



Detecting zoonotic and non-zoonotic pathogens in livestock and their ticks in Corsican wetlands

Baptiste Defaye¹  | Sara Moutailler² | Sébastien Grech-Angelini³  |
Clémence Galon² | Sandrine Ferrandi³ | Vanina Pasqualini¹ | Yann Quilichini¹

¹UMR CNRS SPE 6134 – Université de Corse Pascal Paoli, Corte, France

²ANSES, INRAE, Ecole Nationale Vétérinaire d'Alfort, UMR BIPAR, Laboratoire de Santé Animale, Maisons-Alfort, France

³Groupement Technique Vétérinaire de Corse, Corte, France

Correspondence

Baptiste Defaye and Yann Quilichini, UMR CNRS SPE 6134 – Université de Corse Pascal Paoli, Corte 20250, France.
Email: defaye_b@univ-corse.fr; quilichini_y@univ-corse.fr

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Abstract

Background: Corsica is a large French island in the Mediterranean Sea with high human and animal migration rates, especially near wetlands where these migrations are particularly frequent. Among the livestock populations, cattle and sheep are widely present all across the entire Mediterranean region. Trade can be responsible for the circulation of numerous pathogens and their vectors, thereby representing a health and economic threat for the livestock industry.

Objectives: The objective of our study was to investigate the presence of pathogens in cattle and sheep farms in the wetlands of Corsica using a high-throughput screening technique.

Methods: In our study, blood samples and ticks were collected from cattle and sheep in 20 municipalities near Corsican wetlands to screen for the presence of various types of pathogens. The samples were processed using a high-throughput screening technique based on real-time microfluidic PCR: 45 pathogens were screened in 47 samples simultaneously.

Results: A total of 372 cattle and 74 sheep were sampled, and 444 ticks were collected from cattle. Out of the eight tick species detected, the main one was *Rhipicephalus bursa* (38.7% of the ticks collected). From cattle blood samples, one species and two genera were found: *Anaplasma marginale*, *Trypanosoma* sp. and *Babesia* sp. in respectively 61.5%, 58.3% and 12.2% of the cattle blood samples. From sheep blood samples, 74.3% were positive for *Anaplasma* sp, 2.7% for *Anaplasma ovis* and 1.4% for *Anaplasma capra*. This is the first report of *A. ovis* DNA in blood samples from sheep in Corsica. Out of 444 the tick samples, 114 were positive: 77.2% for *Rickettsia aeschlimannii*, 20.2% for *Rickettsia* sp., 3.5% for *Babesia* sp. and 1.8% for *Anaplasma* sp. Among them, 2.7% were co-infected with *R. aeschlimannii* and *Babesia* sp.

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Conclusions: Our results confirm the extent of possible circulation of different pathogens near Corsican wetlands, not only in ticks collected from livestock but also directly in cattle and sheep, with two (*Trypanosoma* sp. and *Babesia* sp.) being detected for the first time in cattle, one for the first time in sheep (*A. ovis*) and one for the first time in Corsica (*A. capra*)

KEYWORDS

Anaplasma, *Babesia*, cattle, high-throughput screening technique, *Rickettsia*, sheep, tick-borne pathogens, ticks, trypanosoma, wetlands

1 | INTRODUCTION

Livestock rearing appeared early in the Mediterranean region with cattle, goat, pig and sheep (Seder, 2008). Today, in the early 21st-century, grazing pastures represent half the agricultural pasturelands and more than 130 million ha (Pardini, 2004). Livestock are highly affected by all types of pathogens (e.g. bacteria, parasites, viruses) which can cause important economic losses. For instance, €1.660 billion was spent in 2013 in Europe just for animal diseases control including viral diseases like the avian influenza and African swine fever, bacterial diseases such as bovine tuberculosis and brucellosis, and parasite diseases such as toxoplasmosis in pig and sheep, or cryptosporidiosis in cattle (Costa & Akdeniz, 2019; Knap & Doeschl-Wilson, 2020; Mévélec et al., 2020; Thomson et al., 2017). In the Mediterranean Basin, sheep are the main livestock species, especially in North Africa and Eastern Mediterranean countries, followed by cattle and goat (Montgomery, 2014). Combined with their role in foodborne diseases and their interaction with humans, livestock can interact with wild animals, all of which may increase the potential risk of spread or creation of a disease reservoir in the animal population by these interactions, such as for bovine tuberculosis (Cowie et al., 2016). One of the main areas of interaction are feeding areas, which can be human-managed pastures or natural wetlands (Cowie et al., 2016). In 2019, the main livestock species raised in Corsica was sheep, with a total over 100,000 heads, followed by cattle, pig and goat (Chambre d'agriculture Corse, 2021).

Livestock are frequently present in wetlands and their interactions, particularly with wild ungulates (such as wild boar) can occur (Robertson, 1997). Wetlands are key areas for human activities, biodiversity and historically providing one of the main watering and resting areas for both livestock and humans and highly impact the breeding and road construction (Bacon, 1987; Fornell-Muñoz & Guerrero, 2019; Hammer, 1989). They represent 2–3% of the land area in the Mediterranean basin; nevertheless, they regroup more than 30% of the vertebrate biodiversity. However, even if wetlands represent a major importance in the biodiversity and animals and human wellbeing these various activities are disturbance factors of the wetlands ecology such as the water use due to human and agricultural activities, the impact of agriculture chemicals and the livestock grazing (Middleton, 2016; Taylor et al., 2021). Unsurprisingly, these habitats are important for public health given their role in vector proliferation and pathogen trans-

mission (Jourdain et al., 2007; Rabou et al., 2015; Rey et al., 2012). Furthermore, depending on the ecosystem, the diversity and the prevalence of ectoparasite communities and pathogens can change (Dudek, 2014).

Ticks (Acarida) are the leading vectors of veterinary pathogens and the second, after mosquitos, of human pathogens (Nicholson et al., 2019; Parola & Raoult, 2001). Furthermore, ticks are responsible of the transmission, circulation and maintenance of pathogens between different groups of animals all over the world. They allow for the maintenance and transmission of tick-borne pathogens in a natural cycle that involves feeding on the blood of their intermediate and final animal hosts and accidental human hosts (de la Fuente et al., 2008). Ticks can transmit a wide spectrum of bacteria, viruses and parasites. These tick-borne pathogens are known to be both pathogens of veterinary importance and zoonotic pathogens harmful for humans (Sonenshine, 2014). Many different animals can be reservoirs. Worldwide, one of the largest groups of reservoirs is probably ungulates (wild or domestic) as the livestock (Eldridge & Edman, 2003). The livestock are highly affect by various tick-borne pathogens (TBPs) as a target and like host of tick carrying pathogens of sanitary importance such as the bacteria responsible of the Lyme disease and the CCHF virus (Dernat Sylvain et al., 2021). In the Mediterranean Basin, more precisely, the livestock are among the most studied and reported animals host of pathogens and ectoparasites. They also belong the main targets of various ticks' genera as *Rhipicephalus* and *Hyalomma*. By these ticks' genera infestations, the livestock can be targets or reservoir of several pathogens as the causative agents of piroplasmosis, Lyme disease and Q fever (Defaye et al., 2022; Estrada-Peña, 2004). This potential role of target and reservoir is particularly important in Corsica where livestock represents more than 270,000 animals for a human population of 322,000 and coupled with both a lack of knowledge of the farmer about the ticks and TBPs; and under estimation of their risk (Chambre d'agriculture Corse, 2021; Dernat Sylvain et al., 2021). Recently, in two surveys of ticks, nine species were found in Corsica: *Ixodes ricinus*, *Rhipicephalus bursa*, *Rh. sanguineus* s.l., *Rh. (Bo.) annulatus*, *Hyalomma marginatum*, *Hy. scupense*, *Haemaphysalis sulcata*, *Hae. punctata* and *Dermacentor marginatus* (Grech-Angelini et al., 2016). Eight species were found on Corsican cattle. Out of the eight species, *Rh. bursa* was the most commonly found on cattle (>50% of the ticks collected on cattle), with only *Hae. sulcata* not being sampled at all on cattle. In sheep, three

species were identified: *Rh. bursa* (91% of the collected ticks), followed by *H. marginatum* and *Rh. sanguineus* s.l. (Grech-Angelini et al., 2016).

The aims of this study were (i) to determine the main tick species of cattle and sheep in Corsican wetland areas and (ii) to investigate the potential occurrence of zoonotic and non-zoonotic pathogens in ticks and hosts (livestock) from Corsican wetlands. To do so, we focused our screening efforts on the detection of 34 species and 11 genera of bacteria, viruses and parasites with a high impact on animal and human health suspected to be present in Corsica.

2 | METHODS

2.1 | Sites and animal samples

Corsica is the largest French island in the Mediterranean Sea. It is located 15 km from the closest Italian land mass (the island of Sardinia) and 160 km from the nearest French coast. It is characterised by a mild Mediterranean climate and a wide diversity of landscapes, such as wetlands (mainly on the coastline), forests and mountains (elevation of up to 2706 m). Corsica is divided into two administrative *départements* (Haute-Corse and Corse-du-Sud), with a population of 322,000, which increases by a factor of 10 during the tourist season (summer) with approximately 3 million tourists. Sampling was carried out in wetlands, which can be classified into five categories: lagoon, river and river mouth, artificial lake, altitude lake and temporary pool. In this study, all samples were collected in coastal wetlands including lagoon, artificial lake and river mouth.

A total of 372 cattle and 74 sheep were sampled across Corsica on respectively 22 and 3 farms during the winter and spring seasons in 2019 (February to June) and winter in 2020 (October 2019 to February 2020). The farm choose for the study were farm included in the prophylactic program of the Corsican veterinary groups and located near coastal wetlands (Figure 1). For cattle, 288 blood samples and 444 ticks were collected in 18 municipalities, and for sheep, 74 blood samples were collected in 3 municipalities. Samples were collected only from animals older than 6 months of age. Every blood sample was collected in an EDTA tube by veterinarians as part of national surveillance program for animal diseases. All samples were stored at -80°C within a few hours after sampling until further analysis.

