

FREE-RANGING UNGULATES AS HOSTS OF IXODID TICKS AND TICK-BORNE AGENTS IN THE MALÉ KARPATY MTS (SOUTH-WESTERN SLOVAKIA)

Kocianová E.¹, Špitalská E.¹, Berthová L.¹, Svitálková Z.², Mahríková L.², Kazimírová M.², Schnittger L.³

¹ Institute of Virology, SAS, Dúbravská cesta 9, 845 05 Bratislava, SR ,

² Institute of Zoology, SAS, Dúbravská cesta 9, 845 06 Bratislava, SR

³Instituto de Patobiología, CICVyA, INTA-Castelar, 1686 Hurlingham, Prov. de Buenos Aires, Argentina



Introduction: Free-ranging ungulates are obligate hosts for adult and subadult stages of *Ixodes ricinus* ticks. In collaboration with local hunters, spleen and feeding ticks were collected from game animals shot in deciduous forests in the Malé Karpaty Mts during 2011-2014.



Material and methods: Tissue samples (spleen, blood, skin) and ticks feeding on free-ranging ungulates were obtained from **suburban** (Bratislava forest park, Železná studnička) and **natural** (Fúgelka, Harmónia) sites in the **Malé Karpaty Mts** during 2011-2014. Ticks were collected from all examined species, except wild boar, from May to December. The following microorganisms were detected in the biological samples: **rickettsiae** (PCR, targeting the *gltA* gene followed by sequencing), **boreliae** (PCR, 5S-23S rRNA, followed by RFLP), **Coxiella burnetii** (PCR, *com1* gene), **Anaplasma phagocytophilum** (real-time PCR, *msp2* gene), **babesiae** (PCR, *18S rRNA* gene, followed by sequencing) and **Candidatus Neorhlichia mikurensis** (CNM, real-time PCR, *groEL* gene).

Results: Ninety-two ungulates of five species - roe deer (*Capreolus capreolus*), red deer (*Cervus elaphus*), mouflon (*Ovis aries musimon*), fallow deer (*Dama dama*) and wild boar (*Sus scrofa*) were screened for tick-borne microorganisms. Ticks were obtained from all examined species. In the natural site and suburban site, 51.4% (18/35) and 36.8% (21/57) game were infested by ticks, respectively. *Ixodes ricinus* dominated (1524 ind: 90.5% larvae, 8.2% nymphs, 1% females and 0.3% males). *Haemaphysalis concinna* were also present (206 ind.: 82% larvae and 17.9% nymphs). In feeding ticks, overall prevalence of rickettsiae (*R. helvetica*, *R. monacensis* and *Rickettsia sp.*) was 13.2%. *R. helvetica* was detected in all development stages of *I. ricinus*, *R. monacensis* only in larvae.

Prevalence of *A. phagocytophilum* in adult and subadult *I. ricinus* feeding on deer species was 78.0%, while the prevalence of *Theileria sp.* and *Babesia venatorum* was 36.4%.

C. burnetii was detected in 2.6% of *I. ricinus* removed from mouflons, fallow deer and roe deer. Presence of **CNM**, *B. garinii*, *B. afzelii* and *B. valaisiana* was sporadically detected in subadult and adult ticks.

A. phagocytophilum was detected in spleen of wild boar (29.2%) and ruminants (88.1%).

Deer were found to be infected with *Babesia sp.* / *Theileria sp.* (31.8%). Phylogenetic analysis using partial sequences of the *18S rRNA* gene showed that the isolates from feeding ticks and deer spleen clustered with previously described isolates of *T. capreoli* / *Theileria sp.*

Spleens and blood of game animals were negative for rickettsiae, *C. burnetii*, CNM and borreliae.

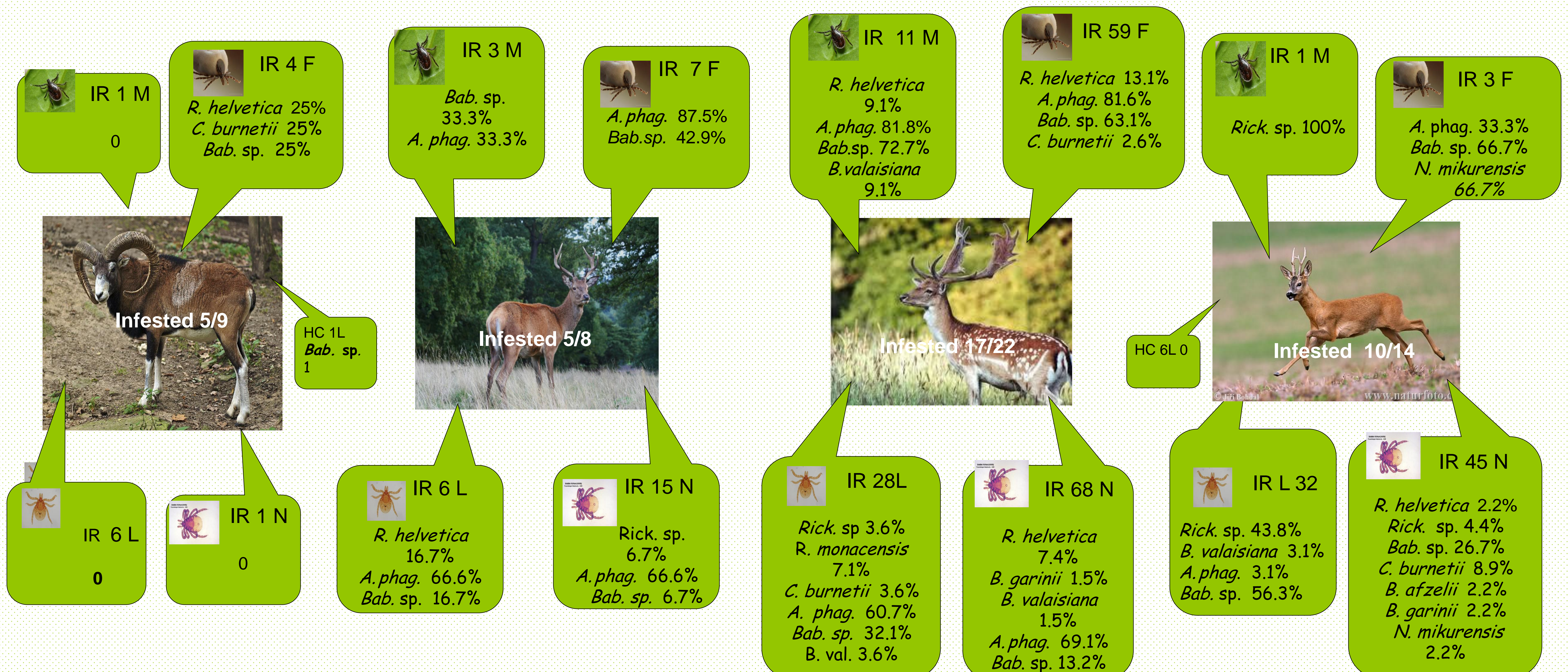


Fig. 1 Occurrence and prevalence of tick-borne pathogens in ticks feeding on free-ranging ungulates in the Malé Karpaty Mts (2011-2014).

Conclusions: The results show that free-ranging ungulates are good sentinels for transport of ticks, infected with the screened microorganisms, but are probably reservoirs only for *A. phagocytophilum* and *Theileria spp.*, suggesting the occurrence of natural foci in the studied sites of Slovakia.