National School of Veterinary Medecin of Sidi Thabet

International Center for Agricultural Research in the Dry Areas

National Agronomic Institute of Tunisia

First detection and molecular identification of *Neospora caninum* from naturally infected cattle and sheep in North Africa

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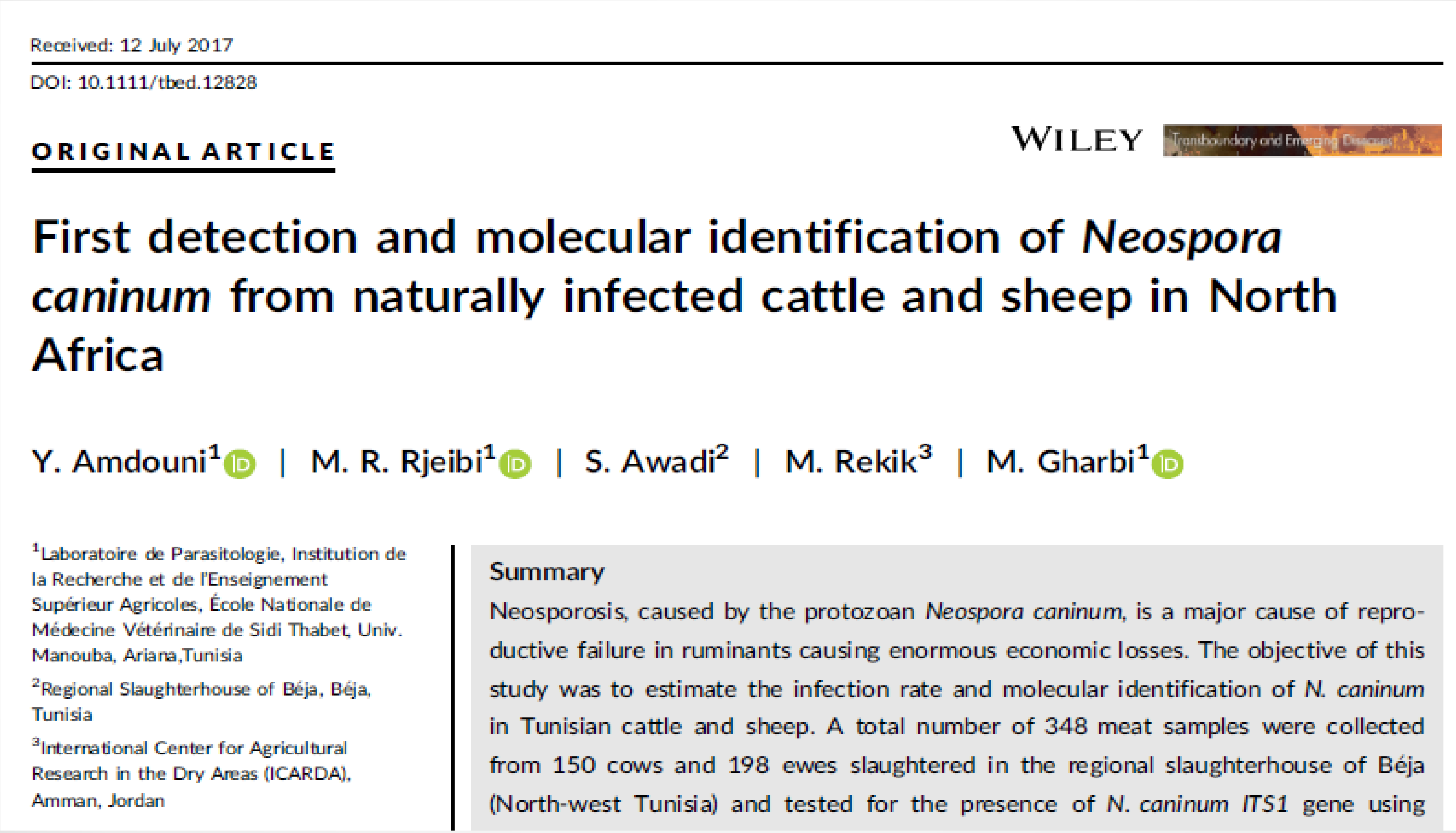

