# **NarCoS: Integrating genomic surveillance of SARS-CoV-2 positive clinical samples in Slovak republic**

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More than two years have passed since the World Health Organisation announced the global pandemic of SARS-CoV-2 virus with major impact on healthcare, economy in virtually all countries around the world. Genomic variability of the coronavirus led to emergence of novel phylogenetic variants with increased infection rate and partia evasion from specific immunity. Therefore, one of key tasks in pandemic management has been the genomic surveillance of clinical COVID-19 cases in all countries. Although our group had sequenced the first six clinical case as early as March 2020, systematically organised weekly sequencing has not started until March 2021. The sequencing efforts in Slovakia are coordinated by the national Public health authority. Based on lower number of cases in early 2021, the original planned sample throughput was project up to 500 samples per week and four laboratories were involved. With the emergence of Delta and Omicron variants the required sample number has grown almost four times. This led to increase in analysed samples in participating laboratories and adding of further two sequencing laboratories, but with limited experience with NGS technology and absent experience with bioinformatics processing. To ensure reliable per case analysis of clinical samples in six Illumina systems based sequencing laboratories, metadata transfer automation, unified variant calling and interpretation and batch upload to GISAID and ENA database as well as fast reporting to TESSY database, we developed an web based integrated information system for sequencing management, data and metadata transfer and automated batch reporting and uploading to relevant databases. Uniquely tuned in-house variant calling pipeline allowed us to unify the analysis of all samples from Slovakia. The name of the system is NarCoS. Aggregate results visualisations are used for reporting purposes for Healthcare ministry pandemic commission for prompt situation assessment and management. We continue to further develop the system, currently focusing on the integration of sequencing based wastewater monitoring for SARS-CoV-2 variants.