In the 21st century, humanity has witnessed three epidemics caused by coronaviruses namely severe acute respiratory syndrome coronavirus (SARS-CoV), Middle East respiratory syndrome coronavirus (MERS-CoV), and novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Among these, SARS-CoV-2 has greater transmission and mortality rate. Coronavirus disease 2019 (COVID-19) emerged in 2019 and is caused by infection with a human betacoronavirus SARS-CoV-2. Coronaviruses are enveloped viruses that possess the largest genome among other RNA viruses. They are characterized by genetic variability and evolve rapidly, changing their antigenic profile, tissue tropism, or host range. The genome of SARS-CoV-2 is a single-stranded positive-sense RNA approximately 29,9 kb in length. Sequence analysis of complete SARS-CoV-2 genomes revealed that three main variants (A, B, and C) distinguished by amino acid changes. The COVID-19 can present a variety of manifestations ranging from no symptoms or mild disease to severe pneumonia or multi-organ failure with hypercytokinemia. The findings indicate that old age and comorbidities could predict a poor outcome. The genetic factors that could predict the severe course of the SARS-CoV-2 infection and disease remain unknown.

We hypothesize that the genetic diversity of the SARS-CoV-2 may contribute to virulence and viral pathogenesis, while the polymorphism located in host genes may influence the cytokine secretion and the clinical course of the COVID-19. The studies that define the factors in patients with COVID-19 associated with the mild or severe outcome are important and needed to be carried out.

The project will determine the sequences of the SARS-CoV-2 genomes isolated from Polish patients and identify viral and host factors involved in SARS-CoV-2 infection, and establish whether these factors can be detected in COVID-19 patients as biomarkers predicting the clinical outcome of the disease. Project objectives include characteristics of SARS-CoV-2 genomes prevalent among Polish patients, identification of major polymorphisms of the selected host genes responsible for a severe course of SARS-CoV-2 infection, assessment of the host's immune response during the COVID-19 disease, and designing of the assay for quantification of the SARS-CoV-2 genomic RNA. The results of these studies will provide information about the prevalence, genotype distribution, antigenic variation of the viral structures, potential correlations between viral genotype and pathogenicity, and host factors involved in COVID-19 outcome.

The studies that define risk factors associated with the clinical course of the COVID-19 disease are needed to be performed. Since most people infected with SARS-CoV-2 are asymptomatic while others die, searching for factors that cause serious outcomes is a high-priority area for research. There is still no data concerning the SARS-CoV-2 genetic variability in Poland. Analysis of the sequences of the SARS-CoV-2 cases are vital to understand the genetic evolution of the virus. The project results may provide new insight into the virulence and pathogenesis, as well as possible strategies for the use of diagnostic tools, vaccination, and antiviral therapy.