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ORIGINAL ARTICLE

WILEY Transboundary and Emerging Diseases

First detection and molecular identification of *Neospora caninum* from naturally infected cattle and sheep in North Africa

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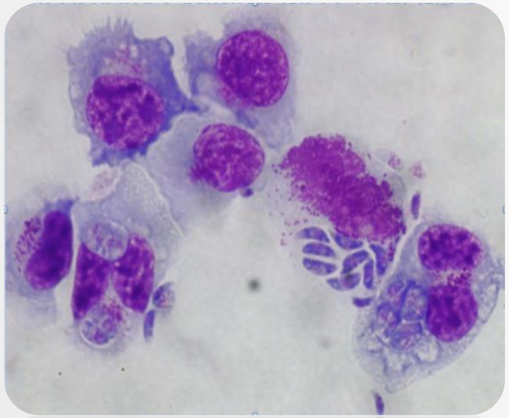
Summary

Neosporosis, caused by the protozoan *Neospora caninum*, is a major cause of reproductive failure in ruminants causing enormous economic losses. The objective of this study was to estimate the infection rate and molecular identification of *N. caninum* in Tunisian cattle and sheep. A total number of 348 meat samples were collected from 150 cows and 198 ewes slaughtered in the regional slaughterhouse of Béja (North-west Tunisia) and tested for the presence of *N. caninum* *ITS1* gene using

- **Background**
- **Objectifs**
- **Methodology**
- **Résultats & Discussion**
- **Conclusion**

