



**P 40 Tick-borne *Anaplasma phagocytophilum* – an emerging pathogen?  
Analysis of *Anaplasma* in ticks detached from humans**

Monika Kozak Ljunggren<sup>a</sup>, Peter Wilhelmsson<sup>a</sup>, Pontus Lindblom<sup>a</sup>, Linda Fryland<sup>b</sup>, Liselott Lindvall<sup>c</sup>, Mari-Ann Åkesson<sup>b</sup>, Christina Ekerfelt<sup>b</sup>, Jan Ernerudh<sup>b</sup>, Pia Forsberg<sup>c</sup>, Per-Eric Lindgren<sup>a,d</sup>

<sup>a</sup> Division of Medical Microbiology, Dept. of Clinical and Experimental Medicine, Linköping University, S-581 85 Linköping, Sweden

<sup>b</sup> Division of Clinical Immunology, Dept. of Clinical and Experimental Medicine, Linköping University, S-581 85 Linköping, Sweden

<sup>c</sup> Division of Infectious Medicine, Dept. of Clinical and Experimental Medicine, Linköping University, S-581 85 Linköping, Sweden

<sup>d</sup> Division of Microbiology, Ryhov County Hospital, S-551 85 Jönköping, Sweden

Human granulocytic anaplasmosis (HGA) may be regarded as an emerging disease due to its recent discovery and a constant increase in the number of cases in Europe and North America. Infections with *A. phagocytophilum* lead to a febrile illness of varying severity, with a risk of immunosuppression that may influence the outcome of coinfections, e.g. borreliosis. According to recent studies, the seroprevalence of *A. phagocytophilum* infection is between 8 and 28% in Sweden. In Europe, tick infection rates vary among countries, 1.2–44%. The main vector for the pathogen is *Ixodes ricinus*, however, there are little data on the frequency of tick infection and thus the risk for HGA. The aim of this study was to determine the prevalence of *A. phagocytophilum* in ticks that had bitten humans and to estimate the risk of acquiring HGA in different regions of Sweden.

Ticks that had bitten humans were collected in 2007–2010. Total DNA and RNA, which was transcribed to cDNA, were extracted from ticks. To detect and quantify *A. phagocytophilum*, a TaqMan real-time PCR assay targeting the 16S rRNA gene was optimized and used. The assay utilizes a species-specific primer pair generating a 150-bp product together with a hydrolysis probe. The use of cDNA offered a 100-fold greater sensitivity compared to DNA-based analysis. Strain variation was investigated by sequencing an 850-bp fragment of the 16S rRNA gene.

Among the 380 ticks collected in Sweden in 2007, 6 were positive for *A. phagocytophilum* giving a prevalence of 1.6%. In 2008, 3.2% of the ticks were positive for *A. phagocytophilum*. All ticks collected belonged to *I. ricinus*, 30% of the *Anaplasma*-containing ticks were adults and 70% were nymphs. In 7 cases, the tick was coinfecting with *Borrelia* spp. The overall rate of coinfection was 0.8%. The quantity of bacteria per tick varied from 1 to 600,000.