

Cancer is a second, after cardiovascular diseases, cause of death worldwide and its proper diagnosis and treatment is still challenging. Among all cancer types, renal cell carcinoma (RCC) is one of the 10th most common and ccRCC is the most frequently diagnosed subtype of RCC (about 70-80% of cases of RCC). Due to the lack of specific symptoms and diagnostic methods, ccRCC is frequently misdiagnosed or detected as another abdominal disease. The most common symptoms of ccRCC include pain, hematuria and high temperature. As those symptoms are mostly observed in a late disease stage (e.g. cancer in metastasis stage), available treatment might be ineffective. In most cases, ccRCC is diagnosed by noninvasive diagnostic imaging during investigation of another abdominal disorder. Nowadays, there is still a lack of specific and selective diagnostic methods for early detection of ccRCC.

Well known background of ccRCC development covers genetic, biological (obesity) and environmental (smoking habits) factors. However, the pathomechanisms underlying the disease progression have not been fully explained yet. In this case, there is a need for further investigation to fully understand and explain molecular mechanisms of RCC development.

Nowadays, metabolomics seems to be one of the most powerful tools in plausible biomarkers evaluation within a wide range of diseases (e.g. cancer, metabolic diseases as well as cardiovascular diseases). Metabolomics is focused on determination of low-molecular-weight compounds, namely metabolites. Those compounds as a last reflection of biochemical processes constitute a great representation of current organisms' status, both physiological and pathophysiological. For metabolomics studies, several types of biological materials can be used. Mainly, metabolite profiles determined in blood (plasma, serum) or urine are easy to analyze due to small invasiveness of samples' collection, simultaneously providing reflection of systemic changes in the organism. As a result, the relationship between qualitative as well as quantitative changes in metabolites' profile and disease state, are determined.

In the proposed project, metabolomics approach will be applied to investigate metabolomics profiles characteristic for ccRCC. The main aim of the study will be to determine metabolites with plausible potential to explain pathomechanisms of the disease development. Furthermore, the hypothesis about relationship between changes in metabolite profiles as a result of ccRCC and different histopathological stages of the diseases, will be verified.

At first, the determination of as many metabolites as possible in plasma and urine samples derived from patients with diagnosed ccRCC, will be conducted. For this purpose complementary analytical techniques such as liquid and gas chromatography, capillary electrophoresis coupled with mass spectrometry, as well as nuclear magnetic resonance, will be applied. The qualitative differences between studied groups will be determined by the use of advanced statistical methods. The research will be carried out in collaboration with world known specialists from the University in Toulouse and Madrid. Statistically significant metabolites selected in the first step of the project can give a better insight into molecular pathomechanisms of ccRCC. Next phase of the project will provide information on relationship between quantitative changes in metabolite levels and ccRCC. Combination of those two stages of the project will provide an explanation of the processes at the molecular level underlying ccRCC development.

As a result, proposed studies would provide an explanation of processes underlying ccRCC. In the future, obtained results might be used for optimization of new, more sensitive diagnostic methods as well as development of more effective treatment.