Background

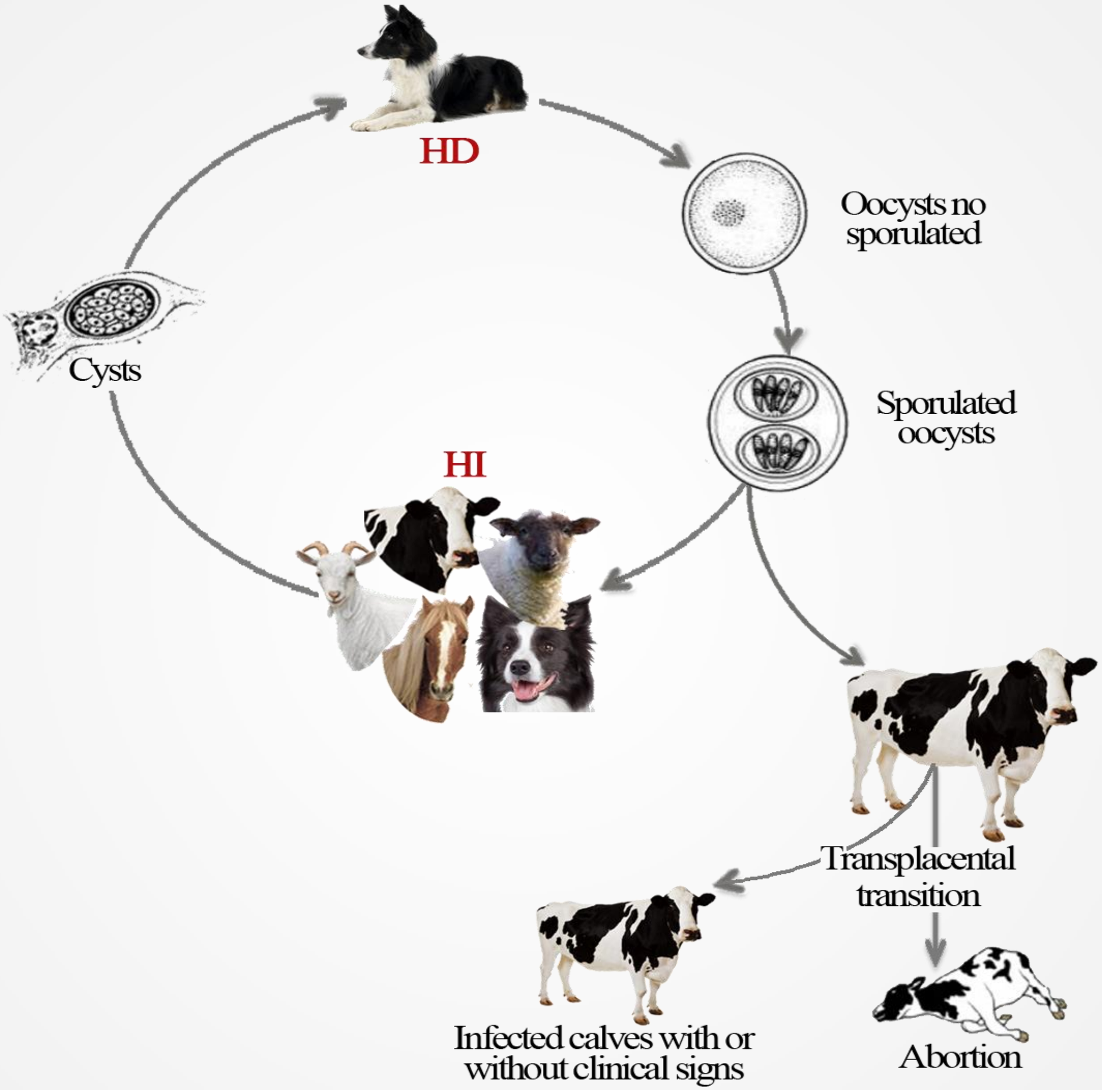


Neospora caninum

An obligate intracellular apicomplexan parasite closely related to *Toxoplasma gondii* and represents an important causative agent of abortions in cattle, worldwide (Reichel et al. 2014).

First reported in Norway in dogs (Bjerkas et al, 1984; Dubey et al, 1988), which are considered to be both intermediate and definitive hosts for *N. caninum*.

