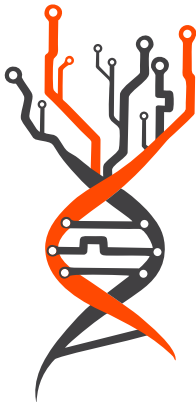


#BelBi2024 • Belgrade, Serbia

BOOK OF ABSTRACTS



5th Belgrade Bioinformatics Conference

17 - 20 JUNE 2024

EDITORS

Dr. Ivana Morić

Dr. Valentina Đorđević

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FOREWORD

We are pleased to announce the successful conclusion of the 5th Belgrade Bioinformatics Conference - BelBi2024, where numerous high-quality scientific contributions were presented. We sincerely thank all participants and proudly present a book of abstracts that not only reflects the scientific richness and diversity of the conference, but also serves as a lasting memento of this remarkable event.

This international conference was jointly organized by several research institutions, faculties, and scientific societies from Serbia. It covered a wide range of topics from the fields of computational biology, bioinformatics, biomedical informatics, and health informatics. The main goal of BelBi 2024 was to promote contacts between scientists of all levels, provide a platform for the exchange of experiences and present the latest advances in their fields. We hope that BelBi2024 was a valuable platform for researchers from all over the world to meet, build new collaborations and expand professional networks.

We are grateful and proud that we were able to welcome over 250 researchers from 21 countries from three continents. The conference included 24 scientific sessions with more than 68 oral presentations (including eight keynote lectures), 54 poster presentations, three hands-on workshops and three satellite events – the MICOS-EU competition, the TranSYS final conference and Shere the IDEA session. We also organized two industry presentations and two

panel discussions - “Building Skills for the Future: Masters 4.0 in Bioinformatics” and “BIO4 Campus: Transforming Science into Business”. We also presented the first BelBi art exhibition inspired by scientific discoveries, entitled “IMGGE Magnificent Cell Dance”. And finally, we are particularly proud of the “Future Keynote Speakers” program, which enabled students from faculties across Serbia to attend this year’s keynote lectures and panel discussions for free.

We would like to thank all the members of the International Advisory Board and the International Program Committee for their efforts and help that contributed to the success of this event. We are very grateful to the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, the SAIGE project and the Chamber of Commerce and Industry of Serbia for their support. Finally, the local organizing committee is very grateful to all sponsors of the conference - BGI & MGI, Elta’90MS, PacBio & East Diagnostics, Alfa Genetics, Vivogen, LKB, Altium, Telekom Srbija, Labena, AlphaMed, Galen Fokus, Superlab, Kefo, RNIDS, Danau Lab Beograd, RTC and Biomedica, and we hope that they will stay with us for many years to come.

Thank you once again to all who contributed to the success of BelBi2024. We look forward to seeing you at future conferences.

Warm regards,
Belgrade, July 2024

*Dr. Valentina Đorđević
& Dr. Ivana Morić,*
On behalf of BelBi2024
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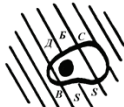
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Flash talks

Genome-wide association study identified genetic signal in cystatin genes associated with Long COVID-19

Marija Laban-Lazovic¹, Marko Zecevic^{2,3}, Nikola Kotur², Vladimir Gasic², Bojan Ristivojevic², Vesna Skodric-Trifunovic^{1,4}, Tatjana Adzic-Vukicevic^{1,4}, Branka Zukic², Sonja Pavlovic² and Biljana Stankovic^{2,*}

¹ Clinic of Pulmonology, University Clinical Centre of Serbia, Belgrade, Serbia

² Institute of Molecular Genetics and Genetic Engineering, University of Belgrade, Serbia

³ Velsera, Belgrade, Serbia

⁴ Faculty of Medicine, University of Belgrade, Serbia

biljana.stankovic@imgge.bg.ac.rs

Long COVID-19 is characterized by symptoms that persist for more than three months after the acute phase of a SARS-CoV-2 infection. It can affect individuals who had both severe and mild cases of COVID-19. The genetic predisposition to this condition remains largely unexplored.

This study aimed to identify genomic loci associated with Long COVID-19. The study included 92 patients with confirmed infection with SARS-CoV-2 during the delta variant wave and treated in hospital settings. These patients were monitored for up to six months after the acute infection. All patients were genotyped using the Illumina Infinium global screening array, which covers over 700,000 genomic variants. Imputation was employed to expand the number of variants to 12,001,939 using the 1kGP Phase 3 human reference panels. We conducted a genome-wide association analysis using an in-house built pipeline on the Cancer Genomic Cloud platform.

Our results identified association signals in the 20p11.21 genomic locus, with the lead variant being rs1275745396 ($p = 6.181 \times 10^{-8}$), located within cystatin genes (*CST3*, *CST4*, *CST1*). The cystatin family consists of cysteine protease inhibitors, involved in various physiological processes. Previous literature has linked serum and saliva cystatin levels to COVID-19 severity and outcomes. Moreover, cystatin's role in taste perception has been recognized previously, which is in line with the well-known perturbations in sensory perception caused by COVID-19. This study is the first to find a genetic association between cystatin genes and Long COVID-19. Further research is necessary to elucidate the role of the cystatin protein family and the biological processes underlying Long COVID-19. A deeper understanding of Long COVID-19 can inform the development of preventive and therapeutic strategies.

Keywords: GWAS, Long COVID-19, cystatins

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