

## Summary

*Anaplasma phagocytophilum* is a common intracellular bacterial parasite of the order Rickettsiales. These microorganisms can be transferred between hosts by vector transmission by ticks from *Ixodes* genus. The constant presence and circulation of *A. phagocytophilum* in the natural environment is provided by natural reservoirs of these bacteria, which include e.g. wild ungulates. Studies presented in three publications included in this dissertation concern the determination of the prevalence and genotyping of *A. phagocytophilum* strains among Polish populations of wild ungulates: red deer, roe deer, fallow deer, wild boar, Eurasian moose and European bison; and in farm animals: red deer and fallow deer.

**The first publication**, concerned the detection of *Anaplasma phagocytophilum* in wild boars. The presence of bacteria was found in 20% of the tested animals. Genotyping and phylogenetic analysis of three partial genetic markers: *16S* rDNA, *groEL* and *ankA* allowed to prove that *A. phagocytophilum* isolated from wild boars are potentially pathogenic for humans, belong to ecotype and cluster I. **The second article** describes the presence of *A. phagocytophilum* in cervids. In roe deer and red deer, the prevalence was over 50%, in moose it was 18%, and in fallow deer no bacteria of the genus *Anaplasma* were detected. In the studied group of farmed red and fallow deer, the presence of *A. phagocytophilum* was detected only in the first species. Additionally, 3 haplotypes of the *16S* rDNA partial gene has been described, two of them has been previously noted, and the third one is new. **The third publication**, concerned the genotyping and prevalence of *A. phagocytophilum* strains isolated from two species of the largest wild ruminants: European bison and Eurasian moose. Prevalence in bison was 24%, and the examination of two additional moose specimens supplemented the data from the second publication and the prevalence in this species was over 30%. Analysis of amplified genetic markers from *A. phagocytophilum* isolates from European bison characterized these strains as ecotype I and cluster IV, isolates from Eurasian moose to two ecotypes - I and II and to cluster I. All three genetic markers: *groEL*, *ankA* and *16S* rDNA, from moose and bison, are identical or grouped with HGA strains, means that detected *Anaplasma phagocytophilum* strains may be potentially pathogenic to humans. To comprehensively describe the issues dispute in the dissertation, unpublished results of genotyping of *A. phagocytophilum* strains from red deer and roe deer are attached. Genotyping of a red deer strains showed that the *A. phagocytophilum* bacteria present in these hosts belong to the ecotype and cluster I. More various were strains isolated from roe deer individuals. These strains were assigned to ecotypes I and II and to clusters I and II.

In summary, 305 individuals of ungulates from 6 species were examined. All bacteria detected by molecular methods belonged to one species – *Anaplasma phagocytophilum*. Sequence analysis of the partial *16S* rDNA gene and phylogenetic analysis of the *ankA* and *groEL* partial genes allowed to confirm that ungulates in Poland are natural reservoirs of *A. phagocytophilum* and there are strains potentially zoonotic for humans among them.