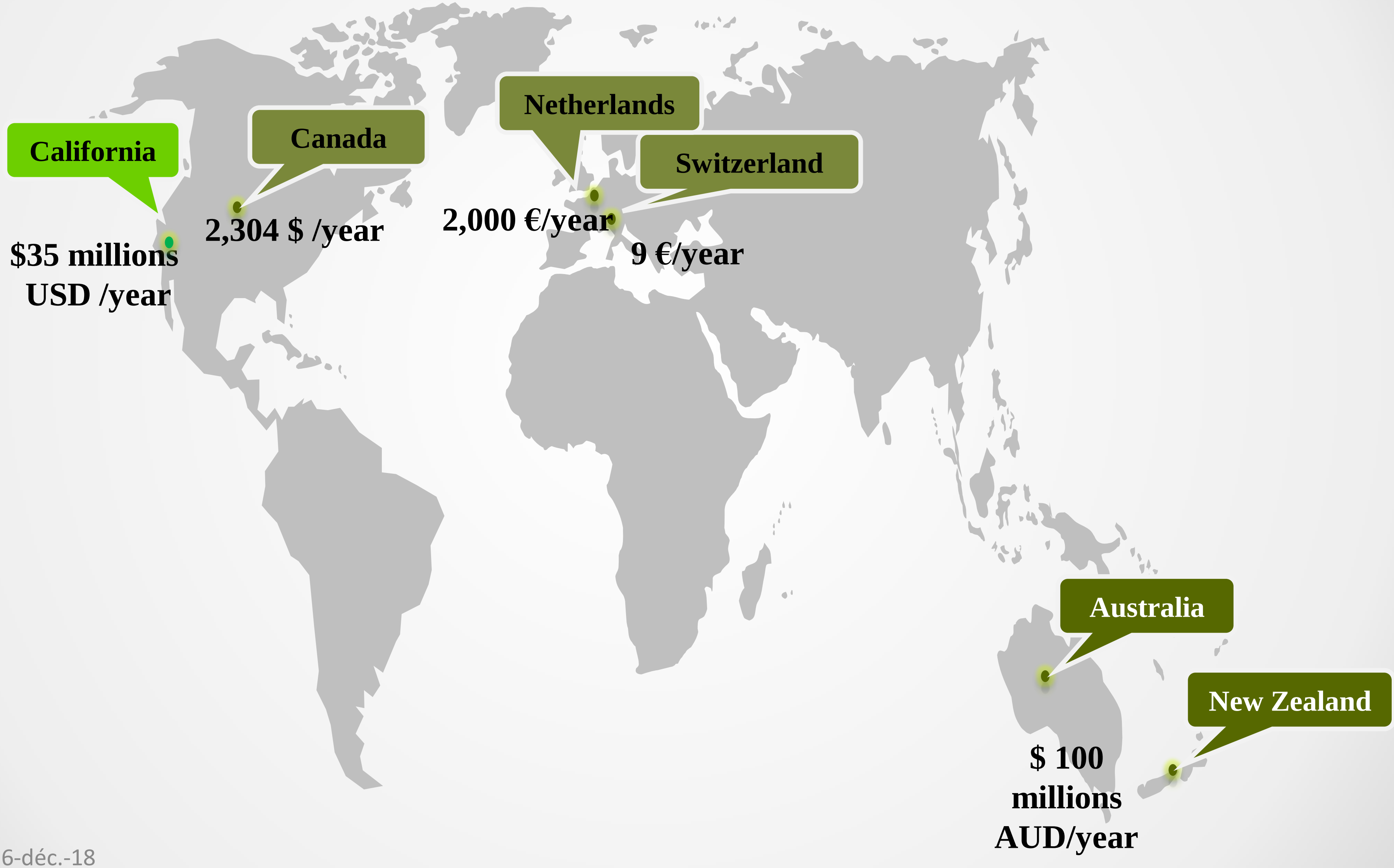
Background



HI : Intermediate host
HD : Definitive host

Background

Economic losses (Dubey et al., 2007)



California

$35 millions USD /year

Canada

2,304 $ /year

Netherlands

2,000 €/year

Switzerland

9 €/year

Australia

$ 100 millions AUD/year

New Zealand

Objectifs

01

Estimate the infection rate of *Neospora caninum* in Tunisian cattle and sheep

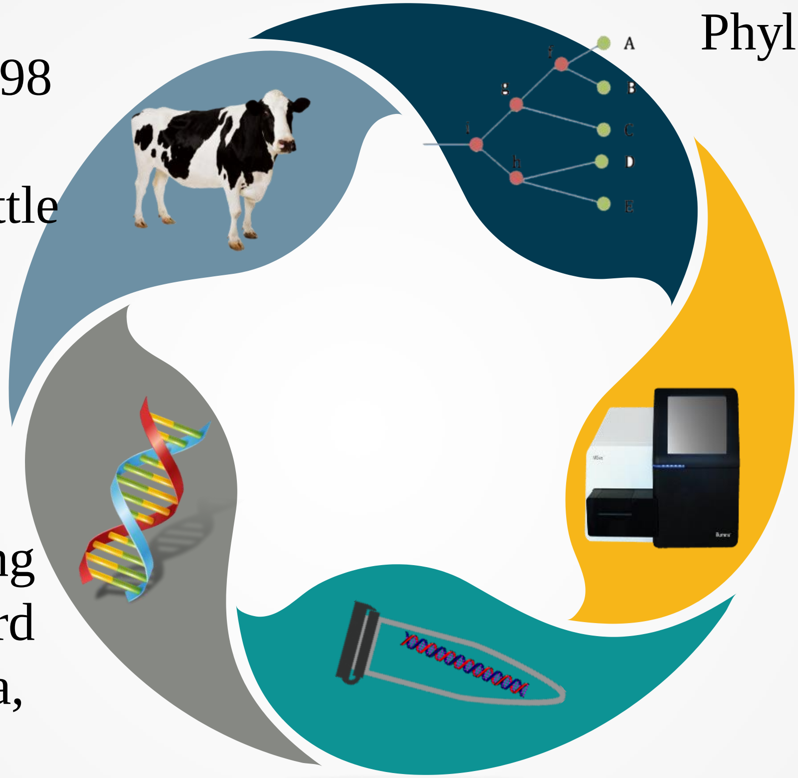
02

Estimate the risk factors associated with *Nospora caninum* infection

03

Phylogenetic analysis of *Neospora caninum* in Tunisian cattle and sheep

Methodology



Collect of 150 and 198 meat samples respectively from cattle and sheep

DNA extraction using gnomique (kit Wizard Genomics (Promega, Madisson)

