Currently six human coronaviruses are known: HCoV-229E and HCoV-OC43 recognized already in 1960's, and four new pathogens: SARS-CoV (identified in 2003), HCoV-NL63 (identified in 2004), HCoV-HKU1 (identified 2005) and MERS-CoV, which emerged and was identified in 2012. Human coronaviruses are generally associated with respiratory tract infections, though some reports also suggest association of these pathogens with gastroenteritis. The severity of the disease depends on the viral species involved, though patient-related factors (e.g., age, general health status) are also of importance.

Within this project we will try to improve our understanding of the virus' biology and to answer a very important question: why two closely related viruses cause different disease?

How are we going to do this? There are several factors that determine, which cells will be infected and which species will be targeted. The most important here is the cellular receptor, the site where virus attaches to the host's cell. Critical analysis of the literature and our results strongly suggests that the second factor is constituted by proteins responsible for activation of the virus at appropriate time, releasing it to start the infection. Our studies will aim to understand how and where this activation occurs.

What will be the benefit? First, we will better understand the infection dynamics, second, we will be able to better assess the risk of interspecies transfer, third, we will try to develop novel and superior *in vitro* culture models allowing us to develop novel drugs or vaccines.