Identification of *Rickettsia* species in ticks from ruminants in Lebanon

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INTRODUCTION

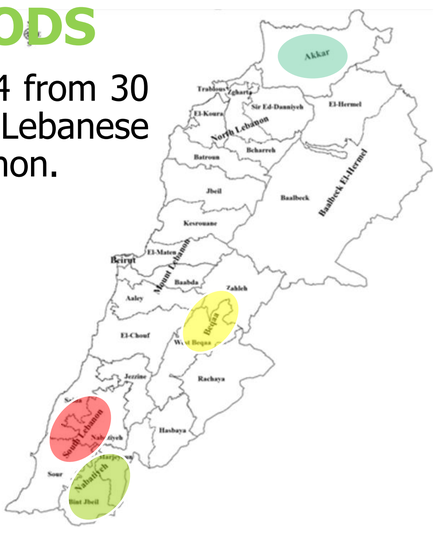
Rickettsie are tick-borne emerging pathogens recognized as important agents of human tick-borne diseases worldwide. Spotted Fever Group (SFG) rickettsiae are important agents of human tick-borne diseases (1). Information on SFG *Rickettsia* and their vectors is not available from Lebanon. A deep knowledge of pathogen prevalence in ticks would have a key role in the control of tick-borne diseases.

AIMS OF THE WORK

Aim of this study was the identification and characterization of Spotted Fever Group (SFG) rickettsiae in ticks from ruminants in Lebanon.

MATERIALS AND METHODS

A total of 88 adult hard ticks was collected in 2014 from 30 Lebanese farms of ruminants in the following Lebanese provinces: Akkar, Bekaa, Nabatieh and South-Lebanon.



Ticks were collected from cattle, sheep and goats.

Ticks were stored in alcohol and identified according to morphological keys (2).

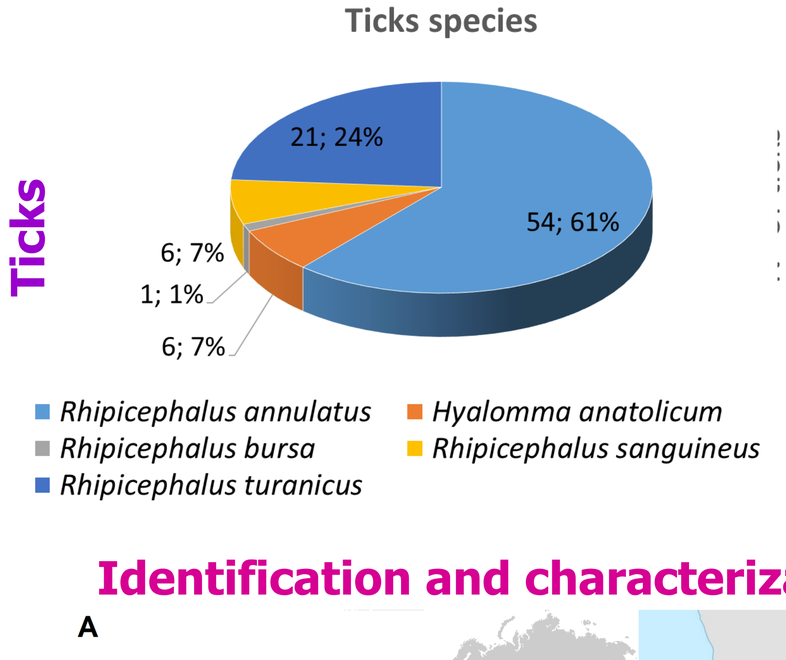
Each tick was cut in two halves. Total DNA was extracted from one-half of each tick using commercial kits.