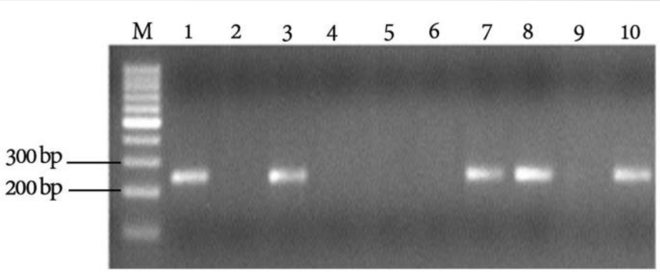
Universal PCRs & spécific PCRs (détection of *N. caninum*).

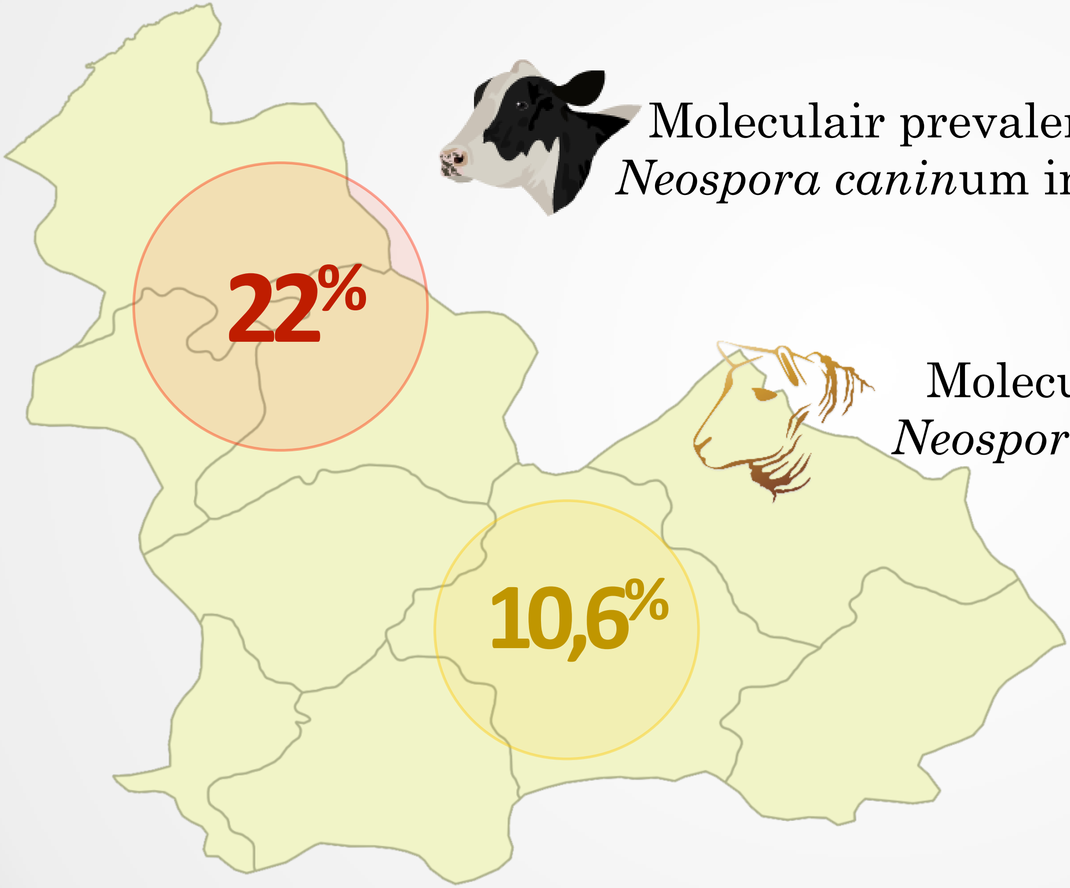
Sequencing of PCR products

Phylogenetic analysis

Résultats & discussion

- **Molecular prevalence**





