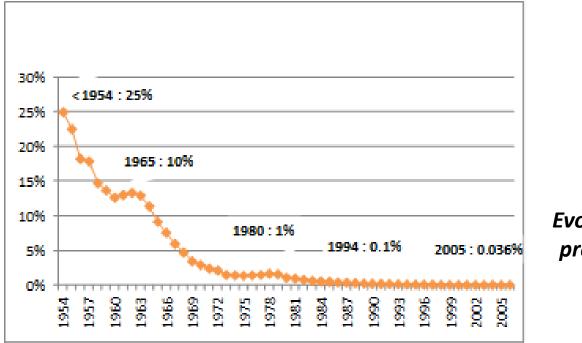




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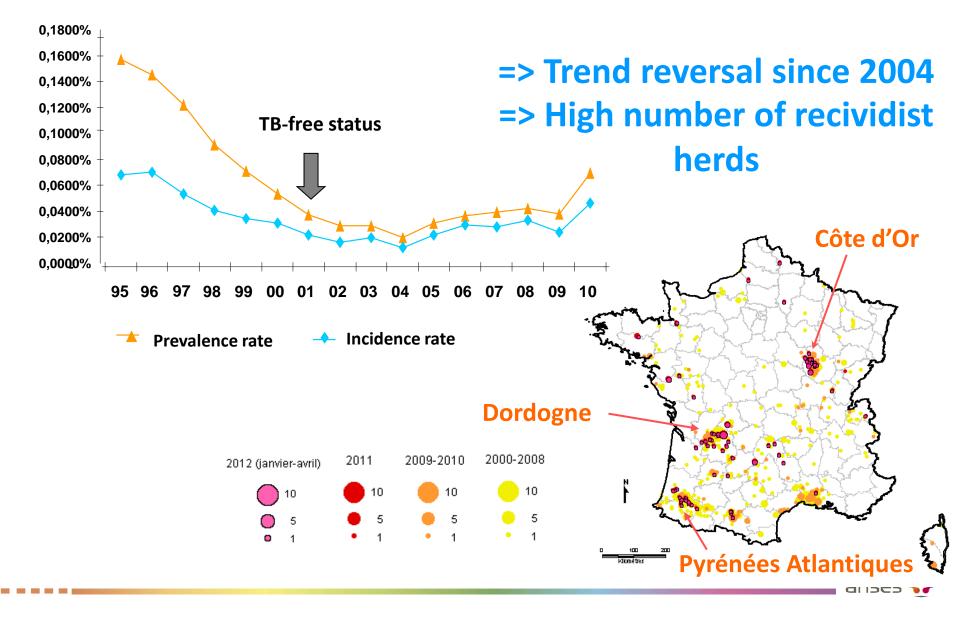
#### Historical background of bTB in French cattle

- **1954** : start of the eradication plan (voluntary)
- 1965 : the eradication plan becomes compulsory
  => tuberculin test and slaughter
- 2001 : France « officially free of bTB »



Evolution of annual prevalence rate in French herds

#### Historical background of bTB in French cattle



### First detection of bTB in wildlife: Brotonne forest

# January 2001: 3 hunted red deer with typical lung and hepatic tuberculous lesions : *M. bovis* isolation







# First detection of bTB in wildlife: Brotonne forest

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Species	No. of the second secon			
Year	2001/2	2005/6	2001/2	2005/6
Nb of hunted animals	72	138	85	155
Prevalence lesions %	18	25	29	42
Prevalence <i>M. bovis</i> %	13	24	7– 30	14 – 42

PhD thesis of Gina Zanella

#### Comparative study of lesions in deer and wild boars

Difference in the type of lesions: deer more contagious Difference in the lesion score between species

