

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), associated with coronavirus disease 2019 (COVID-19), is a novel pathogen recently introduced to the human population. The emergence of SARS-CoV-2 evolved into a worldwide outbreak, with the first Polish cases in February/March 2020. The expanding use of genomic technologies has unprecedentedly allowed the rapid and continuous update of the phylodynamic evolution of this virus. Novel variants bear mutations affecting viral transmissibility and pathogenicity require constant phylogenetic updates to inform public responses and vaccine studies. During the first wave of the epidemic in Poland, the virus was less diverse genetically. On the other hand, in the second wave of pandemics observed in autumn 2020, the molecular diversity of the virus has increased in line with an explosive number of cases and significant mortality. From November 2020 to December 2021, the frequencies of the spike mutations increased by several folds, most likely reflecting the increasing dynamic of the infection in the population and a high number of circulating viral strains in the susceptible population. As shown, this increment was associated with the increasing prevalence of variants of concern like B.1.1.7(Alpha), B.1.617.2 (Delta), and lastly, BA.1 (Omicron), which naturally contains some of the spike mutations, the accumulation of deletions, and other substitutions. Recombination, the transfer of genetic information between molecules derived from different organisms, is a fundamental process in evolution because it can generate novel genetic variation. It has been proposed recently that the global SARS-CoV-2 genome sequence data contain signals of recombination across the pandemic. In the present study, we will present molecular surveillance data on SARS-Cov-2 variant evolution and search possibility of the recombination process in the five most populated European Union states, including Germany, France, Italy, Spain, and Poland.

Further, we will track specific mutations in the viral lineages analysis to characterize spike protein changes. We will be based on sequences from publicly available databases and genomes sequenced in our laboratory. Continuous tracing of emerging virus lineages should be focused on variants of interests and variants of concern, and the evolution of spike mutations. Phylodynamic studies identify the introductory events with the subsequent spread of the virus and its divergence into clades. Increasing molecular variability of pandemics might have resulted in the number of cases related to expanding infections with variants of concern and likely emerged by the recombination process.

Additionally, expanding the variants bearing mutations related to optimized transmissibility and potentially higher virulence might have contributed to the epidemic waves. Continuous surveillance allows the follow-up of virus evolutionary variability and the risks associated with the emergence of new variants. Consequently, the characterization of recombination in SARS-CoV-2 is essential for the temporal population dynamics of the currently ongoing pandemic.