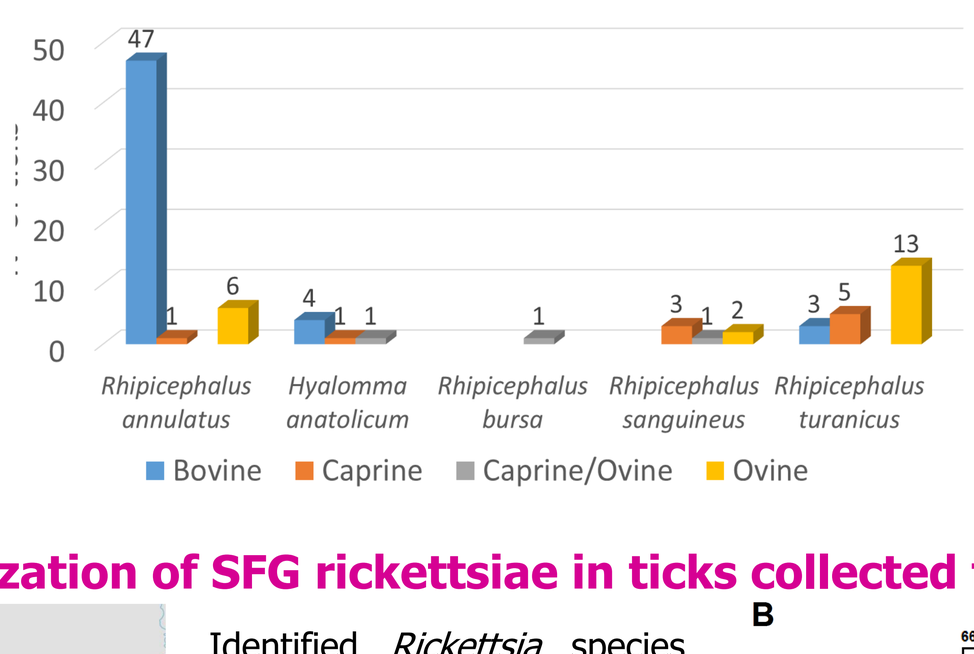
Rickettsia spp. identification and characterization (3, 4)

- PCR and sequencing of fragments of 17 kDa protein, *ompA*, *ompB*, *gltA*, *atpA*, *dnaK*, *dnaA*, *recA* and *16S rRNA*.
- *ompA-ompB* multilocus sequence analysis
- *ompA in silico PstI* and *RsaI* restriction analysis

Sequences were aligned using MAFFT and analysed through MEGA 6.