2.2 | DNA extraction and PCR pre-amplification

Ticks were washed in ethanol and distilled water and then morphologically determined to the species level using species keys (Estrada-Peña, 2004; Pérez-Eid, 2007). Prior to extraction, ticks were crushed in microtubes filled with six metal beads by using a Fisherbrand™ bead mill 24 homogeniser (Thermo Fisher, USA) at 5500 rpm for 20 s. Tick DNA was extracted using a NucleoSpin™ Tissue kit (Macherey-Nagel, Germany). For blood samples, a Nucleospin Quickpure Blood kit (Macherey-Nagel, Germany) was used according to the manufacturer's instructions. All ticks from the same animal were pooled by species,

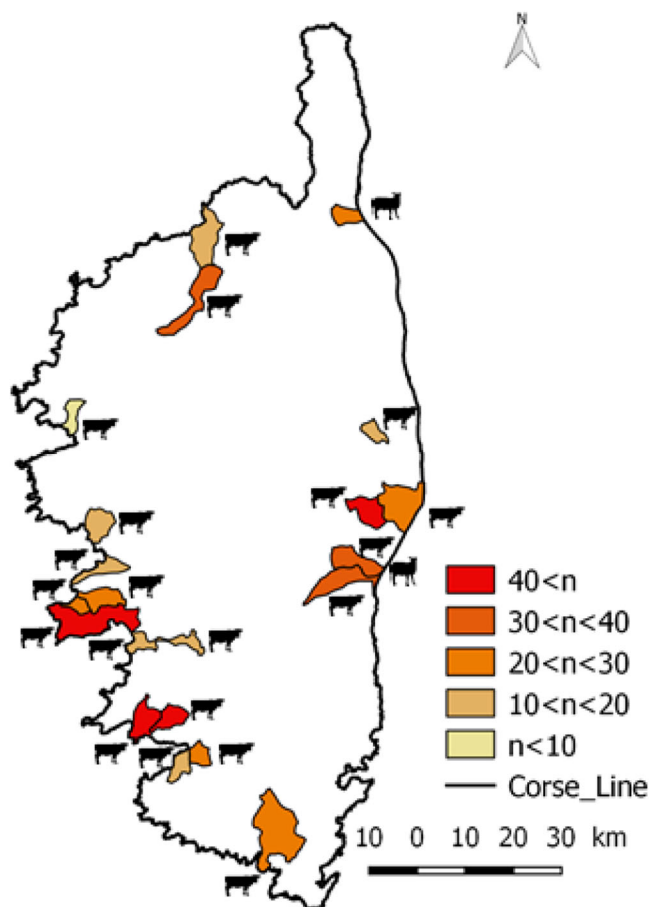


FIGURE 1 Map of Corsica showing the municipalities samples (n = number of animal sampled by municipalities)

stage and sex (minimum number of ticks = 1; maximum number of ticks = 8).

To improve the detection of pathogen DNA, total DNA was pre-amplified by using the PreAmp Master Mix according to the manufacturer's instructions (Fluidigm, California, USA). Prior to the experiments, primers targeting different pathogens were pooled by combining an equal volume of each primer (200 nM final each). The experiment was performed with 1 μl of PreAmp Master Mix, 1.25 μl of pooled primer mix, 1.5 μl distilled water and 1.25 μl DNA for a final volume of 5 μl . Pre-amplification was performed as follows: 1 cycle at 95°C for 2 min, 14 cycles at 95°C for 15 s and 60°C for 4 min. Amplified samples were diluted to 1:10. The pre-amplified DNAs were stored at -20°C until further use.

2.3 | Assay design

Pathogens and their targeted genes were *Anaplasma* spp. (16S rRNA), *A. marginale* (msp1b), *A. phagocytophilum* (msp2), *Borrelia* spp. (23S rRNA), *Bo. burgdorferi* s.s. (rpoB), *Bo. afzelii* (flagellin), *Bo. miyamotoi* (glpQ), *Bo. lusitanae* (rpoB), *Bo. spielmanii* (flagellin), *Rickettsia* spp. (gltA), *R. slovacica* (23S-5S ITS), *R. helvetica* (23S-5S ITS), *R. aeschlimanii*

TABLE 1 List of pathogens, targets and primers/probes created for microfluidic real-time PCR screening

Pathogen	Name	Sequence	Length (nucleotides)	Gene	Gene reference
<i>Aujeszkys disease viral agent</i>	Aujv_gp50_F	CTTTATCGAGTACGCCGACTG	225	gp50	Y14834.1
	Av_gp50_R	AACGGGCACTCTTGCCCC			
	Av_gp50_P	CAGATCTTTGGGCGCTGCCGGC			
<i>Chlamydia psittaci</i>	Chl_psi_16S-23S_F	ACGCCGTGAATACGTTCCC	214	16S-23S rRNA	U68450.1
	Chl_psi_16S-23S_R	AGTCAAACCGTCCTAAGACAG			
	Chl_psi_16S-23S_P	CCTTGTACACACCGCCCGTCACATC			
<i>Haemoproteus spp.</i>	Hae_cytB_F	ATATGCATGCTACTGGTGCTAC	240	cytochrome B	AF465579.1
	Hae_cytB_R	CAAATCCATGAAACAAGTCCAGG			
	Hae_cytB_P	CGGTTGCACCCAGAACTCATTGAC			
<i>Leptospira spp.</i>	Lep_Lipl32_F	CTCTATGTTTGGATTCTGCCC	158	lipL32	MK541891.1
	Lep_Lipl32_R	CCAAGTATCAAACCAATGTGGC			
	Lep_Lipl32_P	ATTGATTTTTCTTCTGCGGTAGCCGCTTTG			
<i>Leucocytozoon spp.</i>	Leu_cytB_F	GGGTATGTCTTACCATGGGG	177	cytochrome B	KF717066.1
	Leu_cytB_R	AATTGCTAGTGCTACGAATGGG			
	Leu_cytB_P	AAATGAGTTTTTGGGGAGCAACCGTTATTAC			
<i>Plasmodium spp.</i>	Pla_ssrRNA_F	ATATAGAAACTGCGAACGGCTC	339	ssrRNA	MK650620.1
	Pla_ssrRNA_R	TTTCTCAGGCTCCCTCTCC			
	Pla_ssrRNA_P	CTCTAATCCCCGTTACCCGTCATAGC			
<i>Rickettsia monacensis</i>	Ric_mon_F	CTCGGTGCCGCTACTTTAAAC	192	ompB	KU961543.1
	Ric_mon_R	GAGCACCGCCAATAAGAGC			
	Ric_mon_P	AGTGCCGATGCAAATACTCCGGTGAC			
<i>Trypanosoma spp.</i>	Try_18SRNA_F	GTAATTCAGCTCCAAAAGCG	178	18S rRNA	EU596263.1
	Try_18SRNA_R	TCAGGAAGGAACCACTCCC			
	Try_18SRNA_P	ACCTCAAGGGCATGGGTCACCAATCC			

(23S-5S ITS), *R. massiliae* (23S-5S ITS), *R. conorii* (23S-5S ITS), *C. burnetii* (idc, IS1111), *N. mikurensis* (16S rRNA), *Bartonella spp.* (ssrA), *Ba. henselae* (pap31), *Ba. quintana* (bqtR), *Ehrlichia spp.* (16S rRNA), *E. ruminatum* (dsb), *Hepatozoon spp.* (18S rRNA), *To. gondii*, *B. microti* (CCTeta), *B. bigemina* (18S rRNA), *B. vogeli* (hsp70), *B. caballii* (rap1), *B. bovis* (CCTeta), *B. ovis* (18S rRNA), *B. divergens* (hsp70), *T. equi* (ema1), *T. annulata* (18S rRNA), *Leishmania spp.* (hsp70), *L. infantum* (ITS) and *African swine fever virus* (Vp72). Primers and probes were designed by Gondard et al. (2018), Grech-Angelini et al. (2020) and Michelet et al. (2014). The set of primers and probes created especially for this study is listed in the Table 1.

2.4 | DNA amplification and microfluidic real-time PCR

The detection of the vector-borne pathogen targets was performed on pre-amplified DNA by using the BioMark™ real-time PCR system (Fluidigm, California, USA) for high-throughput microfluidic real-time PCR amplification using the 48.48 Dynamic Array™ (Fluidigm). Fluidigm chips can carry out 2304 real time PCR reactions simultaneously with

48 PCR mixes on 48 samples placed in individual wells prior to transfer to individual chambers for the reaction. The thermal cycling conditions were 50°C for 2 min, 95°C for 10 min and 40 cycles at 95°C for 15 s and 60°C for 1 min. One negative water control, one inhibitory molecule control (*E. coli* EDL933 strain) and one DNA extraction control (animal species target) were added to each array. *E. coli*-specific primers and probes were used.

2.5 | Confirmation of pathogen detection

The confirmation of the pathogen detection was performed using nested PCR or real-time PCR targeting a gene other than the one used in the microfluidic experiment. The targets and primers were selected from the literature when available or newly designed for this study. The positive sequences after gel migration of the nested PCR product were sent to Eurofins MWG Operon (Cologne, Germany) for sequencing and assembled using BioEdit software (Ibis Biosciences, Carlsbad, CA, USA). An online BLAST (National Center for Biotechnology Information) was used to identify the sequenced organisms. All targeted genes and primer sequences from the literature are described in Gondard

TABLE 2 List of pathogens, targets and primers/probes used for confirmation by real-time PCR

Pathogen	Name	Sequence	Length (nucleotide)	Genes	Genes references
<i>Aujeszký's disease viral agent</i>	Aujv_gp50_F2	AACATCCTCACCGACTTCATG	158	gp50	Y14834.1
	Av_gp50_R2	CTGGTAGAACGGCGTCAGG			
	Av_gp50_P2	AATCGCATCACGTCCACGCCCC			
<i>Chlamydia psittaci</i>	Chl_psi_16S-23S_F2	AGTAATCTTCGGCGAGCTGG	177	16S-23S rRNA	U68450.1
	Chl_psi_16S-23S_R2	CGCTACTTAGGGAATCTCTTTG			
	Chl_psi_16S-23S_P2	TATAAAGCTATGACCCGGAGGTCTCCG			
<i>Haemoproteus</i> spp.	Hae_cytB_F2	CCTTGGGGTCAAATGAGTTTC	231	cytochrome B	AF465579.1
	Hae_cytB_R2	AAGCCGTATCATATCCTAAAGG			
	Hae_cytB_P2	CCTGGACTTGTTCATGGATTGTGGAGG			
<i>Leptospira</i> spp.	Lep_Lipl32_F2	CTCTATGTTTGGATTCTGCC	158	lipL32	MK541891.1
	Lep_Lipl32_R2	CCAAGTATCAAACCAATGTGGC			
	Lep_Lipl32_P2	ATTGATTTTTCTTCTGGGGTAGCCGCTTTG			
<i>Leucocytozoon</i> spp.	Leu_cytB_F2	GAGTTTCTGGGGAGCTACTG	197	cytochrome B	KU842391.1
	Leu_cytB_R2	GGATTAGTGCTACCTGAATATG			
	Leu_cytB_P2	TGAATAAATACAATTGCTAGTGCTACGAATGG			
<i>Plasmodium</i> spp.	Pla_ssrRNA_F2	TCGAGTTTCTGACCTATCAGC	264	ssrRNA	MK650620.1
	Pla_ssrRNA_R2	AGACTTGCCCTCCAATTGTTAC			
	Pla_ssrRNA_P2	TGGCCTTGCAATTGTTATTCTTGTCACTACC			
<i>Trypanosoma</i> spp.	Try_18SRNA_F2	CAACACGGGGAACCTTACCAG	141	18SRNA	EU596263.1
	Try_18SRNA_R2	ATCCTACTGGGCAGCTTGG			
	Try_18SRNA_P2	CAGGGTGAGGATTGACAGATTGAGTGTTTC			

et al. (2018) and Michelet et al. (2014). The set of primers/probes created for this publication is listed in Table 2.

