Charikleia Karageorgiou, Ph.D.

Postdoctoral Researcher, Department of Biological Sciences, University at Buffalo
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EDUCATION & ACADEMIC POSITIONS

Jan 2023 – Present	Postdoctoral Researcher, Dept. Biological Sciences, University at Buffalo, SUNY, NY, USA. Mentor: Dr. Omer Gokcumen
Dec 2021 – July 2022	Research Fellow, Foundation for Research and Technology Hellas - Institute of Computer Science, Computational BioMedicine Laboratory, Greece. Supervisor: Dr. Pavlos Pavlidis
Aug 2021 – Feb 2022	Visiting PhD Researcher, Foundation for Research and Technology Hellas - Institute of Molecular Biology and Biotechnology, Greece. Funded by Marie Skłodowska-Curie Actions - Research and Innovation Staff Exchange (RISE). Supervisor: Prof. John Vontas
Sept 2017 – Sept 2022	PhD *summa cum laude*, Evolutionary Genetics and Genomics, Universitat Autònoma de Barcelona, Spain. Supervisors: Dr. Francisco Rodríguez-Trelles & Dr. Rosa Tarrío
Feb 2021 – June 2021	PhD Internship, University of Zürich, Switzerland. Supervisor: Dr. Martin Kapun
Sept 2016 – July 2017	MSc Bioinformatics, Universitat Autònoma de Barcelona, Spain.
July 2015 – Dec 2016	Research Assistant, Grup de Genòmica, Bioinformàtica i Biologia Evolutiva, Universitat Autònoma de Barcelona, Spain.
Sept 2014 – July 2015	MSc Advanced Genetics, Universitat Autònoma de Barcelona, Spain.
Sept 2011 – June 2014	BSc (Hons) Biomedicine, University of East Anglia, United Kingdom.

PUBLICATIONS & PREPRINTS

* denotes co-first authorship, # denotes corresponding author

10. Acharjee, M., Humphrey, K., Lactaoen, V., **Karageorgiou, C.**, Liu, B., Gokcumen, O. and Rusche, L#. 2025. The deacetylase Sir2 is the primary sensor driving transcriptional changes in response to low NAD+ in the yeast *Kluyveromyces lactis*. *Submitted.*

9. **Karageorgiou, C.**, Ruhl S. and Gokcumen, O.#, 2025. Convergent evolution through independent rearrangements in the primate amylase locus. *bioRxiv:* *https://doi.org/10.1101/2025.08.14.670395*

8. Scheer, K., Landau, L.J.B., Jorgensen, K., **Karageorgiou, C.**, Siao, L., Alkan, C., Morales-Rivera, A.M., Osbourne, C., Garcia, O., Pearson, L., Kiyamu, M., Rivera-Chira, M., Leon-Velarde, F., Lee, F., Brutsaert, T., Bigham, A.W.# and Gokcumen, O.#, 2025. Adaptive Increase of Amylase Gene Copy Number in Peruvians Driven by Potato-rich Diets. *In revision*.

7. Running, L.*, Cristobal, J.R.*, **Karageorgiou, C.**, Camdzic, M., Aguilar, J.M.N., Gokcumen, O., Aga, D.S.# and Atilla-Gokcumen, G.E.#, 2024. Investigating the Mechanism of Neurotoxic Effects of PFAS in Differentiated Neuronal Cells through Transcriptomics and Lipidomics Analysis. *ACS Chemical Neuroscience, 15*(24), pp.4568-4579.

6. Yilmaz, F.*, **Karageorgiou, C.***, Kim, K.*, Pajic, P., Scheer, K., Human Genome Structural Variation Consortium, Beck, C.R., Torregrossa, A.M., Lee, C.# and Gokcumen, O.#, 2024. Reconstruction of the human amylase locus reveals ancient duplications seeding modern-day variation. *Science*, *386*(6724), p.eadn0609.

5. Papadadonakis, S., Kioukis, A., **Karageorgiou, C.**, and Pavlidis, P.[#] 2024. Evoluti2on of gene regulatory networks by means of selection and random genetic drift. *PeerJ*, *12*, e17918.

4. **Karageorgiou, C.**, Gokcumen, O. and Dennis, M.[#], 2024. Deciphering the Role of Structural Variation in Human Evolution: A Functional Perspective. *Current Opinion in Genetics & Development, 88,* p.102240. doi:10.1016/j.gde.2024.102240

3. Labbé, F., et al., 2023. Genomic analysis of two phlebotomine sand fly vectors of *Leishmania* from the New and Old World. *PLoS Neglected Tropical Diseases*, *17*(4), p.e0010862. doi:10.1371/journal.pntd.0010862

2. **Karageorgiou, C.**[#], Tarrío, R.[#] and Rodríguez-Trelles, F.[#], 2020. The Cyclically Seasonal *Drosophila subobscura* Inversion O_7 Originated From Fragile Genomic Sites and Relocated Immunity and Metabolic Genes. *Frontiers in genetics*, *11*, p.1190.

