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BOOK OF ABSTRACTS



4th Belgrade Bioinformatics Conference

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FOREWORD

Dear colleagues and friends,

The 4th Belgrade Bioinformatics Conference - BelBi2023, where many high-quality scientific contributions were presented, has just ended. With great thanks to all participants, we now proudly present a book of abstracts that both reflects the scientific abundance and diversity of the conference and serves as a reminder of a memorable event.

Several research institutions, faculties, and scientific societies from Serbia joined forces in organizing this international conference, which covered numerous topics in computational biology, bioinformatics, and biomedical and health informatics. The main goal of BelBi2023 was to foster contact between scientists, both early stage career and senior researchers, allowing them to share experiences and latest advances in their fields. We sincerely hope that BelBi2023 has served as a platform for researchers from around the world to meet, initiate new collaborations, and expand professional contacts, and that all of you would become a part of the growing BelBi community.

We are grateful and proud to have welcomed more than 250 researchers from 21 countries. We have had 28 scientific sessions, consisting of more than 60 lectures (including eight Keynote talks), 47 presented posters, as well as three workshops and one satellite event – COST action. We have also organized seven industry lectures, including the NGS Challenge,

two Meet the Expert Sessions, and one Business Coffee Break where ten start-up companies took part. And finally, the future BIO4 campus was presented and first panel on Serbia's resources for storage and analyses of genetic data was organized.

We would like to thank all the members of the International Advisory Board and the International Program Committee for their efforts and help in making this event a success. We are very grateful to the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, SAIGE project, and UNDP-Serbia for their support. Finally, the Local Organizing Committee is very grateful to all the sponsors of the conference - BGI, Illumina & Elta'90MS, PacBio & East Diagnostics, ThermoFisher Scientific & Vivogen, Huawei, Labena, DSP Chromatography, RNIDS, Telekom Srbija, Alfa Genetics, Kefo and Superlab, hoping that they will stay with us for many years to come.

Looking forward to seeing you again at the 5th Belgrade Bioinformatics Conference.

Belgrade, July 2023

*Dr. Valentina Đorđević
& Dr. Ivana Morić,*
On behalf of BelBi2023
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Genomic Surveillance and Phylogenetic Analysis of SARS-CoV-2 Variants in Serbia: Insights into Evolutionary Dynamics and Genetic Diversity

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The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has caused a global pandemic, resulting in significant morbidity and mortality worldwide. Understanding the evolutionary dynamics and genetic diversity of the virus were crucial for virus control and management strategies. With that aim we conducted genomic surveillance and phylogenetic analysis of SARS-CoV-2 variants in Serbia, spanning from March 2020 to the end of January 2023.

Sequencing was conducted using three different platforms: Oxford Nanopore, Ion Torrent AmpliSeq and BGISEQ-500. Consensus sequences obtained using platforms respective software were deposited in the GISAID database. In this study 2109 good-quality sequences were included (doi:10.55876/gis8.230411qh). Pangolin and Nextclade software were utilized for clade, lineage and variant determination, while sequence alignment and construction of the phylogenetic tree was performed using Nextstrain web-based application.

Variant analysis revealed over 125,000 mutations across the 2109 sequences, of which 38% occurred in the S protein encoding gene. The most common mutations involved intragenic single nucleotide variants (88%), followed by intragenic deletions (5%). All sequences were assigned to following 16 clades: 20A, 20B, 20C, 20D, 20E, 20G, 20I, 21J, 21K, 21L, 22A, 22B, 22C, 22D, 22E, and 22F.

Temporal analysis of the variants in Serbia revealed that the Alpha variant was predominant during 2020 and the first three months of 2021. The Delta variant emerged in June 2021, dominating until the end of December 2021, when Omicron variant was detected for the first time, overtaking the dominance for the remaining surveillance period. Notably, the Gamma and Epsilon variants were not detected in the analyzed samples.

Phylogenetic analysis demonstrated that the SARS-CoV-2 variants circulating in Serbia were largely comparable to the variants found in Europe. However, a slight delay in their emergence was observed, potentially attributed to a lower travel rate during that period and a decreased frequency of sequencing in certain months.

Keywords: Sars-CoV-2 variants, Next-generation sequencing, phylogeny, surveillance, Serbia

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