3 | RESULTS

3.1 | Tick collection

A total of 444 ticks were collected on 178 cattle in 18 municipalities close to wetlands (Table 3). Six tick species were identified: *Rhipicephalus bursa* (38.7%), *Rh. sanguineus* s.l. (22.8%), *Rhipicephalus* sp. (17.1%), *Hy. marginatum* (8.6%), *Hy. scupense* (7.2%), *D. marginatus* (0.7%) and *Rh. (Bo.) annulatus* (0.2%). Finally, 4.7% of the ticks could not be determined and were designated as undetermined ticks (Table 3). Regarding their life-cycle stage, 55.6% were nymphs and 44.4% were adults; of these adults 57.4% were partially or fully engorged females and 42.6% were males. No ticks were found on sheep.

3.2 | Pathogens detected in ticks

Out of the 312 tick pools from cattle, 96 pools were positive (30.5%) and three pathogen genera were detected.

The most frequently found pathogen was *Rickettsia* sp., detected in 93 pools; 15 of the pools detected positives to *Rickettsia* sp. could not be determined to the specific level. These bacteria were detected in *Rh. sanguineus* s.l. (46.6%), *Rh. bursa* (33.3%), but only 6.7% for *Rhipicephalus* sp., *Hy. scupense* and undetermined ticks. The remaining 78 pools were positive for *R. aeschlimannii*. This pathogen was mainly found in *Rh. bursa* (41%), with the remaining positive tick species being *Hy. marginatum* (29.5%), *H. scupense* (14.1%), *Rh. sanguineus* s.l. (10.2%), *Rhipicephalus* sp. (3.8%) and unknown (1.4%) (Table 3, Figure 2a). These samples were found to be related to the ompB gene of a *R. aeschlimannii* sequence detected in a *Hy. marginatum* individual in Russia (Genbank: KU961544.1) with an identity between 96% and 100%.

One pool was positive for *Anaplasma* sp. It was composed of *Rh. sanguineus* s.l. ticks collected on a farm in Viggianello (Table 3, Figure 2b). However, sequencing was unsuccessful for *Anaplasma* sp.

Two pools were positive for *Babesia* sp. They were one pool of *Rh. sanguineus* s.l. and one of *Hy. marginatum* both collected on a farm in Figari (Table 3, Figure 2c). Unfortunately, the sequencing of the *Babesia* sp. positive samples was unsuccessful.

Only one pool of *Rh. sanguineus* s.l. ticks was positive for more than one pathogen: *R. aeschlimannii* and *Babesia* sp.

TABLE 3 Tick-borne pathogens and tick distribution on livestock in Corsican wetlands

Municipality (n°)	No. sampled sheep/no. positives (A/Ao/Ac)	No. sampled cattle/no. positives (Am/B/T)	D. marginatus (A/B/R/Ra)	Hy. marginatum (A/B/R/Ra)	Hy. scarpense (A/B/R/Ra)	Rhipicephalus spp.(A/B/R/Ra)	Rh. annulatus (A/B/R/Ra)	Rh. bursa s.l. (A/B/R/Ra)	Rh. sanguineus (A/B/R/Ra)	Undetermined tick species (A/B/R/Ra)	Total ticks from cattle (A/B/R/Ra)
Aghione (1)	-	28/9 (Am), 1 (B), 15 (T)	-	2/1 (Ra)	1/1 (R)	2/2 (Ra)	-	2/2 (Ra)	1/1 (R)	9/0	17/2 (R), 5 (Ra)
Ajaccio (2)	-	38/14 (Am), 1 (B), 22 (T)	-	-	-	16/0	1/0	26/3 (Ra)	14/0	-	57/3 (Ra)
Alata (3)	-	6/6 (Am), 3 (B), 2 (T)	1/0	1/1 (Ra)	1/0	1/0	-	1/0	4/4 (R)	-	9/4 (R), 1 (Ra)
Aleria (4)	-	22/0	-	3/3 (Ra)	3/0	2/0	-	22/3 (Ra)	2/2 (Ra)	2/0	34/8 (Ra)
Calcatoggio (5)	-	10/9 (Am), 4 (T)	-	1/0	-	-	-	-	-	1/0	2/0
Coggia (6)	-	10/10 (Am), 4 (B), 9 (T)	-	1/0	8/0	-	-	-	-	2/1 (R)	11/1 (R)
Figari (7)	-	14/14 (Am), 2 (B), 11 (T)	1/0	4/1 (B), 2 (Ra)	-	6/0	-	9/2 (R), 1 (Ra)	12/3 (B), 3 (R), 6 (Ra)	1/0	33/4 (B), 5 (R), 9 (Ra)
Furiani (8)	25/22 (A), 2 (Ao)	-	-	-	-	-	-	-	-	-	-
Grosseto-Prugna (9)	-	11/1 (Am), 6 (T)	-	6/3 (Ra)	3/3 (Ra)	-	-	1/0	-	-	10/6 (Ra)
Olimi-Capella (10)	-	19/19 (Am), 4 (B), 13 (T)	-	4/3 (Ra)	3/1 (Ra)	12/1 (Ra)	-	2/1 (Ra)	3/0	2/1 (Ra)	26/7 (Ra)
Palasca (11)	-	12/10 (Am), 10 (T)	-	12/9 (Ra)	8/3 (Ra)	-	-	54/3 (R), 26 (Ra)	-	-	74/3 (R), 38 (Ra)
Partinello (12)	-	8/5 (Am), 4 (B), 7 (T)	-	-	-	-	-	-	-	-	-
Propriano (13)	-	10/7 (Am), 3 (B), 4 (T)	-	-	-	1/0	-	8/0	3/0	2/0	14/0
Prunelli-Di-Fiumorbo (14)	25/0	8/6 (Am), 4 (T)	-	-	-	-	-	-	-	-	-

(Continues)

TABLE 3 (Continued)

Municipality (n°)	No. sampled sheep/no. positives (A/Ao/Ac)	No. sampled cattle/no. positives (Am/B/T)	<i>D. marginatus</i> (A/B/R/Ra)	<i>Hy. marginatum</i> (A/B/R/Ra)	<i>Hy. scupense</i> (A/B/R/Ra)	<i>Rhipicephalus</i> spp. (A/B/R/Ra)	<i>Rh. annulatus</i> (A/B/R/Ra)	<i>Rh. bursa</i> (A/B/R/Ra)	<i>Rh. sanguineus</i> s.l. (A/B/R/Ra)	Undetermined tick species (A/B/R/Ra)	Total ticks from cattle (A/B/R/Ra)
Serra-Di-Ferro (15)	-	34/29 (Am), 5 (B), 20 (T)	-	-	-	2/2 (Ra)	-	25/2 (R)	14/3 (R)	-	41/5 (R), 2 (Ra)
Serra-Di-Fiumorbo (16)	34/33 (A), 1 (Ac)	-	-	-	-	-	-	-	-	-	-
Sollacaro (17)	-	28/18 (Am), 4 (B), 20 (T)	1/0	-	-	17/0	-	15/1 (Ra)	28/1 (Ra)	1/0	62/2 (Ra)
Tox (18)	-	9/9 (Am), 2 (B), 9 (T)	-	-	-	-	-	1/0	-	-	1/0
Viggianello (19)	-	15/7 (Am), 3 (T)	-	1/0	-	16/0	-	-	8/2 (A)	1/0	26/2 (A)
Villanova (20)	-	16/4 (Am), 2 (B), 9 (T)	-	3/1 (Ra)	5/4 (Ra)	1/1 (R)	-	6/0	12/2 (R), 2 (Ra)	-	27/3 (R), 7 (Ra)
Total sampled/positives	74/55 (A), 1 (Ac), 2 (Ao)	288/177 (Am), 35 (B), 168 (T)	3/0	38/1 (B), 23 (Ra)	32/1 (R), 11 (Ra)	76/1 (R), 5 (Ra)	1/0	172/7 (R), 37 (Ra)	101/2 (A), 3 (B), 13 (R), 11 (Ra)	21/1 (R), 1 (Ra)	444/2 (A), 4 (B), 23 (R), 88 (Ra)

Abbreviations: A, *Anaplasma* spp.; Ac, *A. capra*; Am, *A. marginale*; Ao, *A. ovis*; B, *Babesia* spp.; R, *Rickettsia* spp.; Ra, *R. aeschlimannii*; T, *Trypanosoma* spp.

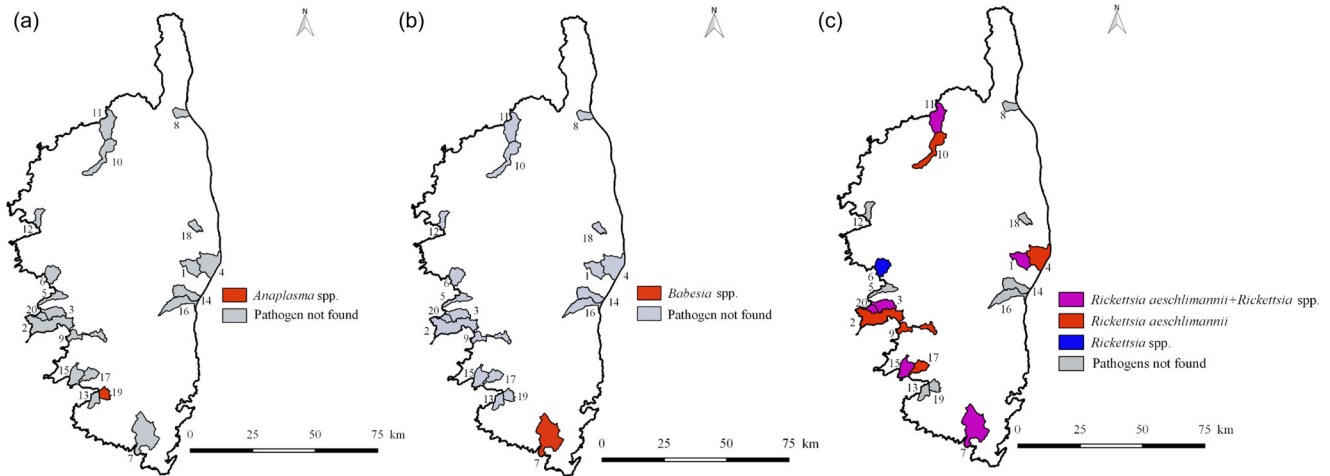


FIGURE 2 Map of Corsica showing the locations of tick samples from cattle positive for *Anaplasma* spp. (a), *Babesia* spp. (b) and *Rickettsia* spp. and *R. aeschlimannii* (c) (1. Aghione, 2. Ajaccio, 3. Alata, 4. Aleria, 5. Calcatoggio, 6. Coggia, 7. Figari, 8. Furiani, 9. Grosseto-Prugna, 10. Olmi-Capella, 11. Palasca, 12. Partinello, 13. Propriano, 14. Prunelli-Di-Fiumurbo, 15. Serra-Di-Ferro, 16. Serra-Di-Fiumorbo, 17. Sollocaro, 18. Tox, 19. Viggianello, 20. Villanova)

3.3 | Pathogens detected in blood samples

From the 362 blood samples (288 cattle and 74 sheep), 79.9% of cattle and 78.4% of sheep were positive for at least one pathogen (Table 3). Bacteria from the genus *Anaplasma* were found in both livestock species (Table 3). In sheep blood samples, two *Anaplasma* species were found: *A. capra* in Serra-Di-Fiumorbo and *A. ovis* in Furiani (Table 3, Figure 3a). The *A. capra* sequence reported was found to be related to one 16S rRNA sequence from a blood sample collected from a Korean water deer in South Korea (GenBank: LC432126.1) with an identity of 98.69%. The *A. ovis* sequence reported was found to be related to a 16S rRNA sequence found in sheep blood in China (GenBank: KX579073.1) with an identity of 99.71%.

