

CURRICULUM VITAE

GERGŐ MIHÁLY BALOGH

Date and place of birth

5th March 1994, Budapest, Hungary

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Education

- **2006-2012:** Krúdy Gyula Secondary School, Nyíregyháza, Hungary
- **2012-2015:** University of Szeged, biology BSc, molecular biology specialization
- **2015-2017:** University of Szeged, biologist MSc, molecular-, immune- and microbiology specialization
- **From 2017:** University of Szeged, Doctoral School of Clinical Medicine

Work history

- **September 2013 – Januar 2016:** Research student, Arabidopsis Molecular Genetics Group, Institute of Plant Biology, HAS BRC, Szeged, Hungary
- **February 2016 – June 2017:** Research student, Algal- and Microbial Genomics Group, Institute of Biochemistry, HAS BRC, Szeged, Hungary
- **September 2017 – July 2021:** PhD student, Department of Dermatology and Allergology, University of Szeged, Hungary
- **August 2021 – December 2021:** assistant research fellow, Department of Dermatology and Allergology, University of Szeged, Hungary
- **From January 2022:** scientific administrator, Systems Immunology Research Group, Institute of Biochemistry, ELKH BRC, Szeged, Hungary

Current research

Our group investigates adaptive immune recognition using computational methods. In the last few years we mainly focused on HLA class I molecules. These proteins present short fragments of peptides, generated in human cells, to cytotoxic T cells. In case of viral infection or the presence of altered self-peptides (in tumors), foreign HLA-bound peptides can appear on the cell surface, serving as a danger signal for T cells. HLA class I molecules show huge diversity in human populations. The peptide binding specificity of these variants might differ. Through the investigation of bound peptide repertoire of HLA molecules, we aim:

1. to show how the presence of different HLA variants in a subject might alter the clinical outcome of patients with infectious diseases or tumors,
2. and to identify immune evasion strategies in the genomes of infectious agents.

Various computational algorithms were developed based on the accumulating *in vitro* data in the last few years. These methods are capable of predicting, what is „visible” for the adaptive immune system through HLA-binding.

In the last 2 years, I used our computational immunology toolbox (R programming language, NetMHCpan algorithm, BLAST etc.) to identify the effects of SARS-CoV-2 mutations on the adaptive immune recognition of the virus. The mutation space of SARS-CoV-2 is dominated by C→U nucleotide changes, mostly generated by an enzyme family of the human innate immunity, APOBEC3. I investigate whether these nucleotide changes increase or decrease the adaptive immune recognition of the virus, and whether there are any evolutionary connections between APOBEC3 activity and the amino acid specificity of different HLA variants.

Prizes

- XXXII. National Conference of Scientific Students' Associations, Biology section, Molecular biology II. subsection (2nd place, 2015)
- Sóni József Scholarship (2015/16)
- Scholarship granted by the city council of Szeged (2016)
- Scholarship of the New National Excellence Programme for MSc students (2016/17)
- Fellowship granted by the Republic (2016/2017)
- SZTE Talent Scholarship (2017)
- Scholarship of the New National Excellence Programme for PhD students (2019/20)
- Stephen W. Kuffler PhD Scholarship (2022)

Important scientific conferences

- Effect of HLA promiscuity on antitumor immunity. Magyar Immunológiai Társaság 47. Vándorgyűlése, Bükkfürdő, Hungary (2018; talk).
- Neoantigen sequence similarity to pathogens and commensals determines immune phenotype of cancer samples and patient survival. AACR Special Conference on Tumor Immunology and Immunotherapy, Boston, USA (2019; poster).
- Neoantigen sequence similarity to pathogens and commensals determines immune phenotype of cancer samples and patient survival. 4th Annual Symposium on Physical Concepts and Computational Models in Immunology, online (2020; poster).
- Láthatóvá tenni a láthatatlant: az APOBEC3 mutagenezis hatása a SARS-CoV-2 adaptív immunfelismerésére. Magyar Immunológiai Társaság 50. Vándorgyűlése, Kecskemét, Hungary (2021; talk).

Released publications

- Manczinger, Máté, et al. "Negative trade-off between neoantigen repertoire breadth and the specificity of HLA-I molecules shapes antitumor immunity." *Nature Cancer* 2.9 (2021): 950-961. (co-first author)
- Koncz, Balázs, et al. "Self-mediated positive selection of T cells sets an obstacle to the recognition of nonself." *Proceedings of the National Academy of Sciences* 118.37 (2021; co-author).

Language skills

- English: intermediate level (B2, complex-type certificate, 2008.)
- Russian: advanced level (C1, complex-type certificate, 2010.)
- Ukrainian: basic level (B1)

Teaching

- R mini-course for students of the Radnóti Miklós Experimental Secondary School, Szeged, Hungary (2019)
- Teaching bioinformatics for Saudi students at the Mawhiba Olympiad Training Camp (King Abdullah University of Science and Technology, Thuwal, Saudi Arabia, 2022)