The aim of the research is to determine the status of genetic imprinting of non-protein-coding sequences, as exemplified by microRNAs, in the pig.

The phenomenon of genomic imprinting, also called gametic, genetic or parental belongs to strategies responsible for the regulation of gene expression and means non-equal expression of parental alleles in their offspring. Thus, the paternal imprinting occurs when only the maternal allele is expressed, whereas the maternal imprinting occurs when solely the paternal allele is expressed. The process of parental imprinting leads to some kind of genetic asymmetry between the paternal and maternal parts of the genome, which is why it is now believed that it has arisen as a result of the conflict between parental genes and the battle of the sexes for control over the development of the fetus. For example, "paternal genes" (the imprinting of the maternal allele) promote the development of the trophoblast, which later forms the placenta responsible for the nutrition of the fetus and its growth. Whereas "maternal genes" (the imprinting of the paternal allele) are responsible for the proper formation of the embryo and its development. The explanation of this situation is as follows: for a male, from the genetic point of view, the most important thing is to have a strong descendant as much as possible, which is supposed to ensure its survival. However, in the case of a female, which may have offspring with many males, genetically important is to ensure equal development for each of her children, regardless of who the father is. The fact that imprinted genes often are associated with prenatal growth and development also speaks in favor of this hypothesis.

So far, the phenomenon of genetic imprinting has been discovered only in mammals and flowering plants. It plays a significant role in the development of organisms and their functioning and the disruptions of the imprinting pattern may lead to many diseases, such as: Angelman or ovarian teratoma. The genomic imprinting has been the subject of intensive research, focused mainly on the human and the mouse, aimed at identifying new imprinted genes as well as mechanisms orchestrating this phenomenon. This task, however, is difficult due to the fact that different organisms, tissues and developmental stages are characterized by different patterns of imprinting, which is why there is a need to carry out numerous studies, focused on various species and tissues. Additionally, the situation is further complicated by the fact that protein-coding genes and non-coding RNAs (ncRNAs) show different imprinting features as well as ncRNAs take part in the regulation of genomic imprinting. This is why imprinting-focused research should no more investigate mainly protein-coding genes, because this will hamper getting the whole, real picture of the phenomenon.

As mentioned above, not only protein-coding genes are subjected to imprinting but also non-coding RNAs, which include inter alia microRNAs (miRNAs). A microRNA particle is about 20-23 nucleotides in length, which is why miRNAs are classified as small RNAs. MiRNAs, binding with the transcript of a gene, lead to its translational repression or less frequently degradation, which is why, in consequence, no protein is synthesized. MicroRNAs play substantial roles in the functioning of organisms indirectly regulating various crucial biological processes such as apoptosis or cell proliferation. An additional important feature of microRNAs from the point of view of imprinting analyses and this project is the possibility to form groups (so called clusters) in the genome. Studies of mice and humans have showed that sequences occurring in replicates or in the form of clusters are subjected to genomic imprinting more frequently than single sequences . Therefore, in this proposal, the microRNA clusters were chosen as the subject of the research; which is supposed to increase the probability of finding of imprinted sequences, thereby allowing their analysis.

The proposed project, aiming at analyzing the genetic imprinting of non-protein-coding sequences in the pig, can make an important contribution to the understanding of this phenomenon for several reasons. Firstly, the pig is a species poorly investigated in terms of genomic imprinting. Moreover, its economic importance and physiological similarity to the human (which makes it, according to some researchers, more adequate human model than the mouse) speak in its favor as an research object. Secondly, the aim of the proposed studies is the imprinting analysis of non-protein-coding sequences, as exemplified by microRNAs. As mentioned above, these sequences differ from protein-coding sequences in terms of imprinting features and their roles in this phenomenon. What's more, the number of identified so far miRNAs undergoing imprinting is scarce in comparison to the information concerning protein-coding genes – i.a. in the case of human there are identified 97 imprinted protein-coding genes and 3 miRNA sequences, whereas in the case of pig there are 22 protein-coding genes and 0 miRNAs (GeneImprint data base). Thus this project has been conceived in order to fill the gap in the existing knowledge of genomic imprinting, which may contribute to its better understanding and characteristics as well as it can act as a stimulus to further research.