Trends in **Molecular Biology** • Special issue

Abstract Book

CoMBoS2

2nd Congress of Molecular Biologist of Serbia

ISBN-978-86-82679-15-8

Belgrade • 2023

CoMBoS2 – the Second Congress of Molecular Biologists of Serbia, Abstract Book – Trends in Molecular Biology, Special issue
06-08 October 2023, Belgrade, Serbia
Online Edition
https://www.imgge.bg.ac.rs/lat/o-nama/kapacitet-i-oprema/istrazivacka-delatnost
https://indico.bio.bg.ac.rs/e/CoMBoS2

IMPRESSUM

PUBLISHER:
Institute of Molecular Genetics and Genetic Engineering (IMGGE), University of Belgrade

FOR THE PUBLISHER:
Dr. Sonja **Pavlović**

EDITOR:
Dr. Zorana **Dobrijević**

EDITORIAL REVIEW BOARD:
Prof. Dr. Silvana **Andrić**
Dr. Valentina **Ćirković**
Dr. Ivica **Dimkić**
Prof. Dr. Branko **Jovčić**
Prof. Dr. Gordana **Matić**
Ass. Prof. Dr. Milena **Milutinović**
Dr. Aleksandra **Stanković**
Dr. Nemanja **Stanisavljević**
Dr. Maja **Stoiljković**

EDITOR IN CHIEF:
Prof. Dr. Dušanka **Savić-Pavićević**

DESIGN:
Ivan **Strahinić**

Institute of Molecular Genetics and Genetic Engineering (IMGGE),
University of Belgrade
Belgrade, 2023
ISBN 978-86-7078-173-3

CoMBoS2

Content

PRECISION MEDICINE AND COVID-19: IMPORTANCE OF HOST GENOME PROFILING

Branka Zukic[1]

[1]*Institute of Molecular Genetics and Genetic Engineering, University of Belgrade, Belgrade, Serbia*

Introduction: The clinical picture and the course of the disease in COVID-19 patients, caused by coronavirus SARS-CoV-2, vary from asymptomatic to fatal outcome. As the same agent cause the disease, the individual genomic profile of the patient could contribute to better understanding of this phenomenon. The current knowledge about genetic markers responsible for a wide range of clinical pictures, as well as possible application of individualized treatment, will be presented.

Methods: Variants in genes responsible for predisposition and response to SARS-CoV-2 infection, pharmacogenetic variants related to drugs used in the treatment of COVID-19, nutrigenetic markers in genes relevant for the metabolism of the micronutrients (vitamin D, selenium and zinc) were investigated using GWAS, PCR and sequencing. Genotype data were extracted from database previously obtained using TruSight One Gene Panel (Illumina).

Results: Eleven pharmacogenomics markers in 7 pharmacogenes relevant for COVID-19 treatment and 10 variants affecting the structure and/or function of proteins important for susceptibility and resistance to SARS-CoV-2 infection were identified. Several variants in genes related to micronutrients were associated with severe COVID-19. Moreover, GWAS detected a significant genetic signal associated with COVID-19 related pneumonia.

Conclusion: Multidisciplinary approach, modern sequencing technologies, comprehensive studies with well-characterized patients' groups, as well as the design of robust bioinformatics tools, enable identification of novel human genetic markers associated with COVID-19. Newly gained knowledge will empower the development of the targeted therapy, as well as the implementation of nutrigenomics/pharmacogenomics, leading to the application of precision medicine in the treatment of COVID-19 patients.

Key words: COVID-19; precision medicine; pharmacogenomics; nutrigenomics; GWAS

Acknowledgements: This study was supported by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia (Agreement no. 451-03-47/2023-01/200042).