The *Anaplasma* species detected in cattle was *A. marginale* (Table 3, Figure 3b) in 61.4% of the cattle blood samples. These samples were related to a 16S rRNA sequence detected in cattle blood samples from Iran (GenBank: MK016525.1) and from Cuba (GenBank: MK804764.1) with an identity between 99% and 100% for both.

The parasite genus *Babesia* sp. was found in 35 cattle blood samples in 12 municipalities (Table 3, Figure 3c). The sequencing of *Babesia* sp. was unsuccessful and did not allow the identification of the species.

Out of the 288 cattle blood samples, 168 were positive for *Trypanosoma* sp. in 19 of the 20 sampled municipalities (Table 3, Figure 3d). Unfortunately, the sequencing of *Trypanosoma* sp. was unsuccessful in these samples and the species could not be identified.

From the 230 positive cattle blood samples, 42.7% were positive for one pathogen, 46% for two pathogens and 11.3% for three pathogens (Table 4).

4 | DISCUSSION

Here, we report 1 year of sampling (2019–2020) on farms located near wetlands in 20 municipalities on the French island of Corsica.

TABLE 4 Number of cattle blood samples positives for *Anaplasma marginale*, *Babesia* spp. and/or *Trypanosoma* spp. DNA

Pathogen	Number of positive samples (%)
<i>Anaplasma marginale</i> (only)	55 (19.1%)
<i>Babesia</i> spp. (only)	5 (1.7%)
<i>Trypanosoma</i> spp. (only)	38 (13.2%)
<i>Anaplasma marginale</i> + <i>Babesia</i> spp.	5 (1.7%)
<i>Anaplasma marginale</i> + <i>Trypanosoma</i> spp.	101 (35.1%)
<i>Babesia</i> spp. + <i>Trypanosoma</i> spp.	0 (0%)
<i>Anaplasma marginale</i> + <i>Babesia</i> spp. + <i>Trypanosoma</i> spp.	26 (9.1%)
Number of positive samples	230 (79.9%)
Number of negative samples	58 (20.1%)
Total samples	288 (100%)

The main objective of our study was to screen cattle and sheep blood samples and their ticks for tick-borne pathogens and non-vectorised pathogens (but with a high risk of presence in wetlands) involved in animal and human health threats. In the literature, many pathogens have been found all around the Mediterranean Basin in ticks collected on cattle and sheep or in cattle and sheep blood (Table S1).

4.1 | Tick species collected on cattle

In the Mediterranean region, ticks are present in 14 countries and are highly diverse. About 27 species from six genera carrying tick-borne pathogens were collected on cattle and sheep (Table S1). These genera are widely distributed in the four areas of the Mediterranean Basin: the Balkans, the Maghreb or southern border, the Middle East and Western Europe. In all four areas, cattle and sheep are host to four of the

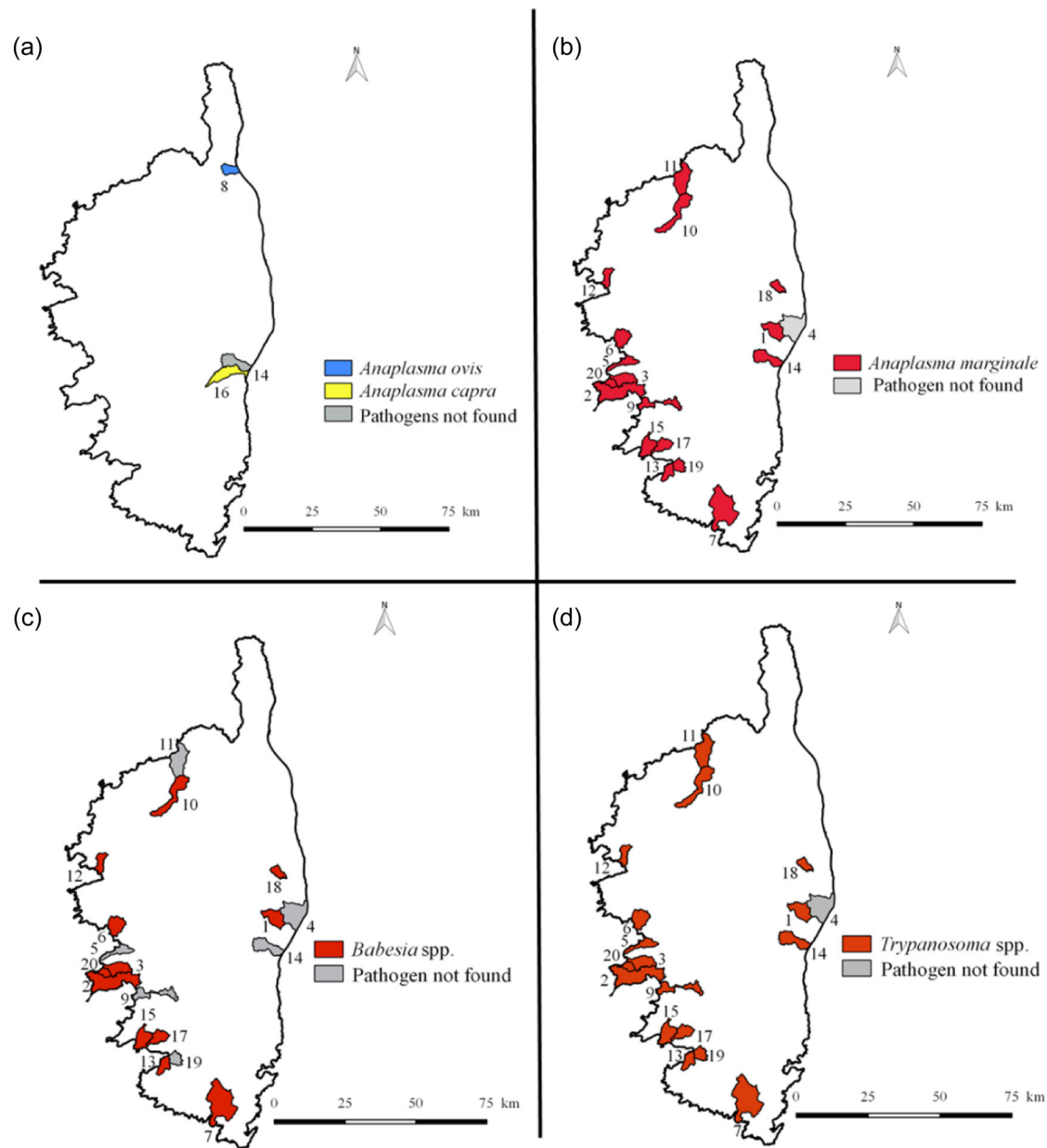


FIGURE 3 Map of Corsica showing locations of sheep blood samples positive for *Anaplasma capra* and *Anaplasma ovis* (a), and cattle blood samples positive for *Anaplasma marginale* (b), *Babesia* spp. (c) and/or *Trypanosoma* spp. (1. Aghione, 2. Ajaccio, 3. Alata, 4. Aleria, 5. Calcatoggio, 6. Coggia, 7. Figari, 8. Furiani, 9. Grosseto-Prugna, 10. Olmi-Capella, 11. Palasca, 12. Partinello, 13. Propriano, 14. Prunelli-Di-Fiumurbo, 15. Serra-Di-Ferro, 16. Serra-Di-Fiumurbo, 17. Solloccaro, 18. Tox, 19. Viggianello, 20. Villanova)

six genera: *Haemaphysalis*, *Hyalomma*, *Ixodes* and *Rhipicephalus*. *Dermacentor* is found in the Balkans, the Middle East and Western Europe on cattle and sheep. Finally, the last genus, *Amblyomma* has only been collected sporadically in Western Europe on cattle. In our study, four of these six genera were found on cattle: *Dermacentor*, *Hyalomma*, *Ixodes* and *Rhipicephalus* (Table S1).

Among these genera, different species are frequently found on cattle or sheep. In the continental areas of the Balkans, the Maghreb, the Middle East and Western Europe, a total of 10 main tick species have been found: the term main species defines the species found with the highest number of tick individuals on the cattle or sheep per study.

Among the genera found in our study, in the *Dermacentor* genus, we identified one species in our study, *D. marginatus*, which has also been found on cattle in Italy and Turkey, and on sheep in Greece, Italy, Spain and Turkey, and can be responsible for the circulation of pathogens such as rickettsiae from the spotted fever group (Buczek et al., 2020). The second one is the *Hyalomma* genus, in which we found two species: *Hy. marginatum* and *Hy. scupense*. *Hyalomma marginatum*, also reported on cattle in Algeria, Spain, France, Greece, Italy and Turkey, and on sheep from Algeria, Cyprus, Greece, Italy and Turkey, is responsible for the transmission of *Babesia* spp., *R. aeschlimannii* and the CCHF virus (Table S1). *Hyalomma scupense* has been found on cattle in Corsica and

sheep in Turkey, and it mainly transmits *Theileria* parasites, but can also transmit the CCHF virus (Gharbi & Aziz Darghouth, 2014). The third tick genus and probably the most frequently encountered tick genus on cattle and sheep was *Rhipicephalus*, with: *Rh. (Bo.) annulatus*, a species known to have a tropism for cattle and responsible for the transmission of *Babesia*. It has been found on cattle in Algeria, Egypt, France, Italy and Lebanon and on sheep in Lebanon and Tunisia (Table S1). *Rhipicephalus bursa*, which has a tropism for domestic ungulates and transmits pathogens/parasites from the *Anaplasma*, *Babesia* and *Theileria* genera, has been found on cattle in nearly every Mediterranean country and on sheep in Algeria, France, Greece, Italy, Lebanon and Tunisia (Table S1). *Rhipicephalus sanguineus* s.l., which targets both dogs and domestic ungulates, has been found in nearly every Mediterranean country on both cattle and sheep (Table S1).

