Eukaryotic genomes contain thousands of non-coding RNAs (ncRNAs) that play key roles in the transcriptional and post-transcriptional regulation of gene expression. Increasing evidence indicates that these types of molecules influence the regulatory responses of plants to biotic stress. The scientific goal of the project is to identify non-coding RNA molecules, with particular emphasis on miRNAs and lncRNAs, in the transcriptomes of oat plants (*Avena sativa* L.) during stress caused by infection by fungi of the genus *Puccinia* and *Blumeria*. Research in the project will be conducted at the transcriptome level using the latest molecular biology techniques, i.e. next-generation sequencing (NGS) technologies based on short (Illumina) and long (Oxford Nanopore) reads, qPCR or dPCR. The research planned in the project will be the first of this type on the structures of non-coding RNA in common oats. The use of artificial inoculation in laboratory conditions and then examination of plant transcripts at an interval after infection will allow us to determine which genes associated with miRNAs and lncRNAs will be activated or silenced and after what time. For a more detailed comparative analysis, sequencing of mRNA structures will be performed to identify common and unique ncRNA sequences in response to disease stress. GO and KEGG analyzes of the obtained results will allow us to answer the questions about which genes and which metabolic pathways are regulated by non-coding RNA structures in response to stress.

Taking into account the growing demand for food, as well as actions aimed at limiting plant protection products, research on this type of structures should be effectively used to discover the molecular mechanisms underlying the development and response to biotic stress. The use of both short- and long-read sequencing technologies seems particularly appropriate for polyploid and repeat-rich genomes, which is reflected in the genome of many cereals, including common oats.