Moleculair prevalence of *Neospora canin*um in cattle

Moleculair prevalence of *Neospora caninum* in sheep

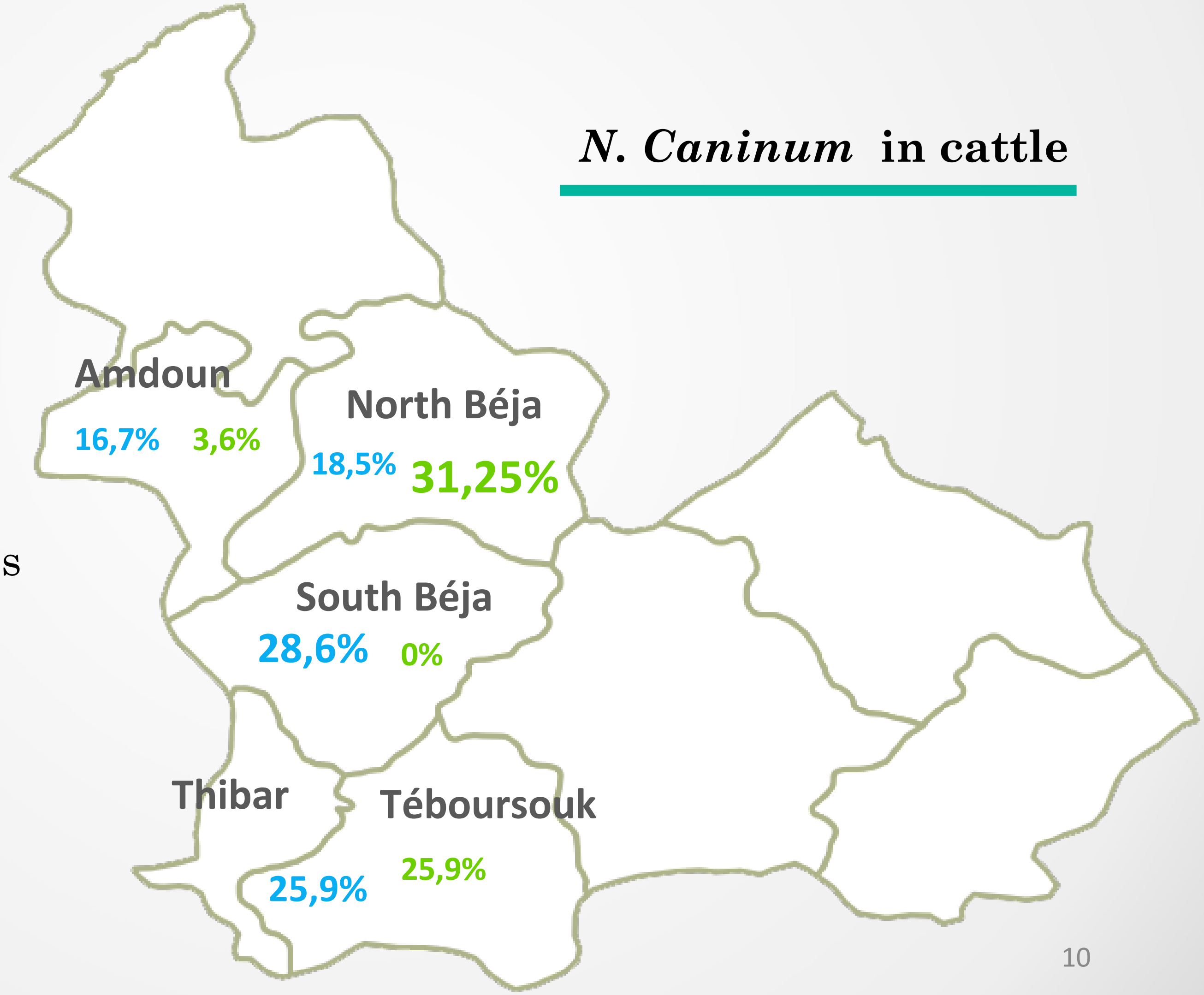
High susceptibility of cattle to *N. caninum* infection (Pan et al., 2004).

