**Appendix A – Statement of Work**

**Research Cooperation Agreement**

**On specific tasks of the INTER-EXCELLENCE II - INTER-ACTION  
- LUAUS25009 project**

*General goal –* Climate change threatens biodiversity, forcing species to adapt or face extinction. Understanding past adaptations can help predict future responses. This project investigates how European bank vole (*Clethrionomys glareolus*) populations adapted after the last glaciation by analyzing their genomes using whole-genome sequencing and climate models. We will identify genomic regions showing elevated geographic and genetic divergence, detect candidate loci involved in local adaptation, and assess gene-environment associations to determine key environmental drivers. Understanding these mechanisms will provide insights into species’ adaptive potential under current and future climate change.

*Collaboration details* – xxx (University of Oklahoma), xxx, and xxx (Institute of Animal Physiology and Genetics, CAS) have been collaborating on climate adaptation research for several years, leading to successful publications in reputable journals. Both research teams have extensive expertise in small mammal genomics, particularly in how population history shapes genetic diversity and adaptive potential across climatic and latitudinal gradients in North America and Europe. xxx and xxx have assembled a comprehensive tissue collection representing vole populations across Europe, Great Britain, and North America. Project LUAUS25009 aims to strengthen and expand collaborations between Czech and U.S. academic institutions, allowing both teams to investigate adaptation, local ancestry, and climate history from a whole-genome perspective. xxx’s lab at the University of Oklahoma has already established protocols for whole-genome sequencing. Within this project, xxx will provide the biological samples, while xxx and her team will perform DNA library preparation and sequencing, and PIs and personnel from both institutions will analyse genomic data and collaborate in resulting publications. The costs of reagents and materials for library preparation and sequencing will be reimbursed through Project LUAUS25009.

*Work to be conducted at the University of Oklahoma (OU)* – Whole genome sequencing on an Illumina platform. This includes preparation of DNA libraries using IDT xGen DNA Lib Prep kit (or similar), normalization and multiplexing using xGen Normalase UDI Primers Plate and IDT xGen Normalase Module, quality checks, and sequencing of genomic libraries through the OMRF (Clinical Genomics Center (CGC). If new and more effective genomic approaches become available during the project, xxx and xxx may decide to implement them, provided they align with the project’s objectives, while the approved budget will remain unchanged.