

## P 17 Diversity and coexistence of tick-borne pathogens in central Germany

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The importance of established and emerging tick-borne pathogens in Central and Northern Europe is steadily increasing, but comprehensive studies on the prevalence and coexistence of several pathogens are rare. To assess the risk of human infections in a frequently visited forest region of Thuringia (Central Germany), a total of 1000 *Ixodes ricinus* ticks were collected in 2006 and 2007 and investigated by PCR targeting the following genes: *Borrelia* spp. – *ospA*, *Anaplasma phagocytophilum* – 16S rRNA gene, *Rickettsia* spp. – *gltA*, *Babesia* spp. – 18S rRNA gene, *Coxiella burnetii* – *IS1111* and *icd*, and *Francisella tularensis* – 16S rRNA gene. Overall, 54.0% of the ticks were infected with at least one pathogen. A broad heterogeneity of *Borrelia* species and *OspA* types was found in 27.0% of the ticks. *A. phagocytophilum* was present in 5.4%, spotted fever group rickettsiae in 14.7%, *Babesia* spp. in 5.0%, and *C. burnetii* in 1.9% of analyzed ticks. None of the ticks was tested positive for *F. tularensis*. Seasonal variations of infection rates were observed for *Borrelia* spp., *A. phagocytophilum*, and *Rickettsia* spp. In 7.6% of ticks, 2 different agents were present, and 1.2% harboured even 3 different pathogens. Our study reports on *C. burnetii* infections in *I. ricinus* ticks in an area where human cases of Q fever occur regularly and *Dermacentor marginatus* is not present. Interestingly, in 10 *C. burnetii*-positive ticks, even copathogens were present indicating the possibility of coinfections in humans in areas where people are exposed to infected ticks and domestic animals. With this study, we extend the knowledge on the coexistence of tick-borne agents in Central Germany, which is a useful basis for risk assessment. Further systematic large-scale investigations are necessary to understand the ecology of *I. ricinus* ticks and interaction in transmission cycles of infectious pathogens they carry.