Résultats & discussion

- Risk factors : Localities

N. Caninum in sheep

***N. Caninum* in cattle**



Close contact with oocysts shed by dogs very often used as shepherd dogs,

Résultats & discussion

Risk factors : Age

Species	Age group	Positive/examined (%SE)	P value
Sheep	<1 ≥1	7/126 (5.6±4) 14/72 (**19.4**±9.1)	0.002*
Cattle	<2 [2-8[≥8	6/54 (**11.1**±8.4) 19/66 (28.8±10.9) 8/30 (26.7±15.8)	0.05*

Table: Association between *N. caninum* infection prevalence and age group

This association with age indicates the presence of an horizontal transmission by ingestion of sporulated oocysts (Figliuolo et al., 2004).

This transmission pathway is indicating the presence of a high abortion risk associated with *N. caninum* infection in naïve ruminants.

Résultats & discussion

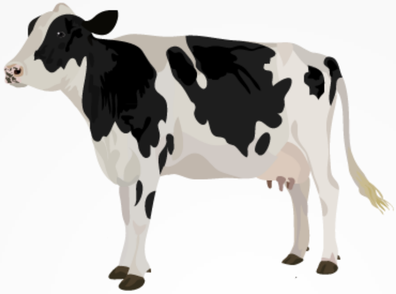
- **Risk factors : Breed**

Compared to Barbarine animals (6.8 4.5%), the infection prevalence by *N. caninum* was higher in Noire de Thibar animals (31.7 14.2%; p < .001).

These results may be due to a higher genetic resistance of local breeds to *N. caninum* in comparison with other breeds and this may be a novel area of research.

