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BOOK OF ABSTRACTS



trap between 2011 and 2013. Meteorological data were obtained from Slovak Hydrometeorological Institute.

A total of 157,785 *Culicoides* were collected, belonging to at least 41 species. During this survey 5 new species for Slovak fauna have been recorded, namely *C. picturatus*, *C. clastrieri*, *C. gejjelensis*, *C. griseidorsum* and *C. odiatus*. The highest species diversity (35 species) and abundance ($\Sigma=97,945$) was in south eastern Slovakia (Michaľany) compared to Tulčik (27 species, $\Sigma=41,670$) and Rozhanovce (31 species, $\Sigma=18,167$). The potential vectors of pathogens, *C. obsoletus/C. scoticus*, were found to be highly abundant with 79% of the total specimen trapped in Tulčik and 68% in Rozhanovce. The second most abundant species were the species of the Pulicaris complex with 14% and 12% respectively. In Michaľany, most of the *Culicoides* captured belonged to the Pulicaris complex (49%) and *C. obsoletus/C. scoticus* (35%). The species of the Nubeculosus complex were present in high abundance (8%) only in this lowland area of south eastern Slovakia. The most abundant species *C. obsoletus/C. scoticus* completed 3 generations throughout the season and 2-3 generations was determined for *C. pulicaris/C. punctatus*.

The population dynamics of *Culicoides* depend on environmental factors and primarily the weather. In general, only few *Culicoides* were collected in temperatures below 8 °C. Statistical analyses showed a positive correlation between *Culicoides* abundance and the average of temperature. The dependence on minimal daily temperature was significant in Michaľany and Rozhanovce. Midge abundance was negatively correlated by wind speed in Tulčik and by relative humidity in Rozhanovce.

Adults' activity of the biting midges was pointed out from April to November meaning a vector free period from December to March. The eastern Slovakia provides suitable biotopes for developments of *Culicoides* especially potential vectors of pathogens.

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GENETIC DIVERSITY OF ANAPLASMA PHAGOCYTOPHILUM AND RESERVOIR COMPETENCE OF WILD LIFE ANIMALS FOR TICK-BORNE PATHOGENS IN NORTHERN ITALY

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Tick borne diseases are zoonoses causing infection in humans and domestic animals. The most spread zoonoses in Europe are the one caused by *Borrelia burgdorferi* sensu lato. *Anaplasma phagocytophilum*, *Babesia* spp., and *Rickettsia* spp. Impact of global, climatic and social changes occurring in recent years has increased incidence of ticks and number of infected people and animals. Movement of ticks into higher altitudes also causes the emergence of new foci.

Our study was carried out in the Valle dei Laghi (northeastern Italian Alps). We have studied the prevalence and genetic variability of *A. phagocytophilum* and its ecological associations with hosts and vectors in the area. 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. In addition 448 larve ticks from wild ungulates, birds and rodents were analyzed for reservoir competence for *A. phagocytophilum*, *Babesia* spp., *B. burgdorferi* s.l. and *Rickettsia* spp.

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.

Moreover, from total of 339 engorged larvae *I. ricinus* ticks from rodents 9.1% were positive for *B. burgdorferi* sensu lato, 5.3% positive for *Rickettsia* spp. and 1.8% positive for *Babesia* spp. From 99 engorged larvae *I. ricinus* ticks from wild ungulates 6% were positive for *A. phagocytophilum*, 6% positive for *Rickettsia* spp. and 1% positive for *Babesia* spp. From 10 engorged larvae *I. ricinus* ticks from birds 80% were positive for *B. burgdorferi* s.l. High degree of genetic variability was observed.

Our study revealed that in mountainous habitats of Northern Italy foci of tick-borne diseases are emerging. Small mammals and wild ungulates are the most important hosts for ticks as well as reservoirs for pathogens, however they participate differently in their ecology and circulation of tick borne agents in natural foci.

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