

AperTO - Archivio Istituzionale Open Access dell'Università di Torino

Prevalence of tick-borne pathogens in Piedmont Region.

This is the author's manuscript

Original Citation:

Availability:

This version is available <http://hdl.handle.net/2318/1760919> since 2020-11-03T09:40:16Z

Terms of use:

Open Access

Anyone can freely access the full text of works made available as "Open Access". Works made available under a Creative Commons license can be used according to the terms and conditions of said license. Use of all other works requires consent of the right holder (author or publisher) if not exempted from copyright protection by the applicable law.

(Article begins on next page)



Prevalence of tick-borne pathogens in Piedmont Region

Topic: Determinants of inter-species and intra-species (including zoonotic) transmissibility of infectious agents



ABSTRACT DETAILS

AUTHORS WITH AN ACCOUNT:



Laura Tomassone
University of Turin, Italy, Italy

LIST OF AUTHORS:

Valerio Carta (1), Veronica Bellavia (1), Federica Verna (1), Alessandra Pautasso (2), Carla Grattarola (1), Barbara Iulini (1), Laura Tomassone (3), Mauro Bardelli (4), Lucia Mandola (1), Simone Peletto (1), Cristina Casalone (1), Rosanna Desiato (1), Maria Caramelli (1)

- 1: Istituto Zooprofilattico Sperimentale PLVA, Italy;
- 2: ASL 1 Imperiese;
- 3: Dipartimento di Scienze Veterinarie, Università degli Studi di Torino;
- 4: ASL VCO

ABSTRACT

Background

Tick-borne diseases are widespread in many European Countries and high incidence has been reported in the past few years. Domestic and wild animals play an important role in promoting the spread of the vector and the pathogens in the territory, whereas the man is usually an occasional host. Tick-bite events has remarkably increased in Piedmont Region (North Western Italy) in humans, where a peak has been observed since 2018.

Objective

The aim of this study was to investigate tick infected by pathogens in Piedmont Region from 2011 to 2019.

Methods

Ticks collected from bitten humans in different areas of Piedmont were studied. They were stored in 70% ethanol (or frozen -20°C) and morphologically identified. A sample collected in at risk population (elderly and minors) was screened by biomolecular essays for the presence of *Borrelia burgdorferi* *sl*, *Rickettsia* *spp.*, and *Anaplasma* *spp.* Pathogen identity was confirmed by sequencing each amplicon. Furthermore, a subset of 57 collected ticks were tested for TBE virus detection.

Results

A total of 2,389 ticks from 2,044 bitten humans from 2011 to 2019 was collected. The most frequently ticks identified belonged to the *Ixodes* genus (N=2,218; 92.84%). 1,850 ticks (77.44%) were identified as *Ixodes ricinus* and 27 (1.13%) as *Ixodes hexagonus*. Some *Ixodes* ticks (N=339; 14.19%) were identified only at genus level due to lack of morphological features. 30 ticks belonged to the *Rhipicephalus* genus (1.17%), 12 (0.50%) to the *Dermacentor* genus and 5 to the *Haemaphysalis* genus (0.21%). Overall, 1,107 tick samples were tested for pathogens. The overall prevalence in all ticks was 29.45% (N=326; 95%CI=26.78-32.23), where at least 1 pathogen was detected. Detected pathogens were *Rickettsia* *spp* (19,69%; 95% CI=17.39-22.16), *Borrelia burgdorferi* *sl*, (7.40%; 95% CI=5.93-9.11), *Anaplasma* *spp.* 2.34% (95% CI=1.54-3.42). Tick Borne Encephalitis virus (TBEV) infection was not detected.

Conclusions

The risk of tick-borne diseases in humans is probably associated with local tick abundance, infection prevalence, density of vertebrate reservoir hosts, climate changes and local information campaign. Further analysis of these factors may help in assessing risks and to guide the implementation of public health policies against tick-borne diseases.