The capercaillie (*Tetrao urogallus*), the largest grouse species in Europe, is known for its distinctive appearance and behavior. Historically, the capercaillie held cultural significance as a popular game species, and it is now recognized as a key umbrella species for forest conservation. Protecting the capercaillie supports not only its survival but also numerous other species dependent on forest ecosystems. However, despite significant conservation efforts, capercaillie populations are rapidly declining across Europe, especially in central and western regions. The primary causes of this decline are identified as habitat destruction, predator pressure, and disturbances caused by human activity.

Recent studies on other animals have highlighted the critical role of the gut microbiome—a complex community of microorganisms—in energy extraction from food and overall health. This relationship is particularly relevant to the capercaillie, which relies on a highly specialized diet of pine and spruce needles, seasonally supplemented with leaves, buds, and fruits from shrubs such as bilberries. These foods, rich in lignocellulose and resins, are difficult to digest without the involvement of specific gut microorganisms. Disruptions in microbiome development, caused by captivity, human-induced stress, or environmental contamination (e.g., heavy metals or polycyclic aromatic hydrocarbons in needles), can severely impact microbiome functionality. Such disturbances may impair nutrient assimilation, weaken the birds' condition, and hinder conservation efforts.

The primary goal of this interdisciplinary project is to investigate the diversity and functionality of the capercaillie microbiome and the associated challenges in lignocellulose biomass degradation using a combination of classical microbiological techniques, advanced DNA sequencing, microfluidics, and metabolic analyses. The main research tasks include:

1. Microbial diversity analysis from capercaillie fecal samples
2. Selection and characterization of lignocellulolytic microorganisms
3. Evaluation of the selected microbial consortia for their capacity for lignocellulosic degradation

The research will be based on non-invasive fecal sample collection from wild populations in Poland and individuals from breeding centers. The project will examine microbiome variability at individual, population, and environmental levels, shedding light on microorganisms essential for the capercaillie's diet and survival.

This study aims to deepen our understanding of the poorly researched capercaillie microbiome and its potential impact on the wellbeing of these birds. The findings could contribute to more effective conservation strategies and reintroduction programs for this endangered species. Additionally, the selected collection of cultured bacteria may have applications beyond conservation. The lignocellulolytic microorganisms identified during the project could support biotechnological innovations, such as bioenergy production from coniferous biomass in the energy sector or improved feeding strategies for related species, such as turkeys in agriculture. The research findings are intended to serve as a foundation for high-quality scientific publications.