To our knowledge, nine tick species have been found on cattle and sheep in Corsica: *Amblyomma variegatum*, responsible for the transmission of *Rickettsia* spp. and *Ehrlichia ruminatum*, which is an African livestock tick and has been sporadically collected on cattle in Corsica (Cicculli et al., 2019b; Yonow, 1995); *D. marginatus*, *Hae. punctata*, *Hy. scupense*, *Hy. marginatum*, *I. ricinus*, *Rh. (Bo.) annulatus*, *Rh. Bursa* and *Rh. sanguineus* s.l. were previously found in exhaustive survey (Grech-Angelini et al., 2016). However, this survey covered the entire island and all seasons. In our study, we focused on wetlands during January-February; the main tick species found belong to the *Rhipicephalus* genus: *Rh. annulatus*, *Rh. bursa* and *Rh. sanguineus* s.l., representing respectively 0.2%, 38.7% and 22.7% of the ticks collected. Prevalence of *Rh. annulatus* was same as previously found and *Rh. bursa* was previously described as the main tick species found on cattle in Corsica (more than 50% of the ticks collected) (Grech-Angelini et al., 2016). However, *Rh. sanguineus* s.l. was represented by only 2.3% of the specimens collected in this previous survey (Grech-Angelini et al., 2016). This genus was followed by the *Hyalomma* genus with two species: *Hy. marginatum* and *Hy. scupense* represented respectively 8.6% and 7.2% of the ticks collected on cattle, which is lower than the *Hy. marginatum* collected (21.5%) and nearly equal to the *Hy. scupense* collected in a previous study (8.7%) (Grech-Angelini et al., 2016). The last species found was *D. marginatus* found in a low proportion (0.7%), which is similar to the one found in the previous study (Grech-Angelini et al., 2016). The tick species found in our study are similar to those reported from an exhaustive survey carried out by Grech-Angelini et al. However, we collected no *Haemaphysalis* and *Ixodes*, which can be attributed to season and altitude. Indeed, most of the *Haemaphysalis* ticks found by Grech-Angelini et al. (2016) were collected in November-December between 400 and 600 m altitude and *Ixodes* ticks in September-October at above 600 m of altitude, whereas we mainly collected our ticks in January-February in wetlands close to sea level. The seasonality of some species such as *Hy. scupense* in January-February and the absence of others such as *Hae. punctata* and *I. ricinus* during these months – which was observed in Grech-Angelini et al. (2016) – may explain the presence of the former species and the absence of the latter two during our sampling period. In addition, specific targeting of the wetlands in our study may also explain the difference between our study and the 2016 survey.

4.2 | Detected pathogens

4.2.1 | *Anaplasma* sp

In our study, the most frequently detected pathogen genus in livestock animal samples was *Anaplasma* sp. in 68.6% of the cattle blood samples and 77.3% of the sheep blood samples. *Anaplasma* is common in the Mediterranean region where it has been detected in cattle and sheep and their ticks in more than 10 countries. Among the six species and two Candidatus species reported, we detected *A. ovis* and *A. capra* in sheep blood samples and *A. marginale* in cattle blood samples.

Anaplasma ovis is responsible for anaplasmosis in small ruminants which can lead to severe anaemia, lower milk production and abortion (Yasini et al., 2012). It is mainly transmitted by *Rhipicephalus* ticks (Cabezas-Cruz et al., 2019; Friedhoff, 1997). In the Mediterranean region, *A. ovis* has already been detected in Algeria, France, Italy and Turkey, in both cattle and sheep, and in sheep in Tunisia. In ticks, it has been detected in Algeria, France, Italy and Morocco (Table S1). *Anaplasma ovis* seems to be mainly distributed in the western part of the Mediterranean Basin and is relatively common in cattle and sheep (Table S1). On Mediterranean islands, it has been detected in Sicily in cattle and sheep, and in Corsica where it has been found in goat flocks with a prevalence of 52.0% (Cabezas-Cruz et al., 2019). In our study, the presence of *A. ovis* DNA was detected in Corsican sheep blood (2.7%) for the first time, but at a lower prevalence (2.7%) than reported in goats (Cabezas-Cruz et al., 2019). The second *Anaplasma* species detected in blood samples was *A. capra*, an emerging zoonotic pathogen targeting small ruminants and humans. *Anaplasma capra* is known to be mainly asymptomatic, but sometimes it can cause fever, myalgia, thrombocytopenia and lymphadenopathy (Li et al., 2015; Peng et al., 2018). Actually, it was mainly reported in Asia (Amer et al., 2019; Peng et al., 2021). However, in the Mediterranean region, it has already been detected in deer in France (Jouglin et al., 2019). The detection of *A. capra* in sheep in our study is the first report of *A. capra* DNA in sheep in the Mediterranean area and in Corsica (Table S1).

The *Anaplasma* species reported in cattle blood samples was *Anaplasma marginale*. *A. marginale* is a bacterium responsible for bovine anaplasmosis occurring across nearly the entire continent of Europe, transmitted by *Rhipicephalus* ticks (Ferrolho et al., 2016; Khodadadi et al., 2021; Martins et al., 2020) and mainly targeting cattle and sheep (Atif, 2015). This bacterial species can cause symptoms such as fever, anaemia, temporal infertility and anorexia (Kocan et al., 2015). *Anaplasma marginale* has been detected in cattle in six Mediterranean countries: Algeria, Egypt, France, Italy, Tunisia and Turkey (Açici et al., 2016; Al-Hosary et al., 2020; Belkahia et al., 2017; Boucheikhchoukh et al., 2018; Ceci et al., 2014; Dahmani et al., 2017). In Italy, *A. marginale* has also been detected in sheep (Torina et al., 2007). In ticks, *A. marginale* has been detected in Egypt, France, Italy and Morocco (Table S1). *Anaplasma marginale* seems to be present in both ticks and domestic animals, especially in western Mediterranean countries. On the Mediterranean islands, *Anaplasma* species has only been detected on French and Italian islands. *Anaplasma marginale* appears to be widespread in Sicily, where it has been detected in cattle, sheep and

ticks. On other islands, this bacterial species has only been detected in Corsica in *Rh. bursa* ticks collected on cattle (Dahmani et al., 2017) (Table S1). In our study, we detected *A. marginale* DNA in cattle at a prevalence of 61.4%, which is lower than the 100% detected in a previous study in cattle (Dahmani et al., 2017). This difference could be explained by difference in the methodology as the number of farm and cattle blood samples which is higher in our study (288 blood samples and 22 farms) compare to Dahmani et al. which was a study on multiple animal (12 samples and one farm). Our result along with the previous discovery of *A. marginale* DNA in ticks collected on cattle indicate the high prevalence of *A. marginale* DNA in Corsican cattle (Cicculi et al., 2019a; Dahmani et al., 2017; Grech-Angelini et al., 2020).

As in the cattle and sheep samples, the *Anaplasma* genus was detected in ticks sampled on cattle. In the Mediterranean region, a total of six species have been detected in a total of nine countries. Among these species, the most frequently detected was *A. phagocytophilum*, found in six countries. It is a pathogen that mainly infects domestic ruminants and lead to symptoms such as fever, anorexia, reduced milk production. It can also be responsible for human granulocytic anaplasmosis with flu-like symptoms or more severe symptoms such as anorexia and depression (Stuen et al., 2013). On Mediterranean islands, *A. phagocytophilum* and *A. marginale* have been detected in Sicily and Corsica. *Anaplasma marginale* has also been detected in Sardinia. In Corsica, this species was detected in 2% of the *Rh. sanguineus* s.l. collected, which is lower than the prevalence found (22%); however, it has been detected at a higher level in *I. ricinus* ticks (Grech-Angelini et al., 2020). In our study, the positive ticks were collected in Viggianello, where *A. marginale* was also found in cattle blood samples.

4.2.2 | *Babesia* sp

The second genus found in cattle blood samples was *Babesia* at a prevalence of 12.2%. This genus is an intracellular protozoan parasite that belongs to the piroplasmid taxon, along with the genus *Theileria*. They mainly infect livestock, pets and rodents in which they can cause piroplasmosis (Beuglet & Moreau, 2015). In humans, *Babesia* parasites can cause moderate symptoms such as myalgia, headache, anorexia as well as severe symptoms with pulmonary oedema, organ dysfunction syndrome and coma, (Vannier et al., 2015). Their primary reservoir is often rodents, which contaminate immature tick stages and the pathogens can be transmitted to domestic ungulates during the adult tick stage (Vannier et al., 2015). The zoonotic species are principally transmitted via *Ixodes* ticks, vector to mainly *B. divergens*, *B. duncani*, *B. microti* and *B. venatorum*. The *Babesia* genus is common in the Mediterranean region where it has been detected in cattle and sheep blood samples in seven countries: Algeria, Egypt, France, Italy, Morocco, Spain and Turkey, with a predominance of *B. bigemina*, the parasite responsible for bovine piroplasmosis (Table S1). On Mediterranean islands, only two species have been detected in cattle: *B. bigemina* and *B. bovis*, both responsible for bovine babesiosis at a prevalence of 26.3% and 20%, respectively in Sicily. From ticks collected on cattle and sheep, this genus has been

detected in Algeria, France, Italy, Palestine and Turkey with a predominance of *B. bigemina* and *B. ovis* (Table S1). In our study, *Babesia* sp. were identified in 3% of the *Rh. sanguineus* s.l. and in 2.6% of the *Hy. marginatum* ticks collected. In Figari, *Babesia* sp. was also found in one cattle blood sample, which indicates that *Babesia* sp. is possibly present in ticks and in cattle in this municipality. Our results demonstrate the presence of *Babesia* sp. in cattle for the first time in Corsica. The presence of *B. bigemina* DNA in ticks on Corsican cattle had already been shown in *Rh. bursa* ticks (Grech-Angelini et al., 2020). The species may be *B. bigemina* or *B. bovis*, which are highly present in the Mediterranean region. However, in our study, we could only identify *Babesia* to the genus level due to unsuccessful sequencing and species determination is still needed.

