

Trends in Molecular Biology · Special issue

Abstract Book

CoMBoS2

2nd Congress of Molecular Biologist of Serbia

ISBN-978-86-82679-15-8

Belgrade • 2023



CoMBoS2 – the Second Congress of Molecular Biologists of Serbia, Abstract Book – Trends in Molecular Biology, Special issue

06-08 October 2023, Belgrade, Serbia

Online Edition

https://www.imgge.bg.ac.rs/lat/o-nama/kapacitet-i-oprema/istrazivackadelatnost

https://indico.bio.bg.ac.rs/e/CoMBoS2

IMPRESSUM

PUBLISHER:

Institute of Molecular Genetics and Genetic Engineering (IMGGE), University of Belgrade

FOR THE PUBLISHER:

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CoMBoS2

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Abstracts

THE ROLE OF THE GUT BACTERIA DURING HOST AGING

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Introduction: Microbial community established in the gut has been recognized as an important factor which influence host aging. Bacteria from the gut co-evolved with the host resulting in mutually beneficial interactions essential for host's wellbeing. This complex crosstalk reflects mainly through the interaction between bacterial macromolecules (e.g., exopolysaccharides) and the host receptors leading to the activation of various cellular pathways. Here, we explore the potential of different lactobacilli, commonly used as probiotics, to activate longevity signalling in *Caenorhabditis elegans*.

Methods: Evaluation of *C. elegans* lifespan and aging parameters (locomotion rate and pharyngeal pumping) were performed by feeding N2 wild-type worms with different *Lactobacillus* species. Worms fed with selected strains were subjected to RNAseq analysis, qPCR and Western blot to evaluate activation of autophagy, immunity, antioxidative response and mitochondrial function. Activation of autophagy was confirmed in DA2123 GFP-labelled LGG-1 transgenic strain and JIN1375 *hlh-30* (tm1978) mutant, while immunity activation was evaluated by using KU25 *pmk-1* (km25) mutant and through nematode killing assays.

Results: Selected strains of lactobacilli promoted health and lifespan of worms through activation of TFEB/HLH-30 dependent autophagy and p38 MAPK/PMK-1 dependent immune response which provided resistance of worms exposed to pathogens. Moreover, RNAseq analysis identified core gene signature associate with exopolysaccharide-induced longevity highlighting involvement of *fmo-2*, *gsto-1*, *nlp-29*, and *clec-47* genes in increased lifespan of the worms.

Conclusion: Analyzed lactobacilli showed potential to promote healthy aging and could be further investigated in order to better understand application of lactobacilli as pro-longevity probiotics.

Key words: Lactobacillus; Caenorhabditis elegans; autophagy; immunity; aging

Acknowledgements: This study was supported by Ministry of Science, Technological Development and Innovation of the Republic of Serbia (Agreement no. 451-03-47/2023-01/200042).