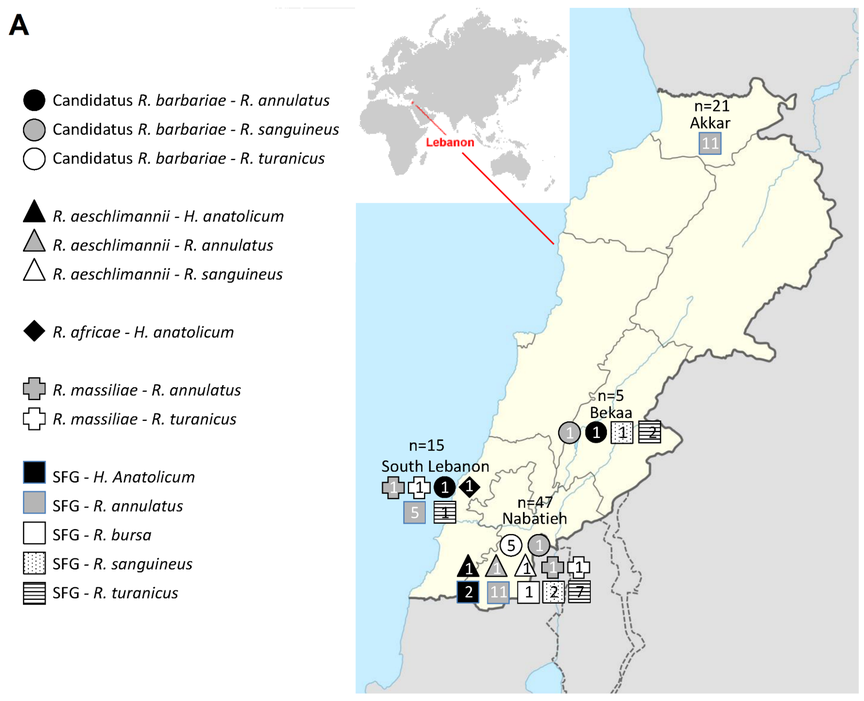
RESULTS





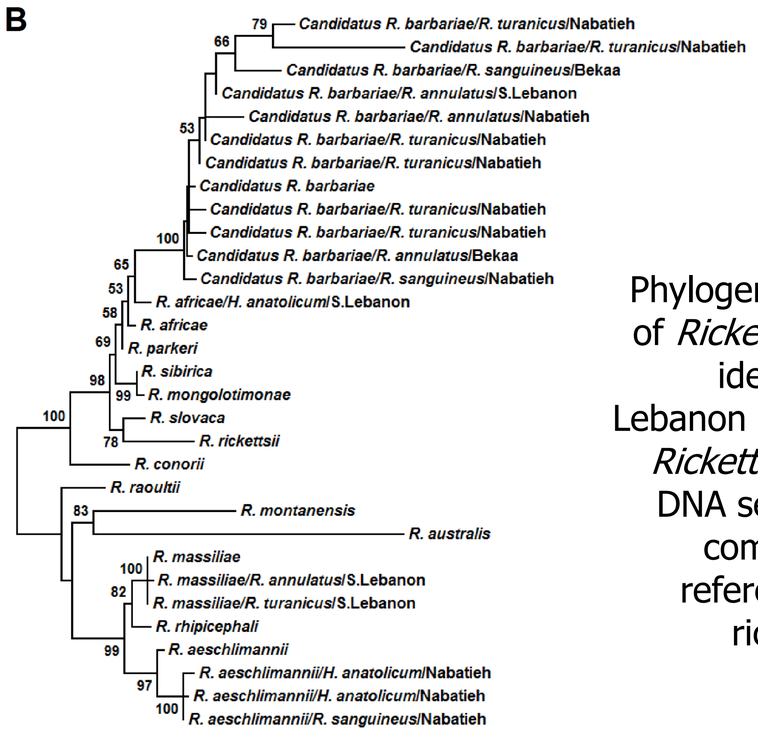
Ticks were screened using the *Rickettsia* spp. 16S rRNA, showing a prevalence of 68.2% (60/88). Among these *Rickettsia* positive samples, 17 were identified at the species level and 43 as SFG rickettsiae based on the multigene genotyping strategy.

Identification and characterization of SFG rickettsiae in ticks collected from ruminants in Lebanon



Identified *Rickettsia* species and ticks in which they were identified. For each Lebanon province, the number of identified *Rickettsia* spp. is reported.

Candidatus *Rickettsia barbariae*, an emerging member of the rickettsial SFG, was identified in 9 samples. *R.massiliae*, *R. aeschlimannii* and *R. africae* were identified in four, three and one tick, respectively.



Phylogenetic tree of *Rickettsia* spp. identified in Lebanon based on *Rickettsia* ompA DNA sequences compared to reference SFG rickettsiae.

R. massiliae (GenBank accession number KR401146), *R. sibirica* (KT345980), *R. slovaca* (KX506733), *R. raoultii* (KX506737), *R.conorii* (KR401144), *R. parkeri* (KJ158741), *R.australis* (AF149108), *R. montanensis* (U43801), *R. rickettsii* (KX544816), *R.rhipicephali* (U43803), *R. mongolotimonae* (DQ097082), Candidatus *R. barbariae* (EU272186) and *R. africae* (KT633262).

CONCLUSIONS

The study showed that SFG rickettsiae with public health relevance involved in human diseases are found in ticks collected in Lebanon, where the widespread distribution of tick vectors and possible livestock animal hosts in contact with humans may favor transmission to humans. These results provided information and suggested further investigation to identify risk factors that will help to diagnose, treat and prevent diseases caused by SFG rickettsiae in this region.

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