1. **Karageorgiou, C.**[#] , Gámez-Visairas, V., Tarrío, R.[#] and Rodríguez-Trelles, F.[#], 2019. Long-read based assembly and synteny analysis of a reference *Drosophila subobscura* genome reveals signatures of structural evolution driven by inversions recombination-suppression effects. *BMC genomics*, *20*(1), p.1-21.

TEACHING & MENTORSHIP

Mentoring:
▫ Carsyn Bonesteel, University at Buffalo, 2024 – Present. BSc Student. Mentoring her independent research project on the evolutionary and functional impact of the hominin-specific *ACOT1* gene duplication on metabolic health.

▫ Rebekah Sheih, University at Buffalo, Summer 2024. BSc REU Student. Supervised her REU project on characterizing the evolutionary history of the *ACOT1* locus.

▫ Eliseo Pampín Bello, Universitat Autònoma de Barcelona, 2017 – 2018. Mentored MSc student and supervised MSc Thesis “Genomic localization and evolutionary history of two aminopeptidase genes long-known to exhibit systematic patterns of spatiotemporal variation in natural populations of *Drosophila”.*

Teaching:
Genetics and Microbiology Department, Universitat Autònoma de Barcelona, 2017 – 2021.
Lectures on *Drosophila morphology, Genetic linkage & mapping, Recombination, and Population Genetics.*

CONFERENCE CONTRIBUTIONS & INVITED TALKS

2025 Convergent evolution through recurrent rearrangements and regulatory rewiring in the primate amylase locus, ***Talk***, ESEB 2025, Barcelona, Spain.

2025 Reconstruction of the human amylase locus reveals ancient duplications seeding modern-day variation, ***Poster***, ESEB 2025, Barcelona, Spain.

2025 Why this locus? Recurrent duplications and extensive structural polymorphism at the amylase locus in humans and non-human primates, ***Talk***, Ecological and Evolutionary Genomics, Gordon Research Conference, Renaissance Tuscany Il Ciocco, Italy.

2025 Convergent evolution through recurrent rearrangements in the primate amylase locus, ***Talk***, Evolution 2025, Athens, GA, USA.

2025 Reconstruction of the human amylase locus reveals ancient duplications seeding modern-day variation, ***Poster***, Evolution 2025, Athens, GA, USA.

2025 Reconstruction of the human amylase locus reveals ancient duplications seeding modern-day variation, ***Talk***, Virtual Evolution 2025, Athens, GA, USA.

2025 Convergent evolution through recurrent rearrangements in the primate amylase locus, ***Talk***, Virtual Evolution 2025, Athens, GA, USA.

2025 Reconstruction of the human amylase locus reveals ancient duplications seeding modern-day variation, ***Invited Seminar Talk***, Brock University, St Catharines, Canada.

2024 Reconstruction of the human amylase locus reveals ancient duplications seeding modern-day variation, ***Poster***, Annual Postdoctoral Research Symposium, University at Buffalo, NY, USA.

2024 Reconstruction of the human amylase locus reveals ancient duplications seeding modern-day variation, ***Talk***, GLAM EvoGen 2024, Syracuse University, NY, USA.

2024 Paleolithic gene duplications primed adaptive evolution of human amylase locus upon agriculture, ***Poster***, SMBE 2024, Puerto Vallarta, Mexico.

2024 Ancient *AMY1* gene duplications primed the amylase locus for adaptive evolution upon the onset of agriculture, ***Invited Seminar Talk***, Biological Sciences Seminar Series, University at Buffalo, NY, USA.

2023 Modeling the evolutionary and functional impact of genomic structural variation in mammalian saliva. ***Poster***, Ecological and Evolutionary Genomics, Gordon Research Conference, Bryant University, RI, USA.

2022 Disentangling the origin of the Cretan wild goat *Capra aegagrus cretica*. ***Talk***, 15th International Congress on the Zoogeography and Ecology of Greece and Adjacent Regions, Mytilene, Greece.

2022 Comparative population genomics of natural populations of *Drosophila subobscura*: Understanding the establishment and maintenance of chromosomal inversion polymorphisms. ***Invited Seminar Talk,*** The Eric Lai Lab, Sloan Kettering Institute, NY, USA.

2022 Comparative population genomics of natural populations of *Drosophila subobscura*: Understanding the establishment and maintenance of chromosomal inversion polymorphisms. ***Invited Seminar Talk,*** Gokcumen Lab, University at Buffalo, NY, USA.

2021 The cyclically seasonal *Drosophila subobscura* inversion O_7 originated from fragile genomic sites and relocated immunity and metabolic genes. ***Poster***, SMBE 2021. Virtual.

2021 The cyclically seasonal *Drosophila subobscura* inversion O_7 originated from fragile genomic sites and relocated immunity and metabolic genes. ***Poster***, SMRT Leiden 2021 – Young Investigator Virtual Conference. Virtual.

