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BOOK OF ABSTRACTS



4th Belgrade Bioinformatics Conference

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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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De novo Genome Assembly of Sweet Chestnut (*Castanea sativa* Mill.) Insights into the Molecular Basis of its Nutritional Properties

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The Sweet Chestnut (*Castanea sativa* Mill.) is a tree species that holds significant economic importance and naturally spreads throughout central-southern Europe and Asia Minor. Its highly nutritious nuts have a unique composition that sets them apart from other nuts, being rich in vitamins, including vitamin C, and B vitamins such as thiamine, niacin, and folate. Over the last few decades, breeding efforts have prioritized the development of sweet chestnut cultivars that are resistant to blight and produce better nuts. However, despite these efforts, molecular genetic studies of the sweet chestnut have been insufficient. To bridge this knowledge gap, we set out to create the first reference genome of the sweet chestnut using whole-genome shotgun paired-end sequencing. Our study involved genome-wide analyses to identify and functionally annotate genes in sweet chestnut, and develop and confirm SSR-SNP markers. Additionally, we have identified and characterized specific genomic loci that enhance the nutritional value of sweet chestnuts. To the best of our knowledge, this is the first study to investigate the genetic loci responsible for determining the nutritional value of chestnuts. We anticipate that our findings will significantly contribute to the development of sweet chestnut cultivars with higher levels of bioactive compounds, minerals, and digestibility, ultimately enhancing the nutritional value of chestnuts.

Keywords: Genome sequencing, sweet chestnut, genomic loci, nutritional value



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