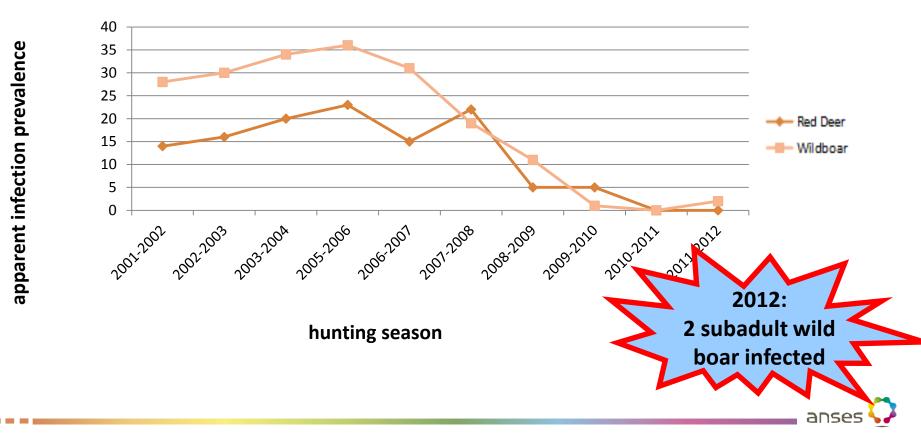
Brotonne forest: important role of deer in the withinspecies and between-species infection spread

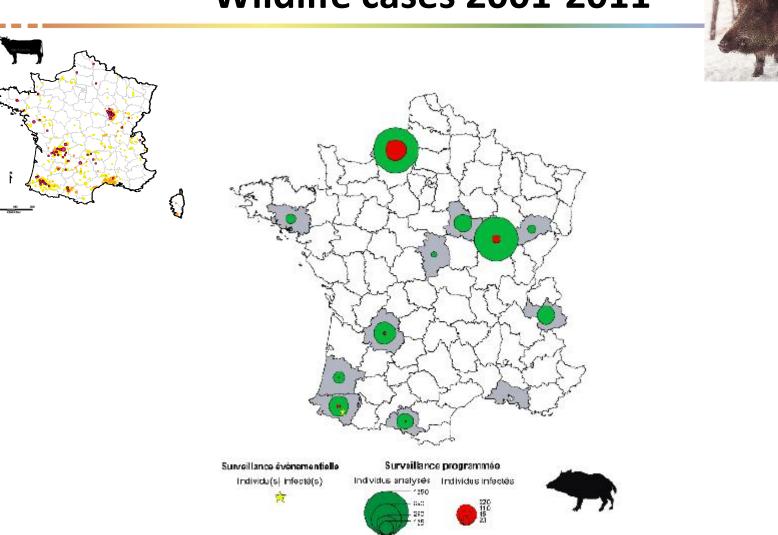
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## First detection of bTB in wildlife: Brotonne forest

#### Since 2006 in the Brotonne forest:

- stamping out of the red deer population
- reduction of wild boar density
- removal of viscera of hunted animals

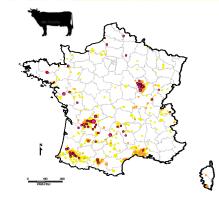


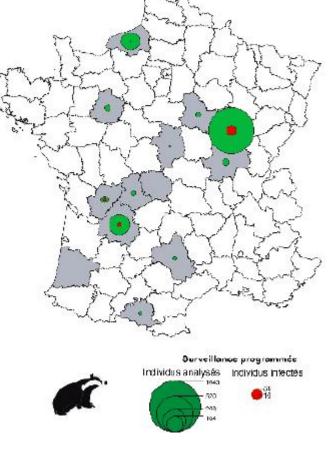


Hars et al. 2012. Dix Ten years of surveillance of bovine tuberculosis in wildlife in France. Inventory and prospects. Bull. épidémio. DGAL/Anses, 52 : 7-8

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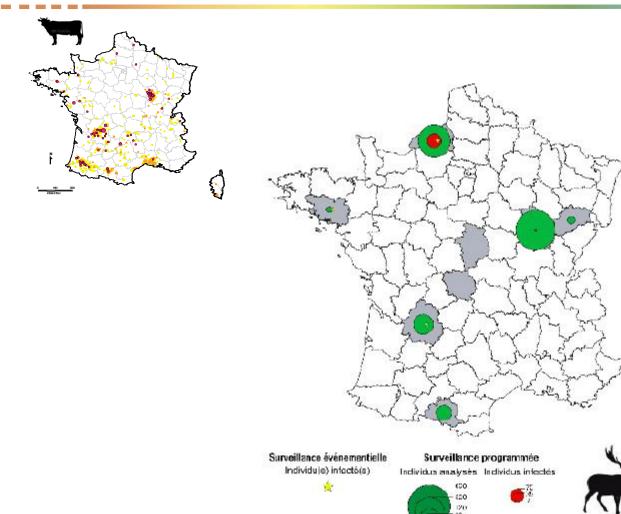


