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CoMBoS2

Content

WELCOME SPEECH

Professor Dušanka **Savić-Pavićević**
President of the Serbian Society
for Molecular Biology

Dr. Melita **Vidaković**
President of the Steering Committee
of the Serbian Society for Molecular Biology

Dear colleagues and friends,

On behalf of the Serbian Society for Molecular Biology (MolBioS), we warmly welcome you to Belgrade for the Second Congress of Molecular Biologists of Serbia (CoMBoS2).

The congress is gathering almost 250 participants from 13 countries (Sweden, United Kingdom, Italy, Switzerland, USA, Australia, Hungary, Czech Republic, Romania, Montenegro, Croatia, Bosnia and Herzegovina, and Serbia).

The program covers various fields of Molecular Biology, including Molecular Biomedicine, Molecular Biotechnology and Molecular Cell Biology, and consists of plenary and invited lectures, the MolBioS award winner lecture, poster sessions and the project corner. Special attention is paid to students and young scientists through the MolBioS Student Session, flash presentations and workshops on state-of-the-art molecular biology methods.

We wish you to be inspired by exciting and outstanding lectures given by renowned scientists and experts, exchange ideas, find opportunities for new collaborations, and have good fun.

WELCOME TO

CoMBoS2

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MolBioS is committed to preserving the memory of the great Serbian scientists who paved the way for fruitful research and education in Molecular Biology in Serbia.

CoMBoS2 is dedicated
to our outstanding teachers
and great scientists

Professor **Ana Savić** (1936-2022)
and Professor **Vladimir Glišin** (1930-2020)

Professor Ana Savić (left photo)
and Professor Vladimir Glišin (right photo)
and the first-generation students
of the study program
Molecular Biology and Physiology
May 1975, Kotor, Yugoslavia

FADS2 GENE VARIANT rs174593 IS ASSOCIATED WITH MULTIPLE SCLEROSIS

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Introduction: The hallmark pathogenic mechanisms of multiple sclerosis (MS) are proposed to be associated with long chain polyunsaturated fatty acids(LC-PUFA)-mediated neuroinflammation, through LC-PUFA-derived pro- and anti-inflammatory eicosanoids. Variants in genes coding for fatty acid desaturases (FADS), the key enzymes in LC-PUFA biosynthesis from essential fatty acids, are associated with changes in circulating LC-PUFA levels. The aim of this study was to investigate the *FADS2* intronic variants, rs174576 (C/A), rs174593 (T/C) and rs174616 (G/A), in association with MS.

Methods: The study involved 124 patients with relapsing-remitting form of MS and 83 healthy control subjects. The *FADS2* gene variants were detected using TaqMan® SNP genotyping assays. Analysis of allele and genotype distributions in patients and controls was done by using the chi-square test.

Results: According to the model of dominant effect of allele, genotypes containing the alternative, C, allele of *FADS2* rs174593 variant were significantly less frequent in MS patients than in controls (MS: TT=57,26%, TC+CC=42,74%; controls: TT=42,17%, TC+CC=57,83%; p=0,03). In addition, the frequency of rs174593 C allele was significantly lower in patients, compared to controls (MS: T=0,76, C=0,24; controls: T=0,67, C=0,33; p=0,04). The frequency distributions of rs174576 and rs174616 alleles and genotypes were not significantly different between the study groups (p>0,05).

Conclusion: The obtained results supply a rationale for further investigation of the association of *FADS2* rs174593 with circulating LC-PUFA levels, in the context of MS. The genotype-LC-PUFA phenotype association could provide guidelines for personalized LC-PUFA supplementation, to potentially ameliorate the disease course and improve the effectiveness of therapy.

Key words: gene; variant; *FADS2*; multiple sclerosis

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