

BOOK OF ABSTRACTS



CONGRESS

OF THE SERBIAN GENETIC SOCIETY

2019 | October
13–17

VRNJAČKA BANJA • SERBIA





Publisher
Serbian Genetic Society,
Belgrade, Serbia
www.dgsgenetika.org.rs

Editors
Branka Vasiljević
Aleksandra Patenković
Nađa Nikolić

Printing
Serbian Genetic Society,
Belgrade, Serbia

Number of copies printed
300

Design
Ivan Strahinić
Ana Kričko

ISBN
978-86-87109-15-5

BOOK OF ABSTRACTS

Abstracts of the 6th CONGRESS OF THE SERBIAN GENETIC SOCIETY



2019 | October
2019

VRNJAČKA BANJA • SERBIA

**MORPHOLOGICAL AND GENETIC ANALYSIS OF FRESHWATER SPONGES
IN SERBIA**

Stefan Andjus¹, Jelena Đuknić¹, Bojana Tubić¹, Nađa Nikolić², Ana Marjanović³,
Marija Branković³, Vera Nikolić⁴, Momir Paunović¹

¹ *University of Belgrade, Institute of Biological Research „Siniša Stanković”,
Belgrade, Serbia*

² *University of Belgrade, School of Dental Medicine, Belgrade, Serbia*

³ *University of Belgrade, School of Medicine, Belgrade, Serbia*

⁴ *University of Belgrade, Faculty of Biology, Belgrade, Serbia*

stefan.andjus@ibiss.bg.ac.rs

Sponges in Serbian rivers and lakes have not been extensively studied. Hence, the aim of this work was to undertake an investigation of the distribution and phylogenetics of sponge species in Serbian waterbodies. A total of 83 localities on 17 rivers and 10 lakes have been investigated. Sponges (62 specimens) were found at 22 localities only. Sponge determination was done using a combination of morphological and genetic studies. Light microscopy and scanning electron microscopy were applied for spicule analysis while the D3 domain of 28S DNA was amplified and sequenced for genetic determination. The following five sponge species were identified: *E. fluviatilis*, *S. lacustris*, *E. muelleri*, *T. horrida* and *E. fragilis*. The sequence of the Serbian *E. fragilis* differed in two base pairs compared to Estonian *E. fragilis* (sequence obtained from the database of the National Center for Biotechnology Information, U.S. National Library of Medicine – NCBI), the previously deposited sequence on NCBI from Estonian *E. fragilis*. The sequence of *T. horrida* from our study is the first partial 28S sequence deposited for this species in the NCBI. A phylogenetic tree based on the 340bp sequences was also generated. It showed distinctive clades and was concordant with the results of the morphological analysis.

FRESHWATER SPONGES, 28S rDNA, PHYLOGENETICS