

Vector-Borne Diseases: Impact of Climate Change on Vectors and Rodent Reservoirs
Berlin, 27 & 28 September 2007

Ticks, rodents and tick-borne diseases in Lithuania and Norway

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The northward expansion and increased density of *I. ricinus* tick populations in Fennoscandia and increasing incidence of tick-borne diseases could be related to climate change. The prevalence of *Borrelia* genospecies in 2221 *I. ricinus* ticks and 398 rodents collected in different landscapes of Lithuania and Norway were detected. Ticks and rodents tissue were tested for the presence of the *Borrelia* spirochetes DNA using PCR. As targets for DNA amplification of pathogens were used *fla* and *OspA* genes of *B. burgdorferi* s.l. genome. In ticks, the overall prevalence of *B. burgdorferi* s.l. infection was 14% in Lithuania, and 5.6% in Norway. The highest prevalence of *B. burgdorferi* s.l. (20% in Lithuania; 21.2% in Norway) was found in deciduous and mixed forests. A lower prevalence (7.4% in Lithuania) was determined in pine forests and in the coastal zone coastal (4.7% in Norway), and the least prevalence (2.4% in Lithuania; 0.6% in Norway) was found in grasslands. In Lithuania, *B. afzelii* genotype was found in 76% of infected ticks, *B.garinii* in 10%, and *B. burgdorferi* s.s. in 7%. Double infections were observed in 1% of the infected ticks, 6% of the *Borrelia* infections were not typed. In Norway, *B. afzelii* was found in 59.4%, *B.garinii* - in 18.8%, and *B. burgdorferi* s.s. - in 9.4% of infected ticks.

The 23.4% (58 out of 248) rodents from Lithuania and 6.7% (10 out of 150) rodents from Norway were infected with *B. afzelii*. In Lithuanian samples, 53% of *M. arvalis*, 22.2 % of *M. agrestis*, 21% of *C. glareolus*, 10.5% of *A. flavicolis* and 6.7% of *A. agrarius* were positive according PCR, in Norway, 4.9 % of *A. sylvaticus* and 5.9% of *A. flavicolis* were infected with *B. afzelii*. *Sciurus vulgaris* harbored both, *B. afzelii* and *B. burgdorferi* s.s. genotypes.

The prevalence of *A. phagocytophilum* and *Babesia divergens* in 364 *I. ricinus* ticks collected in Lithuania and Norway was detected by Taq Man based Real time PCR method. The *msp2* gene of *A.phagocytophilum* and *18sr* RNA gene of *B.divergens* have been chosen as amplification targets in analysis. The overall infection level of *A.phagocytophilum* in Norwegian ticks was 4.5% (rates from 0 to 8.7%), in Lithuanian - 2.9% (rates from 0 to 9.1%). A total of 2.1% ticks were infected with *B. divergens* in Lithuania and 0.9% in Norway. The *A. phagocytophilum* was not found in any of tested ear and spleen samples of 164 small rodents and engorged nymphal ticks collected on rodents.

