Trueperella pyogenes is an opportunistic pathogen causing purulent infections in both livestock and wild animals. This bacterium is a common inhabitant of skin and mucous membranes of the upper respiratory, gastrointestinal, and urogenital tracts of different animal species. In small ruminants, *T. pyogenes* is associated with mastitis, reproductive and respiratory tract infections, and abscesses of different location, including kidney, liver, lung, or lymph nodes. In humans, *T. pyogenes* infections have been rarely reported, most commonly among immunocompromised individuals and after contact with infected animals.

T. pyogenes infections are particularly important in livestock, leading to significant economic losses in animal production. Only limited data about factors promoting the development of *T. pyogenes* infection and determining its course are available. Currently, most of the available literature data are related to the characteristics of isolates from cattle and swine. However, data on the epidemiology of *T. pyogenes* infections and properties of strains occurred in small ruminants are strongly limited. Due to the growing interest in the valuable properties of dairy products and meat from goats and sheep, it seems important to save the health of these animals. The aims of this project are to investigate the phenotypic properties, genotypic characteristics associated with virulence and antimicrobial resistance, and to determine a genetic diversity of *T. pyogenes* strains isolated from small ruminants.

Up to date, little is known about virulence factors, resistance phenotypes and genotypes, as well as genomic variability of caprine and ovine *T. pyogenes* strains. In this project, the isolated *T. pyogenes* strains will be characterized based on the selected phenotypic properties. The antimicrobial resistance profiles, as well as related to them resistance genotypes will be determined among studied strains. Moreover, all strains will be screened for genes encoding known *T. pyogenes* virulence factors and genes associated with biofilm formation. Nevertheless, the biofilm formation ability of studied strains will be also evaluated using a standard method with crystal violet staining. In this study, highly discriminatory typing methods, including the pulse field gel electrophoresis (PFGE), will be used for genetical differentiation of *T. pyogenes* strains. Moreover, a new multi-locus sequence typing (MLST) scheme for the species *T. pyogenes* will be designed in this project, and it will be the first such assay for strain typing in the genus *Trueperella*. Based on the study results a genetic diversity among the caprine and ovine strains will be evaluated, and a phylogenetic relationship between the strains will be established. Additionally, it is planned to carry out the whole genome sequencing (WGS) for the selected strains belonging to different genetic profiles. A bioinformatic analysis of the obtained sequences, deposited in the GenBank database, will allow to identify putative genes related to antimicrobial resistance and pathogenicity of *T. pyogenes*, and to find genome regions associated with mobile elements such as transposons or integrons, which have not been previously described in this species.

The results of the project will improve the current knowledge about determinants of virulence and antimicrobial resistance in *T. pyogenes*, as well as about their distribution among caprine and ovine strains. Generally, the obtained data allow better understanding the pathogenesis of *T. pyogenes* infections. They will also provide valuable information significant from the epidemiological point of view. Furthermore, it seems that a newly developed MLST scheme for *T. pyogenes* typing will be an especially useful tool for epidemiological investigations of infections caused by this pathogen in various animal species. Importantly, the project results should have a broad significance not only for a control of *T. pyogenes* infections in small ruminant farming, but indirectly also for a public health, in accordance with the One Health concept.