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3rd CONGRESS OF GENETICISTS IN BOSNIA AND HERZEGOVINA WITH INTERNATIONAL PARTICIPATION

The Official Publication of the
Institute for Genetic Engineering and Biotechnology
University of Sarajevo

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3rd Congress of Geneticists in Bosnia and Herzegovina with International Participation – CONGUB&H

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3RD CONGRESS OF GENETICISTS IN BOSNIA AND HERZEGOVINA WITH INTERNATIONAL PARTICIPATION – CONGUB&H

2ND - 4TH OCTOBER 2023, SARAJEVO, BOSNIA AND HERZEGOVINA

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Publisher of *Genetics & Applications*

Institute for Genetic Engineering and Biotechnology, University of Sarajevo

Zmaja od Bosne 8, 71000 Sarajevo, Bosnia and Herzegovina

www.ingeb.unsa.ba

Phone: +387 33 220-926

Fax: +387 33 442-891

ingeb@ingeb.unsa.ba

The abstracts underwent a streamlined submission process, wherein authors retained full responsibility for both the content and the language therein.

Dear colleagues,

With great pleasure and enthusiasm that we extend our warmest welcome to all participants of the Third Congress of Geneticists in Bosnia and Herzegovina with International Participation. This Book of abstracts, as a special issue of the Genetics and Applications, stands as a testament to the remarkable collective effort and intellectual curiosity that brings us together.

In the pages that follow, you will find a diverse and inspiring array of abstracts that represent the cutting-edge research, innovative ideas, and profound insights into various fields and disciplines of genetics. These abstracts reflect the passion and dedication of scholars, researchers, and practitioners who are shaping the present and the future of genetics.

As you delve into the abstracts within these pages, we encourage you to engage, question, and explore. Let this book be your guide through the boundless world of ideas, and may it inspire you to embark on your own journey of inquiry and innovation.

We extend our heartfelt gratitude to all the contributors who have shared their work with us, as well as to the organizing committee, volunteers, and sponsors who have made this event possible. Your dedication and commitment are the driving force behind the success of this abstract book and the Congress in general.

We hope that the knowledge and inspiration you gain from the contents of this book will serve as a catalyst for further research, collaboration, and personal growth. Together, let us continue to push the boundaries of knowledge and make a positive impact on our world.

Thank you for joining us in this celebration of intellectual exploration and discovery. We wish you an enriching and thought-provoking journey through the abstracts.

Warm regards,

Prof. dr. Kasim Bajrović,
Editor-in-Chief

Environmental Genetics and Ecotoxicology *Poster presentation*

REVERSE TRANSCRIPTION-QUANTITATIVE PCR (RT-QPCR) WITHOUT THE NEED FOR REMOVAL OF TEMPLATE DNA

Đermić Damir[1], Santini Nunzia[2], Esposito Alessandro[2], Feliciello Maria Chiara[3], Ljubić Sven[1], Feliciello Isidoro[2]

[1]*Ruđer Bošković Institute Division of Molecular Biology, Bijenička cesta 54, Zagreb, Croatia*
[2]*Department of Clinical Medicine and Surgery, University of Naples Federico II, Naples, Italy*
[3]*Department of Statistical Science, Alma Mater Studiorum, University of Bologna, Bologna, Italy*

One of the major problems in transcriptome analysis is inability to completely eliminate template DNA, which is indistinguishable from cDNA, thus resulting in false positive signals. We developed a novel method for transcriptome analysis by RT-qPCR (Reverse-Transcription quantitative Polymerase Chain Reaction), which circumvents the need for elimination of potential DNA contamination, therefore being more precise, simpler and more reproducible than the commonly used methods. The novel procedure involves the use of a modified specific primer during reverse transcription step, which contains mismatched bases, thus producing cDNA molecules not perfectly homologous to genomic DNA. By using the same modified primer in PCR amplification step, only cDNA template is amplified since genomic DNA template is not recognized by the primer. We determined the expression of *Escherichia coli recA* and *sulA* single-copy genes by RT-qPCR using either modified primers, or following the standard procedure. No *recA* and *sulA* sequence amplification was observed using our method unless cDNA was created by reverse transcription. The level of *recA* and sulA sequence amplification was unaffected by genomic DNA elimination from the sample. Conversely, the current method, which uses standard random/oligo-dT primers, showed a false positive signal even when reverse transcription step was skipped and the genomic DNA was (obviously incompletely) eliminated by DNase I treatment. Hence, our method of using a modified primer during cDNA synthesis produces a cDNA-specific PCR signal that is unaffected by genomic DNA and therefore quantifies gene expression much more accurately than the standard, commonly used method.

Keywords: *Escherichia coli*; improved transcriptome analysis; modified primers

Presenting author's e-mail: dermic@irb.hr