Molecular, regulatory mechanisms of animal development, from a fertilized egg to an adult organism are among the most fascinating problems of molecular and cellular biology. Previous studies indicate that the regulation of vertebrate development involves the expression of the *hox* genes. In the post-transcriptional regulation of gene expression, this process involves multiple proteins such as transcription factors, proteins from the Polycomb family and others. Over the last few years, there have been reports on the participation of non-coding RNA (ncRNA) in these processes.

In our research we intend to focus on understanding the role of ncRNA in the kidney development. As our experimental model, we decided to use the cultured human embryonic stem cells, embryonic renal cells, and renal cells isolated from adult individuals. Chosen renal cell cultures reflect the development process of the kidney from an embryo to an adult organism. Besides, we want to examine the effect of the ncRNA neoplastic processes, occurring during the development of renal cancer cells, using the culture cells The results of ncRNA characteristics will be then related to the ncRNA characteristics, present in the kidney tumor samples from Polish patients.

In eukaryotes, there are several types of ncRNA, particularly long (lncRNA), over 200 nt and short (sncRNA), below 200 nt. In addition, the sncRNA group include microRNA, piRNA and tRF RNA, which are substantial fragments of tRNA molecules. Another interesting problem is the potential contribution of a new family of ncRNA, i.e. a circular RNA in cellular processes, including renal cell development. In other words, what types of ncRNA occur in renal cells and what is their characteristics and functions. An excellent way to answer these questions is to use the new generation sequencing methods. Exploiting the methods developed by Illumina company will allow to recognize a panorama of ncRNAs, present in kidney cells and to determine changes in their expression, during development and tumor processes. It should be noted that this technique has previously been used to analyze the sncRNA, occuring in the gonads of domestic swine (Kowalczykiewicz et al. PloS ONE (2014) 9(11) e113249). Besides, deletion of the selected ncRNA using "knockdown" technique shows that ncRNs are involved in the renal cell development and carcinogenesis mechanisms.

A characteristic feature of the RNA molecules is the formation of complex secondary and tertiary structures, which are associated with their function in the cell. In order to explain the function of different types of ncRNA in the renal cell development, we are going to determine their structure using different probes.

Majority of the RNA molecules are present in the form of complexes, formed with various proteins. ncRNAs also form complexes with proteins, and in the case of lncRNA, the number of interacting proteins fluctuates at around several dozen. We would also like to determine in *in vivo* conditions, applying crosslinking protein to RNA molecules method in combination with new methods of sequencing, which proteins interact with the ncRNA in renal cells

Currently, there is a growing interest in RNA epigenetics. We intend to determine through a cellular test, firstly, the presence of modified nucleotides in different ncRNA sncRNA families, and changes in the modification pattern, associated with the renal cell development and carcinogenesis.

Another important problem that we plan to solve is to determine the mechanisms of gene expression regulation in the renal cells. We are going to test the competing endogenous RNA (ceRNA) participation in this mechanism. It is based on the assumption that miRNAs may be related to a number of RNA molecules (eg. mRNA, lncRNA, circRNA). In order to find the target sequences for miRNA, we will use the methods of bioinformatics and confirm experimentally the crosslinking of miRNA binding to specific target sequences for selected lncRNA and circRNA.