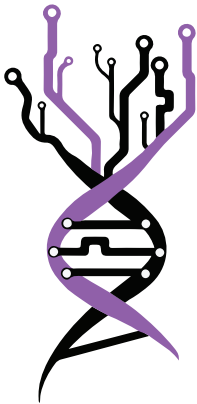


#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



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Dr. Ivana Morić

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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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**Root colonization ability of herbicide-resistant PGP bacteria
evaluated by 16S rRNA metabarcoding**

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In terms of agricultural sustainability, herbicide-resistant, plant growth promoting (PGP) bacteria that can improve crop yield are valuable resource. To exhibit PGP traits, the bacteria must be able to colonize and survive in the rhizosphere.

Upon screening the herbicide-resistant bacterial collection, candidates with the highest PGP potential were grouped into three consortia to evaluate their ability to colonize roots and persist in the natural/local plant microbiome in the pot. Experiments were conducted with seeds of commercial maize hybrids under controlled conditions, with and without herbicide. Colonization ability was evaluated by examining multiple plants from each treatment at two-time points during the experiment. 16S rRNA amplicon community profiling was performed to precisely target the bacterial strains used in the three consortia and investigate how the local microbiome might be altered by the application of the consortia. Bioinformatic analysis was performed using qiime2, clustering of reads into amplicon sequence variants ASVs using the DADA2 plugin, and the taxonomic assignment was based on a customized dataset formed from the 16S rRNA gene sequences of the ten isolates used in this study or by using the Silva rRNA database. For clustering and comparison of ASVs based on sequence similarity, the program cd-hit was used, with the sequence similarity parameter set to 98% to be considered part of the same cluster. The obtained dataset was imported into R using the package qiime2R, and subsequent analyzes and graphs were generated using either the R packages phyloseq, microbiome, or reshape2. We identified seven out of ten inoculated strains in both time points tested and with comparable abundance, indicating that most of the bacterial isolates tested have the ability to colonize the root system of maize. Furthermore, the natural/local microbiome of maize plants is not disturbed by the three consortia used in this study, implying that they are good candidates for future biotechnological applications.

Keywords: metabarcoding, 16S, consortium, bacteria, PGP

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