Kristóf A. Törkenczy

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Current Position	
New York Genome Center	

New York, NY New York Genome Center Post-Doctoral Researcher 2020-present Advisor: Dr. Rahul Satija

Education

Oregon Health & Science University (OHSU)

Portland, OR PhD, Molecular and Medical Genetics 2014-2020 Dissertation: Single-cell approaches for deciphering complex

tissue heterogeneity Advisor: Dr. Andrew Adey

Eötvös Loránd University Budapest (ELTE)

2012-2014 M.Sc., Biophysics

Budapest, HU

Copenhagen, DK

Dissertation: Modeling Speciation: resources versus habitats

Advisor: Dr. Géza Meszéna

University of Edinburgh Edinburgh, UK

M.Sc., Quantitative Genetics and Genome Analysis 2011-2012 Dissertation: Could More Apparent Adaptive Evolution on the X

Chromosome Reflect a Recent Population Bottleneck? Advisor:

Dr. Brian Charlesworth

University of Copenhagen, Niels Bohr Institute

Erasmus Grant (physics, biological networks) 2009-2010

Eötvös Loránd University Budapest

Budapest, HU B.Sc., Theoretical Physics 2007-2011

Dissertation: Fitting the Radial Profile of Spiral Galaxies Advisor:

Dr. Zsolt Frei

Academic/teaching experience

Saturday Academy Cancer Genetics Course, Instructor	2017
Cancer Genetics Summer Course, Invited speaker	2018
Molecular Med Tri-Con Single-Cell Short Course, Instructor	2018

2018

2018

Erasmus Scholarship	2009-2010
Erasmus Programme	
BBSRC Masters Training Grant	2011-2012
Biotechnology and Biological Sciences Research Council (UK)	
Tartar Trust fellowship	2016
Oregon Health & Science University	
Helmsley Fellowship	2017
Helmsley Charitable Trust	

Research Leadership Scholarship

Awards and Grants

2017-2018 Oregon Health & Science University

ASHG Reviewers' Choice Abstract

American Society of Human Genetics

OHSU Three Minute Thesis Challenege Winner Oregon Health & Science University

OHSU Health&Wellness Mini-grant 2018

Oregon Health & Science University

IABCR Travel Award 2019

Oregon Health & Science University

Graduate Research Experience

New York Genome Center Post-Doctoral researcher, advisor: Dr. Rahul Satija

New York, NY

2020-present

research topic: Cross-species integration of multi tissue single-cell epigenetic landscapes

- Working on computational framework to integrate single-cell ATAC-seq datasets across tissues
- Identify and annotate shared and species-specific regulatory elements
- Validate finding using CRISPRi

research topic: Mapping epigenetic regulation of wild type and IDH mutant glioblastomas (Dr. Viviane Tabar and Dr. Kenny Yu collaboration)

> Working on computational framework to identify important regulatory TF networks across glioblastoma subtypes via single-cell RNA and single-cell ATAC integration

Oregon Health & Science University

Portland, OR

Graduate researcher, advisor: Dr. Andrew Adey

2015-2020

research topic: Characterization of single-cell epigenetic landscape of triple negative breast cancer

> Developed computational framework for single-cell combinatorial indexed ATACseq analysis

 Describe and delineate the epigenetic drivers for drug persisting triple negative breast cancer cell populations

research topic: Detection of structural variation in single cells

Built CNV detection pipeline for single-cell DNA sequencing data
 Characterized somatic variation in healthy and diseased tissues

Eötvös Loránd University Budapest

Budapest, HU

Masters researcher, advisor: Dr. Géza Meszéna research topic: Speciation and adaptive dynamics

2012-2014

- Developed mathematical model for "mixed" speciation
- Simulated a two patch-two resource multi parametric model to test for criterion of speciation

Oregon Health & Science University

Portland, OR

Summer intern, advisor: Dr. Paul Spellman

summer 2013

research topic: searching for mutational signatures in data from patients

with VHL disease associated familial clear cell carcinoma

University of Edinburgh

Edinburgh, UK

Masters researcher, advisor: Dr. Brian Charlesworth research topic: the faster X-effect and population bottlenecks

2012

- Simulated the evolution of the site frequency spectrum of bi-allelic sites in bottlenecked populations
- Compared a X chromosome diversity to autosome diversity to look for signs of faster X chromosomal adaptive evolution.

Undergraduate Research Experience

Eötvös Loránd University Budapest

Budapest, HU

Undergraduate researcher with Pan-Starrs Research Team advisor: Dr. Zsolt Frei research topic: Pan-Starrs data analysis

2011

- Fitted radial profiles of spiral galaxies via the Sersic profiles
- Worked on developing Sersic index based spiral galaxy classification scheme

Language and Programming Experience

Hungarian (native), English (near-native), Italian (advanced), Bash, C, Fortran, Matlab, Octave, PERL, Python, R

Related Professional Experience

Oregon Museum of Science and Industry Biology lab volunteer 2015-2020 Oregon Bioscience and Symposium Workshop (2017)

Professional and Academic Associations

American Association for the Advancement of Science American Society of Human Genetics OHSU Graduate Student Organization (Vice President) OHSU International Employee Resource Group (Co-chair)

Posters

Torkenczy AK, Meszena G. Modeling Speciation: resources versus habitats. Abstract. OHSU Program for Molecular and Cellular Biology Retreat. Welches, Oregon (2014).

