Klebsiella pneumoniae (*Kp*) is a Gram-negative bacterium from the Enterobacteriaceae family and a component of the human microbiome. Under specific conditions, *Kp* causes dangerous infections, such as sepsis, urinary tract infections, or infections leading to impaired liver function. This species is characterized by an alarming worldwide multidrug resistance. Therefore, *Kp* belongs to the group of pathogens called ESKAPE, i.e. those that escape modern methods of treating the infections they cause. The main virulence factors of *Kp* are capsules (K antigen, CPS, also called capsular polysaccharide and EPS - exopolysaccharide), lipopolysaccharide (LPS, O antigen, endotoxin) and fimbriae. O antigens of *Kp* are seen as a good candidate for promising therapeutic strategies based on active or passive immunization, which means using them as antigens for bactericidal monoclonal recombinant antibodies or vaccine antigens. For such therapy to be effective, it is necessary to have complete knowledge about O antigens, their occurrence and diversity. The O and K antigens determine the O and K serotypes of Kp, respectively. K1 and K2 antigens, which predominate among clinical isolates and hypervirulent strains, are also targets for therapeutic strategies for infections caused by Kp.

For years, the opinion that there was little diversity of O antigens (O serotypes) in Kp. Over the years, 9 O serotypes have been identified, distinguishing *Kp* from other Gram-negative bacteria. For example, 188 O serotypes have been identified for E. coli. Recent years, including research conducted by the leader of this project, have supplemented the knowledge about O antigens to 12 serotypes/subtypes [O1 (variant 1 and 2), O2a, O2afg, O2aeh, O3, O3a, O3b, O4, O5, O7, O8, O12, O13]. Five of them were described in detail by the Principal Investigator of the project (O1v2, O2v2, O3a, O3b, O13) including the effect of insertion sequences in genes for switch between O1/O2v2 to O1/O2v1 phenotype. However, this did not close the door to a very intriguing question: whether it is possible that there are additional new O serotypes in this pathogen. Open-source bioinformatics tools for *Klebsiella* O and K antigen coding sequences, such as Kaptive, provide the answer to this question: “Yes, they exist.”. Depending on the report, it is estimated that we may be dealing with from 2.4 to 17% of non-typeable strains in various collections of *Kp* clinical isolates. The project team established cooperation with the creators of the Kaptive tool (bioinformaticians and epidemiologists), who provided 11 clinical isolates constituting patterns of regions coding O and K antigens for the Kaptive database and algorithms. Preliminary research predicts that among them we will find 11 new O antigens and 8 new K antigens. Establishing cooperation will allow us to link genes with chemical structures and improve algorithms that are widely used by microbiologists for epidemiological surveillance. Additionally, it will be planned to investigate the susceptibility of strains with new serotypes O and K to the action of complement - a mechanism of the innate response of the human immune system and examination of O-antigen specific sera ability to bind and kill encapsulated Kp clinical isolates.

In 2017, the World Health Organization (WHO) classified multidrug-resistant *Kp* isolates as priority 1. Critical, taking into account the availability of drugs effective in preventing such infections. If newly developed therapies based on O and LPS and K antigens are to be effective, expanding knowledge about the structures and diversity of O serotypes is a necessary condition. By implementing the project's objectives, society will gain an advantage in knowledge about possible significant changes in the distribution of O/K serotypes among isolates causing infections, e.g. as a result of antigenic drift.