

Impact of wild mammals' ectoparasites on transmission of different pathogens

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Wild mammals are associated with vector-borne (tick, flea, mite, lice) pathogens that is causing infectious diseases worldwide. Ectoparasites of wild mammals can transmit different pathogens such as *Bartonella*, *Rickettsia*, *Borrelia* and other bacterias or viruses. Human outdoor activities in parks and suburban forests are increasing and providing excellent conditions for contact between wild mammals, vectors and human or domestic animals. Thus, in order to assess risks of infection, is important to know what pathogens can be detected in wild mammals' ectoparasites. For that purpose, we used real-time PCR, nested-PCR, multiplex PCR and vector-borne bacteria flow chip for different pathogens detection. A total 118 ectoparasites were collected (110 ticks and 8 fleas) from road kill wild mammals (*Lepus europaeus*, *Mustela putorius*, *Nyctereutes procyonoides*, *Meles meles*, *Vulpes vulpes*). We identified two tick species (*Ixodes ricinus* and *Dermocentor reticulatus*) and two flea species (*Chaetopsylla globiceps* and *Ctenocephalides canis*). Genus of *Bartonella*, *Rickettsia*, *Borrelia* and *Anaplasma* were detected. *Rickettsia* DNA were found in 23.1% *D. reticulatus* ticks and 13.4% *I. ricinus* ticks, as well in 12.5% fleas of *C.globiceps* species. Sequence analysis of the 17 kDa protein coding gene fragment sequinces showed that sequences are similar to *R. helvetica* and *R. raoultii* species. A total 3.39% tested ectoparasites were infected with the *Bartonella* pathogen. Sequence analysis of the 16S-23S rRNR ITS region fragment sequinces showed that fleas were infected with *B.hensellae* and ticks with *B.schoenbuchensis* species. *Borrelia* spp. and *Anaplasma* spp. were found in 27.1% and 56.8% tested ectoparasites respectively. *Borrelia* DNA were found in 37.5% fleas and 26.4% ticks. *Anaplasma* DNA were found in 59.1% ticks and 25% fleas.