Torkenczy AK, Vitak AS, Adey AC., Highly Multiplexed Single Cell Genome Sequencing for Somatic CNV Characterization. Abstract. OHSU Research Week. Portland, Oregon (2016).

Torkenczy AK, Sinnamon JR, Linhoff MW, Vitak AS, Pliner HA, Trapnell C, Steemers FJ Mandel G, Adey AC. The accessible chromatin landscape of the hippocampus at single-cell resolution. Abstract. ASHG Annual Meeting. San Diego, California (2018).

Oral Presentations

Torkenczy AK, Deep profiling of somatic variation in pancreatic solid tumors at the single-cell level. Oral presentation. OHSU Research Week. Portland, Oregon (2017).

Torkenczy AK, Sequencing thousands of single-cell genomes with combinatorial indexing. Oral presentation. Molecular Med Tri-Con. San Francisco, California (2018).

Torkenczy AK, Integrated single-cell epigenetic analysis reveals cross-species functional conservation. Oral Presentation. CEGS Meeting. New York, New York (2021).

Publications/Creative work

* Co-first Author, equal contribution

A. Peer reviewed

Sinnamon JR*, **Torkenczy AK***, Linhoff MW, Vitak AS, Pliner HA, Trapnell C, Steemers FJ Mandel G, Adey AC. The accessible chromatin landscape of the murine hippocampus at single-cell resolution. *Genome Res.* (2019), co-first authorship

Vitak SA*, **Torkenczy KA***, Rosenkrantz JL, Fields AJ, Christiansen L, Wong MH, Carbone L, Steemers FJ, Adey AC. Sequencing thousands of single-cell genomes with combinatorial indexing. *Nat Methods*. **14:**302–308 (2017) doi:10.1038/nmeth.4154., co-first authorship

Daughtry BL, Rosenkrantz JL, Lazar NH, Fei SS, Redmayne N, **Torkenczy KA**, Adey A, Yan M, Gao L, Park B, Nevonen KA, Carbone L and Chavez SL. Single-cell sequencing of primate preimplantation embryos reveals chromosome elimination via cellular fragmentation and blastomere exclusion. *Genome Res.* **25** (2019), doi:10.1101/gr.239830.118.

Su Y, Pelz, C, Huang, T, **Torkenczy KA**, Wang X, Cherry A, Daniel CJ, Liang J, Nan X, Dai MS, Adey AC, Impey S, Sears RC. Post-translational modification localizes MYC to the nuclear pore basket to regulate a subset of target genes involved in cellular responses to environmental signals. *Genes & development*, **32**:21-22 (2018), 1398-1419.

Mulqueen RM, Pokholok D, Norberg SJ., **Torkenczy KA**, Fields AJ, Sun D, Sinnamon JR, Shendure J, Trapnell C, O'Roak BJ, Xia Z, Steemers FJ, Adey AC. (2018). Highly scalable generation of DNA methylation profiles in single cells. *Nature biotechnology*, **36**(5):428-431.

Thornton CA, Mulqueen RM, **Torkenczy KA**, Nishida A., Lowenstein EG, Fields AJ., Steemers FJ., Zhang W, McConnell HL, Woltjer RL, Mishra A, Wright KM & Adey AC. (2021). Spatially mapped single-cell chromatin accessibility. *Nature methods*, **12**(1274)

B. Preprint

Mulqueen RM, DeRosa AB, Thornton AC, Sayar Z, **Torkenczy AK***, Fields AJ, Wright KM, Nan X, Ramji R, Steemers FJ, O'roak BJ, Adey AC. Improved single-cell ATAC-seq reveals chromatin dynamics of in vitro corticogenesis. *bioRxiv*. (2019) (doi: https://doi.org/10.1101/637256)

Langer E, Farrell AS, Allen-Petersen BL, Daniel CJ, Kresse KM, English IA, Shah V, MacPherson K, Wang X, Pelz C, Turnidge M, Jenny ZP., Doha Z, Kendsersky ND, **Torkenczy AK**, Pelz KR, Fields A, Cohn GM, Dewson GS, Thoma MC, Amery TS, Agarwal A, Link JM, Sheppard BC, Adey AC, Sears RC, The Prolyl Isomerase PIN1 Plays a Critical Role in Fibroblast Differentiation States to Support Pancreatic Cancer. *Manuscript in review*

Torkenczy AK*, Langer E*, Fields AJ, Risom T, Turnidge M, Gray JW, Sears RC, Adey AC. Trametinib driven epigenetic adaptation of cells across multiple triple negative breast cancer cell lines. *Manuscript in review*, co-first authorship

Torkenczy AK, Dalgarno C, Jiang L, Hao Y, Satija R. Integrated single-cell epigenetic analysis reveals cross-species functional conservation. *Manuscript in preparation*