4.2.3 | *Rickettsia aeschlimannii*

The genus *Rickettsia* was only found in ticks, and it was the most frequently detected pathogen genus. It was detected in 25% of the collected ticks. It is composed of many zoonotic agents with diverse pathogenicity, but most of these species can be a threat for human health with symptoms ranging from cutaneous rashes to lymphadenopathy, for example (Blanton, 2019; Davoust et al., 2010). In Corsica, even if the exact impact of *Rickettsia* species is still unknown, diverse species have already been found in animals (*R. aeschlimannii*, *R. africae*, *R. felis*, *R. helvetica*, *R. massiliae* and *R. slovaca*; Cicculi et al., 2019b; Cicculi et al., 2019c; Grech-Angelini et al., 2020; Matsumoto et al., 2004) and a previous sero-epidemiological study showed exposure of 4.8% of the people to these pathogens in Corse-du-Sud (Raoult et al., 1985). The rickettsiae detected belong to the spotted fever group (SFG) rickettsiae. SFG is transmitted exclusively by ticks, which play the roles of both vector and reservoir owing to the trans-stadial and transovarial transmission of these pathogens (Blanton, 2019). Out of the positive ticks, 79.3% were *R. aeschlimannii* and the rest could not be determined to the species level. *Rickettsia aeschlimannii* was first found in *Hy. marginatum* from Morocco. The disease in humans was documented in a man who had travelled to Morocco in 2000 (Beati et al., 1997; Raoult et al., 2002). Given its circulation in *Hy. marginatum*, *R. aeschlimannii* is distributed throughout Africa. In the Mediterranean region, *R. aeschlimannii* is widely distributed in ticks. It has been found in Algeria, Egypt, France, Greece, Lebanon, Spain and Turkey (Table S1). On Mediterranean islands, it has been found in Cyprus with a prevalence of 12% from *Hy. marginatum* collected on goats and sheep (Chochlakis et al., 2012), and on the Greek island of Cephalonia in *Hy. anatolicum excavatum* collected on sheep (Psaroulaki et al., 2006) (Table S1). In Corsica, *R. aeschlimannii* has previously been reported with a prevalence of 23% in ticks collected on cattle and 58% in ticks collected on sheep (Grech-Angelini et al., 2020). It was also detected in *Hy. marginatum* collected on cattle in 2019 (Cicculi et al., 2019c). In our study, we confirmed the presence of *R. aeschlimannii* in ticks collected from cattle at a prevalence similar to that previously found (19.8%), but in a wide diversity of tick species (Table S1). It seems that *R. aeschlimannii* DNA is present in ticks on cattle regardless of the sampling



FIGURE 4 Distribution of *Trypanosoma* spp. in cattle in the Mediterranean region (data from the literature) and in our study (red square)

area. Nevertheless, *R. aeschlimannii* was not detected in cattle or sheep blood.

4.2.4 | *Trypanosoma* sp

Trypanosoma sp. was detected in 58.3% of the cattle blood samples. The *Trypanosoma* genus is mainly known as the pathogen of sleeping sickness in humans, caused by *Tr. brucei*, and Chagas disease, caused by *Tr. cruzi*, in Africa and South America, respectively. It is a ubiquitous genus, infecting a wide range of vertebrates and are mainly transmitted by biting flies, bugs and occasionally ticks (Kaufer et al., 2017). In domestic animals (cattle, horses, sheep, carnivores, etc.), these pathogens are transmitted mechanically by a wide range of biting midges. This protozoan parasite can be transmitted horizontally and vertically (Desquesnes et al., 2013). In the Mediterranean region, two species have been found: *Tr. evansi* responsible for 'surra' a trypanosomiasis with high morbidity and mortality rates in animals (Ereqat et al., 2020). According to the infected animal host, it can be lethal (horses), cause acute disease (dogs) and variable symptoms including lethal symptoms (cattle). However, although it is morphologically similar to *Tr. brucei*, *Tr. evansi* is rarely detected in humans and is still not considered as zoonotic (Desquesnes et al., 2013). It has been found in Algeria, Egypt, Palestine and Tunisia (Figure 3). *Trypanosoma theileri* is a non-pathogenic haemoparasite except for cattle in which it can cause anaemia, abortion, fever and weight loss (Villa et al., 2008). It can be transmitted by tabanid flies and *Hy. anatolicum anatolicum* ticks (Lee et al., 2013). It has been found in Italy and in Spain (Figure 4). To our knowledge, this is the first report of *Trypanosoma* sp. DNA in cattle in Corsica. Unfortunately, the DNA sequence was not readable, so the sequence failed which could be due to divers factors as the quality or a degradation of the DNA extract, the presence of inhibitor or the

efficiency of the Sanger sequencing method used; therefore, parasite isolation or serological surveys are required to confirm its presence.

A total of 44% of the cattle blood samples collected in our study were positive for DNA of more than one pathogen. Co-infection of cattle by multiple pathogens has already been widely observed in different countries, but generally involve pathogens from the same group, genus or species (variants). In our study, co-infection involved three pathogens of different genera: *A. marginale*, *Babesia* sp. and *Trypanosoma* sp. The highest prevalence of co-infection was found for *A. marginale* and *Trypanosoma* sp. which do not belong to the same groups of pathogens and are transmitted by different vectors. This finding shows the variability of exposure of Corsican cattle to different pathogens. However, the presence of *A. marginale* DNA has been confirmed by sequencing, but the specific identity of *Babesia* sp. and *Trypanosoma* sp. could not be determined in our study. Therefore, the isolation of these three pathogens in mono- and co-infected animals is still required to confirm our findings.

4.3 | Potential role of the livestock in the pathogens circulation

As these data shown, a variety of pathogens can be found in Corsican livestock. Some of these pathogens can have a direct impact in the livestock industry in Corsican wetlands as the bacteria of the *Anaplasma* genus reported in cattle and sheep flocks (*A. marginale*, *A. capra* and *A. ovis*) and the *Babesia* genus meanwhile other pathogens as *Rickettsia aeschlimannii* and the genus *Trypanosoma* could be a threat for human health. This show both the role of target and reservoir of the livestock in Corsican wetlands. With the detection of the genera *Anaplasma* and *Babesia* in both tick and animal shown also a potential circulation of those genera between ticks and animals in some municipalities. These

different information support the importance of the veterinary activities near Corsican wetlands in order to prevent livestock to harmful pathogens, monitor the role of sentinels of the livestock to pathogens as *R. aeschlimannii* and *Trypanosoma* sp. However, in order to confirmed our results, further experimentations are require. Among them, the collect of ticks during different season will allow to have a better overview of the pathogens circulating in livestock near Corsican wetlands. In addition, our methodology was based on PCR and it was not possible to confirm the actual presence and circulation of these pathogens. Obviously, serological surveys and pathogen isolations are needed to draw conclusions regarding the actual presence and potential circulation of these pathogens in the livestock population in Corsican wetlands.

5 | CONCLUSION

In our study, we confirmed the presence of pathogen DNA in Corsican cattle, including *A. marginale* and in their ticks, such as *R. aeschlimannii*, *Anaplasma* sp. and *Babesia* sp. In addition, we detected the DNA of *Babesia* sp. and *Trypanosoma* sp. in cattle blood for the first time in Corsica with potential co-infection. The DNA of two different pathogen genera were found in both animals and ticks in the same municipalities: *Babesia* sp. in Figari and *Anaplasma* sp. in Viggianello which suggests the circulation of these pathogens in these municipalities. We also detected for the first time the presence of *Anaplasma capra* and *A. ovis* DNA in sheep flocks in Corsica. Our results are a first step in the characterisation of potential threats regarding these pathogens and farming activities near Corsican wetlands.

AUTHOR CONTRIBUTIONS

Baptiste Defaye: Conceptualisation; data curation; formal analysis; investigation; methodology; visualisation; writing – original draft. Sara Moutailler: Conceptualisation; methodology; resources; validation; writing – review & editing. Sébastien Grech-Angelini: Conceptualisation; investigation; methodology; writing – review & editing. Clémence Galon: Formal analysis; methodology. Sandrine Ferrandi: Conceptualisation; investigation; methodology; writing – review & editing. Vanina Pasqualini: Project administration; resources; supervision; validation; writing – review & editing. Yann Quilichini: Conceptualisation; methodology; project administration; resources; supervision; validation; writing – review & editing.

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COMPETING INTERESTS

The authors declare that they have no competing interests.

DATA AVAILABILITY STATEMENT

The authors confirm that the data supporting the findings of this study are available within the article and its supplementary material. Raw data that support the findings of this study are available from the corresponding author, upon reasonable request.

ETHICAL STATEMENT

Ethical review and approval were waived for this study. The samples were collected by veterinarians during tuberculosis prevention campaigns and brucellosis monitoring and not specifically for this study. The study complies with the current French laws and followed conservation guidelines. Therefore, approval of the ethics committee was not required.

ORCID

Baptiste Defaye  <https://orcid.org/0000-0002-5252-8574>

Sébastien Grech-Angelini  <https://orcid.org/0000-0003-4133-6726>

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REFERENCES

- Açı, M., Bölükbaşı, C. S., Pekmezci, G. Z., Gürler, A. T., Umur, Ş., Karaer, K. Z., Çakmak, A., Nalbantoğlu, A. S., & Nişbet, C. (2016). Seroepidemiological survey of bovine tick-borne infections in the Black Sea Region of Turkey. *Turkish Journal of Veterinary and Animal Sciences*, 40, 170–174. <https://doi.org/10.3906/vet-1506-3>
- Al-Hosary, A., Răileanu, C., Tauchmann, O., Fischer, S., Nijhof, A. M., & Silaghi, C. (2020). Epidemiology and genotyping of anaplasma marginale and co-infection with piroplasms and other anaplasmatocae in cattle and buffaloes from Egypt. *Parasites Vectors*, 13, 495. <https://doi.org/10.1186/s13071-020-04372-z>
- Amer, S., Kim, S., Yun, Y., & Na, K.-J. (2019). Novel variants of the newly emerged *Anaplasma capra* from Korean water deer (*Hydropotes inermis argyropus*) in South Korea. *Parasites Vectors*, 12, 365. <https://doi.org/10.1186/s13071-019-3622-5>
- Atif, F. A. (2015). *Anaplasma marginale* and *Anaplasma phagocytophilum*: Rickettsiales pathogens of veterinary and public health significance. *Parasitology Research*, 114, 3941–3957. <https://doi.org/10.1007/s00436-015-4698-2>
- Bacon, P. R. (1987). Use of wetlands for tourism in the insular Caribbean. *Annals of Tourism Research*, 14, 104–117. [https://doi.org/10.1016/0160-7383\(87\)90050-8](https://doi.org/10.1016/0160-7383(87)90050-8)
- Beati, L., Meskini, M., Thiers, B., & Raoult, D. (1997). *Rickettsia aeschlimannii* sp. nov., a new spotted fever group *Rickettsia* associated with *Hyalomma*