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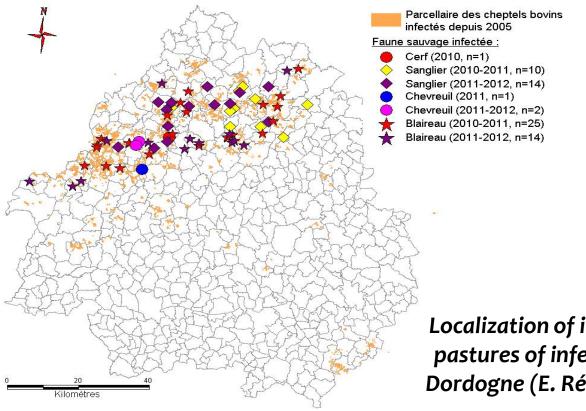
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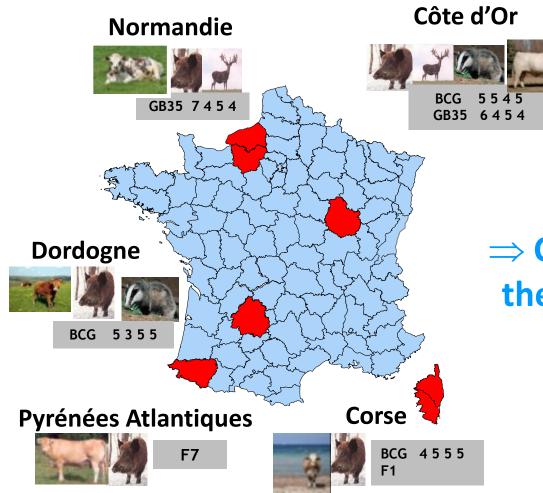
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#### **Dordogne :**

# more than 500 red deer and wild boars tested in 2006 (all negative). First cases detected in 2010



Localization of infected wildlife and pastures of infected cattle herds in Dordogne (E. Réveillaud, Vet. thesis)



#### ⇒ Cattle and wildlife share the same *M. bovis* strains per region

ML Boschiroli. National reference laboratory

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•What are the roles of wildlife in the bTB epidemiology in France ?

Maintenance host? Spill over host? Sentinel of cattle infections?

• If wildlife is a reservoir, how can we limit the spill back of bTB from wildlife to cattle ?

How to quantify and qualify those contacts? How to limit those contacts? Interest of vaccinating wildlife ?

• How to optimize a surveillance program in wildlife? Sampling strategy and diagnostic tools ?



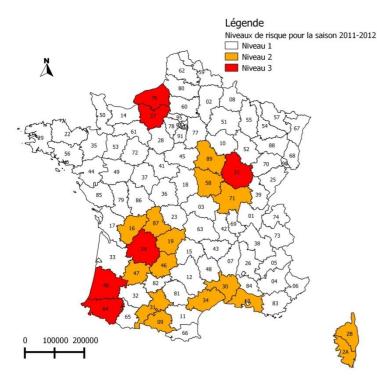
- •What are the roles of wildlife in the bTB epidemiology in France ?
- If wildlife is a reservoir, how can we limit the spill back of bTB from wildlife to cattle ?
- How to optimize a surveillance program in wildlife?
- Is the environment a bacterium reservoir in areas where the infection reemerges ?
- What is the impact of hunting practices on infection prevalence in wildlife?
- How to reconcile hunters and farmers interests ?
- How to deal with game parks and supplier game farms?