2019 Long-read based assembly and synteny analysis of a reference *Drosophila subobscura* genome reveals signatures of structural evolution driven by inversions recombination-suppression effects. ***Poster***, VII Jornada de Bioinformatica i Genomica, Barcelona, Spain.

2019 Long-read based assembly and synteny analysis of a reference *Drosophila subobscura* genome reveals signatures of structural evolution driven by inversions recombination-suppression effects. ***Poster***, European Drosophila Research Conference (EDRC), Lausanne, Switzerland.

2019 Comparative population genomics of natural populations of *Drosophila subobscura.* ***Talk***, VII Jornades de Biorecerca UABio. Universitat Autònoma de Barcelona. Barcelona, Spain.

2018 The genome of *Drosophila subobscura*. ***Talk***, VI Jornades de Biorecerca UABio. Universitat Autònoma de Barcelona, Barcelona, Spain.

OUTREACH & SERVICE

August 2025 Outreach Organizer – *Breaking Bread: Exploring the Evolution of Amylase in Humans*. Evolution, Diversity, Art and Community, Festa Major de Gràcia & ESEB 2025, Barcelona, Spain. Organized and led a bilingual (English/Spanish) public outreach activity on human evolution and the amylase locus, selected as part of ESEB's outreach initiative. Co-organizer: Thomas Hitchcock.

July 2025	Co-Chair, GRC Power Hour™ – Gordon Research Conference (GRC) on Evolutionary and Ecological Genomics: *Dynamics of Ecological and Evolutionary Change*, Lucca, Italy.
July 2025	Chair for the Gordon Research Seminar (GRS) Ecological and Evolutionary Genomics: *Elucidating the Evolutionary Dynamics of Adaptation in Fluctuating Environments*, Lucca, Italy. Co-chair: Joaquin Nunez.
May 2025	Moderator, Virtual Evolution 2025 Conference, Sessions: *Population Genetics Theory* and *Molecular Evolution*
May 2025	Organization Committee for *Paving Pathways: A multi-panel symposium highlighting scientists in various post-graduate biomedical careers*, Buffalo, USA.
2025 – Present	Organizer of "Talk Nerdy to Me", a monthly event dedicated to public speaking and science communication, aimed at making research accessible to general audiences.
July 2024	Organizer for Society for Molecular Biology and Evolution 2024 Symposium: *Deciphering the functional and adaptive effects of genomic structural variation*, Puerto Vallarta, Mexico.
2024 – Present	Organizer, Postdoctoral Meetups, University at Buffalo, USA – Initiated and coordinated regular gatherings to build a supportive community, foster open communication and encourage interdisciplinary exchange.
2022 – Present	Organizer for Genome Structure Evolution and Anthropology Seminar Series, Buffalo Evolutionary and Anthropological Genomics Lab, University at Buffalo, USA.
Editor:	Associate Editor for *Heredity* (2025–)
Reviewer for:	Molecular Biology and Evolution, Nature Communications, Genome Research, Genetics, The American Journal of Human Genetics,The Leakey Foundation (Grant review).
Guest-Editor:	*Heredity*, Special Issue: *Functional and Adaptive Effects of Genomic Structural Variation*, edited with Omer Gokcumen, Megan Dennis, and Ellen Leffler. 2024-2025.
Training:	GSA Journals Peer Review Training Program, Winter 2025. eLife Early-Career Reviewers Pool, Spring 2025.
Memberships:	Genetics Society of America (GSA), Society for Molecular Biology and Evolution (SMBE), Society for the Study of Evolution (SSE), European Society for Evolutionary Biology (ESEB), The Genetics Society (GS).

HONORS & AWARDS

2025	DeLill Nasser Award for Professional Development in Genetics, Genetics Society of America. ($1,000)
2022	*Summa Cum Laude*, PhD Defense, Universitat Autònoma de Barcelona, Spain.
2020	Swiss-European Mobility Programme (SEMP) Grant (440 CHF/month, declined due to COVID-19 pandemic)
2017 – 2022	PIF PhD fellowship from the Universitat Autònoma de Barcelona, Spain. (~75,000 €)

MEDIA HIGHLIGHTS & PRESS COVERAGE

2024	Yilmaz et al. Reconstruction of the human amylase locus reveals ancient duplications seeding modern-day variation. Press release. Highlights: *NYT*, *Discover*, *CNN*, *NBC*. *Highlighted in the NIH Director's blog, as review highlight in Cell Genomics, PLOS SciComm "Top Stories in Human Evolution of 2024, Leakey Foundation Podcast "Top Human Origins Discoveries of 2024."*

PROGRAMMING LANGUAGES

Bash, Python, R, MySQL, HTML, Perl

SOFTWARE & TOOLS

The *Drosophila subobscura* Genome Browser: A genomic visualization and exploration platform for *Drosophila subobscura*, featuring annotated genes, sequence variants (SNPs and indels), transposable elements, inversion breakpoints and reuse and synteny information.

Updated September 2025