Detection of *Anaplasma phagocytophilum, Coxiella burnetii* and *Rickettsia* spp from animals and ticks in a rural area of Latium Region

Macrì G.[1], Maroli M.[2], Salvato L.[1], Scarpulla M.[1]

[1]Istituto Zooprofilattico Sperimentale delle Regioni Lazio e Toscana - Sede di Roma.
[2]Istituto Superiore di Sanità - Roma

AIM The aim of the study was to investigate the presence of some tick-borne bacteria, acting as agent of zoonotic diseases, in a northern rural area of Latium Region. In particular, bacteria of *Anaplasma*, *Rickettsia* and *Coxiella* genus were investigated in bovine and equine using serological and molecular analysis and the occurrence of selected pathogens were also studied in ticks.

MATERIAL AND METHODS Ticks: a total of 934 ticks from animals (n=325) or free living (n=609) were collected and morphologically identified. Of 934 ticks some were pooled cause their dimension and laboratory needs, giving a total of 151 tick samples. Five tick species were recognized, being *Ixodes ricinus* the most abundant (48.1%), followed by *Rhipicephalus bursa* (24.1%), *R.* (*Boophilus*) *annulatus* (22.2%), *R. sanguineus* (2.8%), *Hyalomma marginatum* (2.3%) and *Ripicephalus* spp. (0.5%). *R. sanguineus* was collected only free living, *B. annulatus* only on bovine and *R. bursa* on equine. PCR was performed to detect the presence of *Rickettsia* spp., *Anaplasma phagocytophilum* and *Coxiella burnetii* on 934 ticks: 307 collected from bovine, 18 from equine and 609 free living (167 in meadow and 442 in wooden area).
Animals: a total of 281 blood samples were examined, 271 from bovine and 10 from equine. IFAT and ELISA serological tests were performed on bovine serum samples to detect antibodies against A. phagocytophilum and C. burnetii, while only A. phagocytophilum was investigated on equine samples. PCR was performed on buffy coat or blood coagulum to detect A. phagocytophilum and Rickettsia spp. DNA.

RESULTS Serological analysis performed on bovine samples scored positive for *C. burnetii* (4,5%) and *A. phagocytophilum* (49%) while PCR on buffy coat or coagulum were negative for A. phagocytophilum and Rickettsia spp. DNA. None of the equine blood samples showed positive results. Of 151 tick samples, 19 were found to be positive for A. phagocytophilum DNA in B. annulatus (3/151) and I. ricinus (3/151), Rickettsia spp. DNA in I. ricinus (3/151), R. bursa (1/151), H. marginatum (6/151) and R. sanguineus (1/151), C. burnetii DNA was detected only in B. annulatus (2/151). Minimum and maximum prevalence were calculated considering that some of the positive samples were pooled (see the table below).

Seroprevalence

Pathogenn species	bovine positive samples (%)	equine positive samples (%)
C. burnetii ELISA	13/271 (4.5)	0/10 (0.0)
A. phagocytophilum IFI	133/271 (49.0)	0/10 (0.0)

Prevalence of tick-borne pathogens in ticks by PCR

	bovine		equine		free living	
Pathogenn species	%min	%max	%min	%max	%min	%max
A. phagocytophilum	1.0	5.9	0.0	0.0	0.5	4.8
Rickettsia spp.	2.9	10.8	0.0	0.0	0.3	2.0
C. burnetii	0.7	5.2	0.0	0.0	0.0	0.0

PCR in ticks from bovine

Tick species	samples	ticks	*A.phagocytophilum* positive samples	*Rickettsia spp.* positive samples	*C. burnetii* positive samples
I. ricinus	2	12	0	2	0
R. bursa	11	54	0	1	0
H. marginatum	7	21	0	6	0
B. annulatus	69	220	3	0	2
total	89	307	3	9	2

PCR in free living ticks

Tick species	samples	ticks	*A.phagocytophilum* positive samples	*Rickettsia spp.* positive samples	*C. burnetii* positive samples
I. ricinus	26	404	3	1	0
R. bursa	30	167	0	0	0
H. marginatum	2	2	0	0	0
Rhipicephalus spp.	1	5	0	0	0
R. sanguineus	10	31	0	1	0
total	59	609	3	2	0

CONCLUSIONS

The results herein presented show that A. phagocytophilum, C. burnetii and Rickettsia spp. occur in the studied areas suggesting the different role played by tick species in pathogen transmission and risk for human and animal infection. Further studies would be necessary to corroborate data collected and to improve knowledge on presence and distribution of bacteria investigated.

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