Molecular-biological and serological tools for the diagnosis of canine and equine babesiosis in Switzerland

Heinz Sager, Alexa Oppliger, Laura Muggli, Marie-José Porchet, Caroline Frey, Norbert Müller, Bruno Gottstein
Institut of Parasitology, University of Bern, CH-3001 Bern.

Key words
Babesia, Theileria, Rhipicephalus, Dermacentor, PCR

Aim of the study
Babesiosis in dogs and horses is caused by protozoan parasites including Babesia canis for dogs, while horses are affected by B. caballi and Theileria equi. For a long time both, canine and equine babesiosis, were assumed to be typical travelers diseases, but within the last years more and more cases were found in patients that had no anamnestic sojourn outside Switzerland. Therefore, these parasites become more and more relevant for Swiss veterinarians and the local animal population. The aim of the present project was to prepare laboratory tools suitable to diagnose canine and equine babesiosis/prioplasmosis, and to apply those tools in an explorative study on (a) the occurrence of autochthonous and imported cases of babesiosis in dogs and horses in our country and (b) respective tick hosts.

Material and methods
For routine diagnosis of Babesia-infection in dogs and horses, investigation of Giemsa-stained blood-smears (capillary blood) for acute stage diease, and antibody detection by IFAT for chronic stage diease are the appropriate tools. Speciation of Babesia was performed by PCR, which was subsequently developed into a new real-time PCR, suitable for routine diagnosis, but also for testing Giemsa-stained blood smears and ticks.

Results and significance
Overall, 99 horses of Switzerland (either with clinically suspected babesiosis or at risk of infection) were tested in the present study. One of these horses yielded a positive Giemsa-stained blood smear at diagnosis, subsequently confirmed as T. equi by PCR. From 14 clinically suspected cases of canine babesiosis, 5 were parasitologically positive, and all 5 cases yielded B. canis canis by PCR.
A total of 1'864 ticks were collected from mainly dogs and horses. 34 (1.8%) specimen were Dermacentor reticulates, 64 (3.4%) were Rhipicephalus sanguineus and the rest (94.8%) Ixodes spp.. All R. sanguineus ticks were negative by Babesia-PCR, while 3 (9%) out of the 34 D. reticulates specimen were PCR-postive for Babesia-DNA. Subsequent sequencing revealed a high similarity with Babesia sp. Genotype EU1.
Global warming, ecological changes in the potential habitat of ticks, increasing host- and vector-populations and increasing mobility of dog owners may be responsible for an autochthonous risk of infection for Babesia spp., and further surveillance is suggested to tackle this problem.

Publications, posters and presentations
Porchet, MJ.; Sager, H.; Muggli, L.; Oppliger, A.; Müller, N.; Frey, C.; Gottstein, B. Etude épidémiologique descriptive de la Babésiose canine dans la Région Lémanique. Schweiz. Arch. Tierheilkd. 149: 457-465 (2007).
Porchet, MJ.; Sager, H.; Muggli, L.; Oppliger, A.; Müller, N.; Frey, C.; Gottstein, B. A descriptive epidemiological study on canine babesiosis in the Lake Geneva region. WAAVP, Gent/Belgium, August 19-23, 2007.

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