- marginatum* ticks. *International Journal of Systematic Bacteriology*, 47, 548–554. <https://doi.org/10.1099/00207713-47-2-548>
- Belkahlia, H., Ben Said, M., El Mabrouk, N., Saidani, M., Cherni, C., Ben Hassen, M., Bouattour, A., & Messadi, L. (2017). Spatio-temporal variations and genetic diversity of *Anaplasma* spp. in cattle from the north of Tunisia. *Veterinary Microbiology*, 208, 223–230. <https://doi.org/10.1016/j.vetmic.2017.08.004>
- Beuglet, F., & Moreau, Y. (2015). Babesiosis. *New Developments in Major Vector-Borne Diseases Part II: Important Diseases for Veterinarians Scientific and Technical Review*, 34, 627–639. <http://doi.org/10.20506/rst.34.2.2385>
- Blanton, L. S. (2019). The rickettsioses: A practical update. *Infectious Disease Clinics of North America*, 33, 213–229. <https://doi.org/10.1016/j.idc.2018.10.010>
- Boucheikhchoukh, M., Laroche, M., Aouadi, A., Dib, L., Ahmed, B., Raoult, D., & Parola, P. (2018). MALDI-TOF MS identification of ticks of domestic and wild animals in Algeria and molecular detection of associated microorganisms. *Comparative Immunology, Microbiology and Infectious Diseases*, 57, <https://doi.org/10.1016/j.cimid.2018.05.002>
- Buczek, W., Koman-Iżko, A., Buczek, A. M., Buczek, A., Bartosik, K., Kulina, D., & Ciura, D. (2020). Spotted fever group rickettsiae transmitted by dermacentor ticks and determinants of their spread in Europe. *Annals of Agricultural and Environmental Medicine*, 27, 505–511. <https://doi.org/10.26444/aaem/120602>
- Cabezas-Cruz, A., Gallois, M., Fontugne, M., Allain, E., Denoual, M., Moutailler, S., Devillers, E., Zientara, S., Memmi, M., Chauvin, A., Agoulon, A., Vayssier-Taussat, M., & Chartier, C. (2019). Epidemiology and genetic diversity of *Anaplasma ovis* in goats in Corsica, France. *Parasites & Vectors*, 12(3). <https://doi.org/10.1186/s13071-018-3269-7>
- Ceci, L., Iarussi, F., Greco, B., Lacinio, R., Fornelli, S., & Carelli, G. (2014). Retrospective study of hemoparasites in cattle in southern Italy by reverse line blot hybridization. *Journal of Veterinary Medical Science*, 76, 869–875. <https://doi.org/10.1292/jvms.13-0365>
- Chambre d'agriculture Corse, C. (2021). Elevages corses [WWW Document]. Retrieved from <https://corse.chambres-agriculture.fr/lagriculture-corse/elevages-corses/>
- Chochlakis, D., Ioannou, I., Sandalakis, V., Dimitriou, T., Kassinis, N., Papadopoulos, B., Tselentis, Y., & Psaroulaki, A. (2012). Spotted fever group rickettsiae in ticks in Cyprus. *Microbial Ecology*, 63, 314–323. <https://doi.org/10.1007/s00248-011-9926-4>
- Cicculi, V., Capai, L., Quilichini, Y., Masse, S., Fernández-Alvarez, A., Minodier, L., Bompard, P., Charrel, R., & Falchi, A. (2019a). Molecular investigation of tick-borne pathogens in *Ixodid* ticks infesting domestic animals (cattle and sheep) and small rodents (black rats) of Corsica, France. *Ticks and Tick-borne Diseases*, 10, 606–613. <https://doi.org/10.1016/j.ttbdis.2019.02.007>
- Cicculi, V., de Lamballerie, X., Charrel, R., & Falchi, A. (2019b). First molecular detection of *Rickettsia africae* in a tropical bont tick, *Amblyomma variegatum*, collected in Corsica, France. *Experimental & Applied Acarology*, 77, 207–214. <https://doi.org/10.1007/s10493-018-00336-2>
- Cicculi, V., Maestrini, O., Casabianca, F., Villechenaud, N., Charrel, R., de Lamballerie, X., & Falchi, A. (2019c). Molecular detection of spotted-fever group rickettsiae in ticks collected from domestic and wild animals in Corsica, France. *Pathogens*, 8, <https://doi.org/10.3390/pathogens8030138>
- Costa, T., & Akdeniz, N. (2019). A review of the animal disease outbreaks and biosecure animal mortality composting systems. *Waste Management*, 90, 121–131. <https://doi.org/10.1016/j.wasman.2019.04.047>
- Cowie, C. E., Hutchings, M. R., Barasona, J. A., Gortázar, C., Vicente, J., & White, P. C. L. (2016). Interactions between four species in a complex wildlife: Livestock disease community: Implications for *Mycobacterium bovis* maintenance and transmission. *European Journal of Wildlife Research*, 62, 51–64. <https://doi.org/10.1007/s10344-015-0973-x>
- Dahmani, M., Davoust, B., Tahir, D., Raoult, D., Fenollar, F., & Mediannikov, O. (2017). Molecular investigation and phylogeny of anaplasmataceae species infecting domestic animals and ticks in Corsica, France. *Parasites Vectors*, 10, 302. <https://doi.org/10.1186/s13071-017-2233-2>
- Davoust, B., Mediannikov, O., Marié, J.-L., Socolovschi, C., Parola, P., & Raoult, D. (2010). Les animaux vertébrés sont-ils réservoirs de rickettsies? *Bulletin de l'Académie Vétérinaire de France*, 163, 291–302. <https://doi.org/10.4267/2042/48177>
- de la Fuente, J., Estrada-Pena, A., Venzal, J. M., Kocan, K. M., & Sonenshine, D. E. (2008). Overview: Ticks as vectors of pathogens that cause disease in humans and animals. *Frontiers in Bioscience: A Journal and Virtual Library*, 13, 6938–6946. <https://doi.org/10.2741/3200>
- Defaye, B., Moutailler, S., Pasqualini, V., & Quilichini, Y. (2022). Distribution of tick-borne pathogens in domestic animals and their ticks in the countries of the Mediterranean basin between 2000 and 2021: A systematic review. *Microorganisms*, 10, (1236). <https://doi.org/10.3390/microorganisms10061236>
- Dernat, S., Toffoletti, H., Charrier, F., & Johany, F. (2021). Tick-borne disease risks and livestock management: Farmer's knowledge and practices in a Corsican valley (France). *NJAS: Impact in Agricultural and Life Sciences*, 93, 74–97. <https://doi.org/10.1080/27685241.2021.1975977>
- Desquesnes, M., Dargantes, A., Lai, D.-H., Lun, Z.-R., Holzmüller, P., & Jittapalpong, S. (2013). *Trypanosoma evansi* and surra: A review and perspectives on transmission, epidemiology and control, impact, and zoonotic aspects. *BioMed Research International*, 2013, 321237. <https://doi.org/10.1155/2013/321237>
- Dudek, K. (2014). Impact of biodiversity on tick-borne diseases. *Przegląd Epidemiologiczny*, 68, 681–684.
- Eldridge, B. F., & Edman, J. (2003). *Medical entomology: A textbook on public health and veterinary problems caused by arthropods*. Springer Science & Business Media.
- Ereqat, S., Nasereddin, A., Al-Jawabreh, A., Al-Jawabreh, H., Al-Laham, N., & Abdeen, Z. (2020). Prevalence of *Trypanosoma evansi* in livestock in Palestine. *Parasites Vectors*, 13, 21. <https://doi.org/10.1186/s13071-020-3894-9>
- Estrada-Peña, A. (2004). *Ticks of domestic animals in the Mediterranean region: A guide to identification of species*. University of Zaragoza.
- Ferrolho, J., Antunes, S., Santos, A. S., Velez, R., Padre, L., Cabezas-Cruz, A., Santos-Silva, M. M., & Domingos, A. (2016). Detection and phylogenetic characterization of *Theileria* spp. and *Anaplasma marginale* in *Rhipicephalus bursa* in Portugal. *Ticks and Tick-Borne Diseases*, 7, 443–448. <https://doi.org/10.1016/j.ttbdis.2016.01.004>
- Fornell-Muñoz, A., & Guerrero, F. (2019). Mediterranean basin wetlands as a vertebral axis of the territory: Relationships with roman roads and contemporary livestock trails. *National Cultiv*, 14, 61–78. <https://doi.org/10.3167/nc.2019.140104>
- Friedhoff, K. T. (1997). Tick-borne diseases of sheep and goats caused by *Babesia*, *Theileria* or *Anaplasma* spp. *Parassitologia*, 39, 99–109.
- Gharbi, M., & Aziz Darghouth, M. (2014). A review of hyalomma scupense (Acari, Ixodidae) in the Maghreb region: From biology to control. *Parasite*, 21, 2. <https://doi.org/10.1051/parasite/2014002>
- Gondard, M., Michelet, L., Nisavanh, A., Devillers, E., Delannoy, S., Fach, P., Aspan, A., Ullman, K., Chirico, J., Hoffmann, B., van der Wal, F. J., de Koeijer, A., van Solt-Smits, C., Jahfari, S., Sprong, H., Mansfield, K. L., Fooks, A. R., Klitgaard, K., Bødker, R., & Moutailler, S. (2018). Prevalence of tick-borne viruses in *Ixodes ricinus* assessed by high-throughput real-time PCR. *Pathogens and Disease*, 76, <https://doi.org/10.1093/femspd/fty083>
- Grech-Angelini, S., Stachurski, F., Lancelot, R., Boissier, J., Allienne, J.-F., Marco, S., Maestrini, O., & Uilenberg, G. (2016). Ticks (Acari: Ixodidae) infesting cattle and some other domestic and wild hosts on the French Mediterranean island of Corsica. *Parasites & Vectors*, 9, <https://doi.org/10.1186/s13071-016-1876-8>
- Grech-Angelini, S., Stachurski, F., Vayssier-Taussat, M., Devillers, E., Casabianca, F., Lancelot, R., Uilenberg, G., & Moutailler, S. (2020). Tick-borne pathogens in ticks (Acari: Ixodidae) collected from various domestic and wild hosts in Corsica (France), a Mediterranean

