

# Charikleia Karageorgiou, Ph.D.

Postdoctoral Researcher, Department of Biological Sciences, University at Buffalo

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 [Google Scholar](#) |  [ORCID](#) |  [Bluesky](#)

## EDUCATION & ACADEMIC POSITIONS

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Jan 2023 – Present	Postdoctoral Researcher, Dept. Biological Sciences, University at Buffalo, SUNY, NY, USA. Mentor: <u>Dr. Omer Gokcumen</u>
Dec 2021 – July 2022	Research Fellow, Foundation for Research and Technology Hellas - Institute of Computer Science, Computational BioMedicine Laboratory, Greece. Supervisor: <u>Dr. Pavlos Pavlidis</u>
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: <u>Prof. John Vontas</u>
Sept 2017 – Sept 2022	PhD <i>summa cum laude</i> , Evolutionary Genetics and Genomics, Universitat Autònoma de Barcelona, Spain. Supervisors: <u>Dr. Francisco Rodríguez-Trelles</u> & <u>Dr. Rosa Tarrío</u>
Feb 2021 – June 2021	PhD Internship, University of Zürich, Switzerland. Supervisor: <u>Dr. Martin Kapun</u>
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

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\* denotes co-first authorship, # denotes corresponding author

10. Acharjee, M., Humphrey, K., Lactaoen, V., **Karageorgiou, C.**, Liu, B., Gokcumen, O. and Rusche, L.<sup>#</sup>. 2025. The deacetylase Sir2 is the primary sensor driving transcriptional changes in response to low NAD<sup>+</sup> in the yeast *Kluyveromyces lactis*. *Submitted*.
9. **Karageorgiou, C.**, Ruhl S. and Gokcumen, O.<sup>#</sup>, 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.<sup>#</sup> and Gokcumen, O.<sup>#</sup>, 2025. Adaptive Increase of Amylase Gene Copy Number in Peruvians Driven by Potato-rich Diets. *In revision*.
7. Running, L.\*<sup>#</sup>, Cristobal, J.R.\*<sup>#</sup>, **Karageorgiou, C.**, Camdzic, M., Aguilar, J.M.N., Gokcumen, O., Aga, D.S.<sup>#</sup> and Atilla-Gokcumen, G.E.<sup>#</sup>, 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.\*<sup>#</sup>, **Karageorgiou, C.\***, Kim, K.\*<sup>#</sup>, Pajic, P., Scheer, K., Human Genome Structural Variation Consortium, Beck, C.R., Torregrossa, A.M., Lee, C.<sup>#</sup> and Gokcumen, O.<sup>#</sup>, 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.<sup>#</sup> 2024. Evolution of gene regulatory networks by means of selection and random genetic drift. *PeerJ*, 12, e17918.
4. **Karageorgiou, C.**, Gokcumen, O. and Dennis, M.<sup>#</sup>, 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.**<sup>#</sup>, Tarrío, R.<sup>#</sup> and Rodríguez-Trelles, F.<sup>#</sup>, 2020. The Cyclically Seasonal *Drosophila subobscura* Inversion O<sub>7</sub> Originated From Fragile Genomic Sites and Relocated Immunity and Metabolic Genes. *Frontiers in genetics*, 11, p.1190.
1. **Karageorgiou, C.**<sup>#</sup>, Gámez-Visairas, V., Tarrío, R.<sup>#</sup> and Rodríguez-Trelles, F.<sup>#</sup>, 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

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### 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

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- 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**, SBE 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**, 15<sup>th</sup> 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*<sub>7</sub> originated from fragile genomic sites and relocated immunity and metabolic genes. **Poster**, SBE 2021. Virtual.
- 2021 The cyclically seasonal *Drosophila subobscura* inversion *O*<sub>7</sub> 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 Bioinformática i Genòmica, 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 Biocerca UABio. Universitat Autònoma de Barcelona. Barcelona, Spain.
- 2018 The genome of *Drosophila subobscura*. **Talk**, VI Jornades de Biocerca UABio. Universitat Autònoma de Barcelona, Barcelona, Spain.

## OUTREACH & SERVICE

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- 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: <i>Dynamics of Ecological and Evolutionary Change</i> , Lucca, Italy.
July 2025	Chair for the Gordon Research Seminar (GRS) Ecological and Evolutionary Genomics: <i>Elucidating the Evolutionary Dynamics of Adaptation in Fluctuating Environments</i> , Lucca, Italy. Co-chair: Joaquin Nunez.
May 2025	Moderator, Virtual Evolution 2025 Conference, Sessions: <i>Population Genetics Theory and Molecular Evolution</i>
May 2025	Organization Committee for <i>Paving Pathways: A multi-panel symposium highlighting scientists in various post-graduate biomedical careers</i> , 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: <i>Deciphering the functional and adaptive effects of genomic structural variation</i> , 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.
<i>Editor:</i>	Associate Editor for <i>Heredity</i> (2025–)
<i>Reviewer for:</i>	Molecular Biology and Evolution, Nature Communications, Genome Research, Genetics, The American Journal of Human Genetics, The Leakey Foundation (Grant review).
<i>Guest-Editor:</i>	<i>Heredity</i> , Special Issue: <i>Functional and Adaptive Effects of Genomic Structural Variation</i> , edited with Omer Gokcumen, Megan Dennis, and Ellen Leffler. 2024-2025.
<i>Training:</i>	GSA Journals Peer Review Training Program, Winter 2025. eLife Early-Career Reviewers Pool, Spring 2025.
<i>Memberships:</i>	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

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2025	DeLill Nasser Award for Professional Development in Genetics, Genetics Society of America. (\$1,000)
2022	<i>Summa Cum Laude</i> , 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

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

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Bash, Python, R, MySQL, HTML, Perl

## SOFTWARE & TOOLS

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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*