### Sylvatub: a new surveillance system

#### **Objective:**

to detect bTB infection in wildlife species and follow prevalence along time + homogenization of sampling and diagnostic procedures and data centralization



Implemented since october 2011

3 levels of surveillance according to incidence rates in cattle and wildlife

Both active and passive surveillance

Riviere et al. 2012. Bovine tuberculosis surveillance in wildlife in France. WDA-EWDA congress, Lyon – France

## Sylvatub: a new surveillance system

#### **Results 2011/2012** (prevalence of culture positive animals)

- Côte d'Or (infected area of the department)
  - wild boars: 8.1% (95% CI : [4.4 11.8])
  - deer: 0.7% (95% CI : [0.2 3.7])
  - badgers: 2.9% (95% CI : [1 4.8]) –partial results
- Dordogne (infected area of the department)
  - wild boars: 0.8% (95% CI : [0.3 2.7])
  - badgers: 4.2% (95% CI : [2.3 6.1]) partial results
  - 1 roe deer found infected
- Pyrénées Atlantiques (infected area of the department)
  - wild boars: 10.5% (95% CI : [2.6 18.5])
  - •1 badger found infected

No wildlife case outside cattle infected areas Same spoligotypes/VNTR between wildlife and cattle (except one case in Côte d'Or)

#### An example of research program (1)

PhD of Ariane Payne (ONCFS-ENVA-université Lyon1) To assess the risk of transmission of bTB between wildlife (wild boars and badgers) and cattle in Côte d'Or surveillance program Density Level of infection **Risk of** level contacts transmission **Overlap of** habitats other research program M. bovis excretion **M. bovis persistence** in the environment level

# An example of research program (1)

#### • GPS tracking:

- 10 wild boars and 10 badgers fitted with GPS collars
- Adults from different groups
- tracked during 1 to 8 months

#### ⇒ Level of the use of cattle area by wild boars and badgers

- Video surveillance:
  - On selected places in cattle zone (troughs, silage, drinking point, salt lick, farm buildings)
  - Implemented for one year

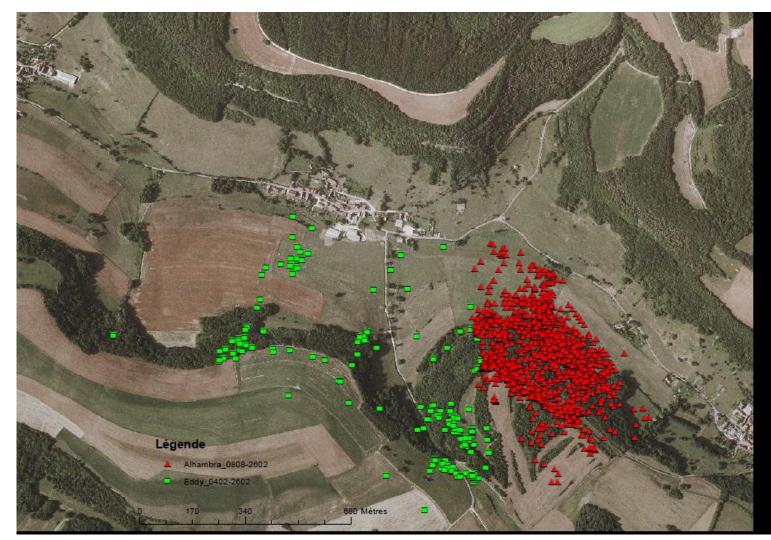


- $\Rightarrow$ Level of frequentation of cattle zone
- $\Rightarrow$ Attractivity of the different places
- ⇒Behaviour observation (opportunity for bTB transmission?)



#### An example of research program (1)

#### **GPS tracking on badgers: example**



GPS fixes (1 fix per 1/2h during the night) of 2 badgers:

•1 female tracked for 6 months (red triangles)

•1 male tracked for 1 month (green squares)



# An example of research program (2)

Is the environment a bacterium reservoir in areas where the infection reemerges ? PhD of Elodie Barbier (Anses-INRA)

=> to determine the prevalence of *M. bovis* and other atypical Mycobacterium in different agroecosystems

=> to determine the impact of the type of soil on *M*. *bovis* presence and survival

#### In progress:

Development of a RT PCR to detect *M. bovis* in water, soil, soil and aquatic fauna Immunocapture strategy for bacteriology and DNA extraction



## Conclusion

French wildlife infected at various levels function of geographical areas and species

=> What is the exact role of wildlife ?

In France, small geographical areas with increased surveillance and monitoring activities: great number of cattle and wildlife strains isolated in these areas since 2004

Can Next Generation Sequencing be used to reconstruct the transmission chains of the infection within each area and to better understand the role of wildlife?





