

Prevalence and genetic variability of *Anaplasma phagocytophilum* in feeding *I. ricinus* from several host species in Northern Italy.

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In Europe, *Anaplasma phagocytophilum* is an emerging tick-borne pathogen with both medical and veterinary importance, being the causative agent of human granulocytic anaplasmosis (HGA) and the tick-borne fever of domestic animals. Its ecology and its molecular diversity in Europe is currently under assessment. Therefore, we have studied the prevalence and genetic variability of *A. phagocytophilum* and its ecological associations with hosts and vectors in the area.

Our study was carried out in the Valle dei Laghi (northeastern Italian Alps). A total of 821 questing *I. ricinus* ticks were collected by dragging and 284 engorged ixodid ticks were collected from humans and from hunted or live-trapped wild-life animals. Further they were analyzed for the prevalence of *A. phagocytophilum*. All positive samples were used for amplification of *groEL* and *msp4* genes for further phylogenetic analysis.

Overall *A. phagocytophilum* prevalence in questing *Ixodes ricinus* ticks was 1.8%, in ticks from various host was: 4.3% in ticks from humans, 9.1% in ticks from dogs, 14.3% in ticks from wild ungulates, 7.7% in ticks from sheep, 10.7% in ticks from birds and 6.1% in ticks from rodents. Prevalence in rodent blood samples (*A. flavicolis*, *M. avellanarius*, *M. glareolus*) was only 0.3%. Phylogenetic analyses of *msp4* and *groEL* showed two distinct enzootic cycles of *A. phagocytophilum* associated with different reservoirs as well as vectors. Strains that infect humans belong to the clade formed out of strains from engorged ticks collected from dogs, wild ungulates, sheep and birds. Strains obtained from rodents are most likely transmitted by other tick vector and may not represent an immediate threat to humans in northern Italy. Our results shows different ecology of *A. phagocytophilum* as it is in United States.