Résultats & discussion

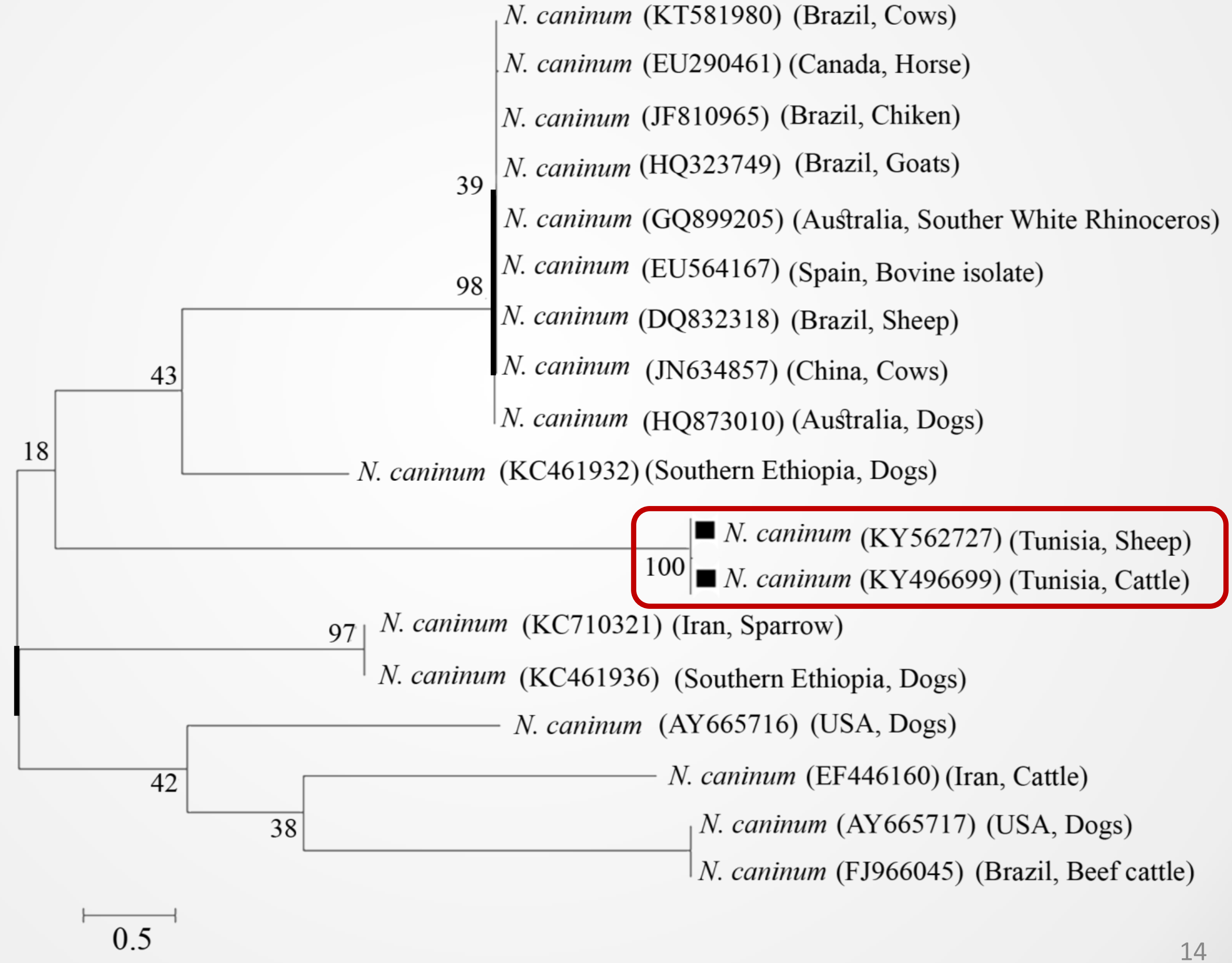
- **Risk factors : Breed**



No differences were depicted in the molecular prevalence of *N. caninum* according to cattle breeds ($p > .05$).

Résultats & discussion

- **Phylogenetic analysis**



Résultats & discussion

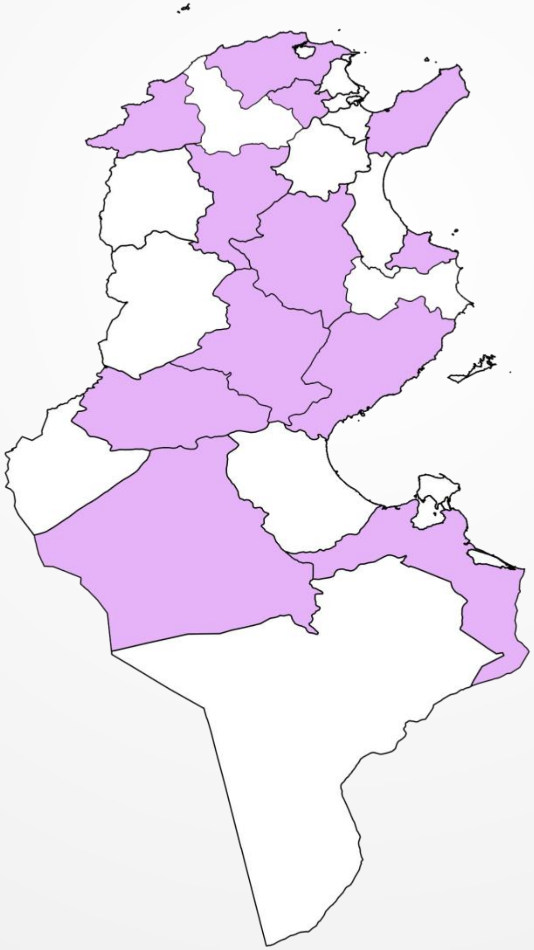
- **Phylogenetic analysis**

Based on the alignment of the two sequences of *N. caninum* from each host species (cattle and sheep), the phylogenetic tree showed two clusters:

- In the first cluster, sequences were close with sequences from Latin America (Brazil), Southern Europe (Spain) and Asia (Australia and China).
- The second cluster included sequences from North America (USA), Africa (Southern Ethiopia) and Asia (Iran).

Conclusion

+++ Studies in other regional slaughterhouses are necessary to estimate the geographical prevalence of *N caninum* infection in Tunisian cattle and sheep and to better explore the role of this parasite in both cattle and sheep abortions.



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Thank you