
P5: Molecular characterization of *Klossiella muris* (Adeleorina, Coccidia, Apicomplexa) detected during field survey of small mammals from Afghanistan

Ulrich SCHOTTE¹, Alfred BINDER¹, Katja GOLLER², Michael FAULDE³, Silke RUHL¹, Sabine SAUER⁴, Mathias SCHLEGEL⁵, Jens P. TEIFKE⁵, Rainer G. ULRICH⁶, **Claudia WYLEZICH²**

¹ Central Institute of the Bundeswehr Medical Service Kiel, Department of Veterinary Medicine, Kronshagen, Germany

² Friedrich-Loeffler-Institut, Institute of Diagnostic Virology, Greifswald - Insel Riems, Germany

³ Central Institute of the Bundeswehr Medical Service Koblenz, Department of Medicine, Koblenz, Germany

⁴ Bundeswehr Medical Academy, Military Medical Research and Development, Munich, Germany

⁵ Friedrich-Loeffler-Institut, Department of Experimental Animal Facilities and Biorisk Management, Greifswald - Insel Riems, Germany

⁶ Friedrich-Loeffler-Institut, Institute of Novel and Emerging Infectious Diseases, Greifswald - Insel Riems, Germany

Small mammals are an important reservoir for causative agents of numerous infectious diseases, including vector-borne diseases, and might therefore represent a threat for humans and animals. In our study, small mammals collected in military camps in Afghanistan were investigated for the presence of apicomplexans using histopathology and molecular methods. For this purpose, well-established and newly developed real-time PCR assays were applied. A high prevalence of apicomplexans was detected in house mice (*Mus musculus*), but also in shrews (*Crocidura cf. suaveolens*) and grey dwarf hamsters (*Cricetulus migratorius*). The further molecular characterization based on partial 18S rRNA gene sequences revealed a close relationship to a cluster of *Hepatozoon* sp. detected in voles of the genus *Microtus*. *Hepatozoon canis* DNA was detected in one house mouse as well as in two *Rhipicephalus* ticks from a dog puppy. In addition, a few house mice were found to be infected with far related adeleorinids showing the highest sequence identity of 91.5% to *Klossiella equi*, the only published *Klossiella* sequence at present. For their better phylogenetic characterization, we did additional metagenomics sequencing of two selected samples. The resulting 18S rRNA gene sequences have a length of 2.4 kb including an insertion of about 0.5 kb and are 100% identical to each other. Histopathology together with organ tropism and detection rates verified this sequence as of *Klossiella muris*. In conclusion, in our study we were able to document naturally occurring protozoan life stages and the additional taxonomic characterization of a well-known commensal in mice.