- island environment. *Transboundary and Emerging Diseases*, 67, 745–757. <https://doi.org/10.1111/tbed.13393>
- Hammer, D. A. (1989). *Constructed wetlands for wastewater treatment: Municipal, industrial and agricultural*. CRC Press.
- Jouglin, M., Blanc, B., de la Cotte, N., Bastian, S., Ortiz, K., & Malandrin, L. (2019). First detection and molecular identification of the zoonotic *Anaplasma capra* in deer in France. *PLoS One*, 14, <https://doi.org/10.1371/journal.pone.0219184>
- Jourdain, E., Gauthier-Clerc, M., Bicout, D., & Sabatier, P. (2007). Bird migration routes and risk for pathogen dispersion into western Mediterranean wetlands. *Emerging Infectious Diseases*, 13, 365–372. <https://doi.org/10.3201/eid1303.060301>
- Kaufer, A., Ellis, J., Stark, D., & Barratt, J. (2017). The evolution of trypanosomatid taxonomy. *Parasites Vectors*, 10, 287. <https://doi.org/10.1186/s13071-017-2204-7>
- Khodadadi, N., Nabavi, R., Sarani, A., Saadati, D., Ganjali, M., Mihalca, A. D., Otranto, D., & Sazmand, A. (2021). Identification of *Anaplasma marginale* in long-eared hedgehogs (*Hemiechinus auritus*) and their *Rhipicephalus turanicus* ticks in Iran. *Ticks and Tick-borne Diseases*, 12, 101641. <https://doi.org/10.1016/j.ttbdis.2020.101641>
- Knap, P. W., & Doeschl-Wilson, A. (2020). Why breed disease-resilient livestock, and how? *Genetics, Selection, Evolution (GSE)*, 52, 60. <https://doi.org/10.1186/s12711-020-00580-4>
- Kocan, K. M., De La Fuente, J., & Cabezas-Cruz, A. (2015). The genus *Anaplasma*: New challenges after reclassification. *Revue Scientifique et Technique (International Office of Epizootics)*, 34, 577.
- Lee, Y.-F., Cheng, C.-C., Chen, J.-S., Lin, N.-N., Hung, Y.-W., Wang, J.-M., Tu, W.-C., Tung, K.-C., & Chiu, Y.-T. (2013). Evidence of intracellular stages in trypanosoma (Megatrypanum) theileri in non-phagocytic mammalian cells. *Veterinary Parasitology*, 191, 228–239. <https://doi.org/10.1016/j.vetpar.2012.08.027>
- Li, H., Zheng, Y.-C., Ma, L., Jia, N., Jiang, B.-G., Jiang, R.-R., Huo, Q.-B., Wang, Y.-W., Liu, H.-B., Chu, Y.-L., Song, Y.-D., Yao, N.-N., Sun, T., Zeng, F.-Y., Dumler, J. S., Jiang, J.-F., & Cao, W.-C. (2015). Human infection with a novel tick-borne *Anaplasma* species in china: A surveillance study. *The Lancet Infectious Diseases*, 15, 663–670. [https://doi.org/10.1016/S1473-3099\(15\)70051-4](https://doi.org/10.1016/S1473-3099(15)70051-4)
- Martins, K. R., Garcia, M. V., Bonatte-Junior, P., Duarte, P. O., de Higa, L. O. S., Csordas, B. G., Barros, J. C., & Andreotti, R. (2020). Correlation between *Rhipicephalus microplus* ticks and *Anaplasma marginale* infection in various cattle breeds in Brazil. *Experimental & Applied Acarology*, 81, 585–598. <https://doi.org/10.1007/s10493-020-00514-1>
- Matsumoto, K., Parola, P., Brouqui, P., & Raoult, D. (2004). *Rickettsia aeschlimannii* in hyalomma ticks from Corsica. *European Journal of Clinical Microbiology & Infectious Diseases*, 23, 732–734. <https://doi.org/10.1007/s10096-004-1190-9>
- Mévélec, M.-N., Lakhri, Z., & Dimier-Poisson, I. (2020). Key limitations and new insights into the *Toxoplasma gondii* parasite stage switching for future vaccine development in human, livestock, and cats. *Frontiers in Cellular and Infection Microbiology*, 10, 607198. <https://doi.org/10.3389/fcimb.2020.607198>
- Michelet, L., Delannoy, S., Devillers, E., Umhang, G., Aspan, A., Juremalm, M., Chirico, J., van der Wal, F. J., Sprong, H., Boye Pihl, T. P., Klitgaard, K., Bødker, R., Fach, P., & Moutailler, S. (2014). High-throughput screening of tick-borne pathogens in Europe. *Frontiers in Cellular and Infection Microbiology*, 4, <https://doi.org/10.3389/fcimb.2014.00103>
- Middleton, B. A. (2016). *Cattle grazing in wetlands*. Berlin, Heidelberg, Berlin: Springer. https://doi.org/10.1007/978-94-007-6172-8_60-2
- Montgomery, R. (2014). Archive: Agriculture statistics – North Africa and Eastern Mediterranean – Statistics explained [WWW Document]. Retrieved from https://ec.europa.eu/eurostat/statistics-explained/index.php?title=Archive:Agriculture_statistics_-_North_Africa_and_Eastern_Mediterranean
- Nicholson, W. L., Sonenshine, D. E., Noden, B. H., & Brown, R. N. (2019). Chapter 27 – Ticks (Ixodida). In G. R. Mullen, & L. A. Durden (Eds.), *Medical and veterinary entomology* (pp. 603–672; 3rd edn.). Academic Press. <https://doi.org/10.1016/B978-0-12-814043-7.00027-3>
- Pardini, A. (2004). Mediterranean pastoral systems and the threat of globalization. In A. Ferchichi (comp.), & A. Ferchichi (collab.) (Eds.), *Réhabilitation des pâturages et des parcours en milieux méditerranéens* (pp. 155–168). Zaragoza: CIHEAM. (Cahiers Options Méditerranéennes; n. 62). 11. Réunion du Sous-Réseau Ressources Fourragères Méditerranéennes du Réseau Coopératif Interrégional FAO-CIHEAM de Recherche et Développement sur les Pâturages et les Cultures Fourragères, 2002/10/29-2002/11/01, Djerba (Tunisia). <http://om.ciheam.org/om/pdf/c62/04600150.pdf>
- Parola, P., & Raoult, D. (2001). Ticks and tickborne bacterial diseases in humans: An emerging infectious threat. *Clinical Infectious Diseases: An Official Publication of the Infectious Diseases Society of America*, 32, 897–928. <https://doi.org/10.1086/319347>
- Peng, Y., Lu, C., Yan, Y., Shi, K., Chen, Q., Zhao, C., Wang, R., Zhang, L., Jian, F., & Ning, C. (2021). The first detection of *Anaplasma capra*, an emerging zoonotic anaplasma sp., in erythrocytes. *Emerging Microbes and Infections*, 10, 226–234. <https://doi.org/10.1080/22221751.2021.1876532>
- Peng, Y., Wang, K., Zhao, S., Yan, Y., Wang, H., Jing, J., Jian, F., Wang, R., Zhang, L., & Ning, C. (2018). Detection and phylogenetic characterization of *Anaplasma capra*: An emerging pathogen in sheep and goats in China. *Frontiers in Cellular and Infection Microbiology*, 8, 283. <https://doi.org/10.3389/fcimb.2018.00283>
- Pérez-Eid, C. (2007). *Les tiques: identification, biologie, importance médicale et vétérinaire*. Cachan, France: Lavoisier.
- Psaroulaki, A., Ragiadakou, D., Kouris, G., Papadopoulos, B., Chaniotis, B., & Tselentis, Y. (2006). Ticks, tick-borne rickettsiae, and *Coxiella burnetii* in the Greek Island of Cephalonia. *Annals of the New York Academy of Sciences*, 1078, 389–399. <https://doi.org/10.1196/annals.1374.077>
- Rabou, A. F. N. A., Yassin, M. M., Sharif, F. A., Al-Agha, M. R., Daher, K. S. A., Ali, A. K. S., & Hamad, D. M. (2015). Inhabitants knowledge on mosquito proliferation and control in the wetland ecosystem of Wadi Gaza, Gaza Strip, Palestine. *IUG Journal of Natural Studies*, 16, 41.
- Raoult, D., Fournier, P.-E., Abboud, P., & Caron, F. (2002). First documented human *Rickettsia aeschlimannii* infection. *Emerging Infectious Diseases*, 8, 748–749. <https://doi.org/10.3201/eid0807.010480>
- Raoult, D., Nicolas, D., De Micco, P., Gallais, H., & Casanova, P. (1985). [Epidemiologic aspects of Mediterraneanan boutonneuse fever in the south of Corsica. *Bulletin De La Societe De Pathologie Exotique Et De Ses Filiales*, 78, 446–451.
- Rey, J. R., Walton, W. E., Wolfe, R. J., Connelly, R., O'Connell, S. M., Berg, J., Sakolsky-Hoop, G. E., & Laderman, A. D. (2012). North American wetlands and mosquito control. *International Journal of Environmental Research and Public Health*, 9, 4537–4605. <https://doi.org/10.3390/ijerph9124537>
- Robertson, A. I. (1997). The effect of livestock on wetlands. In W. D. Williams (Ed.), *Wetlands in a dry land: Understanding for management* (pp. 195–201). Canberra: Environment Australia, Biodiversity Group.
- Sonenshine, D. (2014). *The biology of ticks*. New York: Oxford University Press.
- Stuenkel, S., Granquist, E. G., & Silaghi, C. (2013). *Anaplasma phagocytophilum* – A widespread multi-host pathogen with highly adaptive strategies. *Frontiers in Cellular and Infection Microbiology*, 3, 31. <https://doi.org/10.3389/fcimb.2013.00031>
- Taylor, N. G., Grillas, P., Al Hreisha, H., Balkiz, Ö., Borie, M., Boutron, O., Catita, A., Champagnon, J., Cherif, S., Çiçek, K., Costa, L. T., Dakki, M., Fois, M., Galewski, T., Galli, A., Georgiadis, N. M., Green, A. J., Hermoso, V., Kapedani, R., & Sutherland, W. J. (2021). The future for Mediterranean wetlands: 50 key issues and 50 important conservation research questions. *Regional Environmental Change*, 21, 33. <https://doi.org/10.1007/s10113-020-01743-1>
- Thomson, S., Hamilton, C. A., Hope, J. C., Katzer, F., Mabbott, N. A., Morrison, L. J., & Innes, E. A. (2017). Bovine cryptosporidiosis: Impact, host-parasite

- interaction and control strategies. *Veterinary Research*, 48, 42. <https://doi.org/10.1186/s13567-017-0447-0>
- Torina, A., Vicente, J., Alongi, A., Scimeca, S., Turlá, R., Nicosia, S., Di Marco, V., Caracappa, S., & de la Fuente, J. (2007). Observed prevalence of tick-borne pathogens in domestic animals in Sicily, Italy during 2003–2005. *Zoonoses Public Health*, 54, 8–15. <https://doi.org/10.1111/j.1863-2378.2007.00989.x>
- Vannier, E. G., Diuk-Wasser, M. A., Ben Mamoun, C., & Krause, P. J. (2015). Babesiosis. *Infectious Disease Clinics of North America*, 29, 357–370. <https://doi.org/10.1016/j.idc.2015.02.008>
- Villa, A., Gutierrez, C., Gracia, E., Moreno, B., Chacón, G., Sanz, P. V., Büscher, P., & Touratier, L. (2008). Presence of *Trypanosoma theileri* in Spanish cattle. *Annals of the New York Academy of Sciences*, 1149, 352–354. <https://doi.org/10.1196/annals.1428.016>
- Yasini, S., Khaki, Z., Rahbari, S., Kazemi, B., Amoli, J. S., Gharabaghi, A., & Jalali, S. (2012). Hematologic and clinical aspects of experimental ovine anaplasmosis caused by *Anaplasma ovis* in Iran. *Iranian Journal of Parasitology*, 7, 91–98.
- Yonow, T. (1995). The life-cycle of *Amblyomma variegatum* (Acari: Ixodidae): A literature synthesis with a view to modelling. *International Journal for Parasitology*, 25, 1023–1060. [https://doi.org/10.1016/0020-7519\(95\)00020-3](https://doi.org/10.1016/0020-7519(95)00020-3)
- Zeder, M. A. (2008). Domestication and early agriculture in the Mediterranean basin: Origins, diffusion, and impact. *Proceedings of the National Academy of Sciences*, 105, 11597–11604.

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