Nikolaos Vakirlis, PhD

Email: n.vakirlis@pasteur.gr
Phone: +302106478524
Social: Bluesky, Linkedin
Links: lab website , Google Scholar

Research experience

2024 – (current)	**G4 Group Leader, Evolutionary Genomics Group** Hellenic Pasteur Institute (Greece)
2022 – 2024	**Junior Investigator - Group Leader** Institute for Fundamental Biomedical Research, BSRC “Alexander Fleming” (Greece)
2021 – 2022	**Postdoctoral researcher** Kiel University (Germany) Advisor: Dr. Anne Kupczok (University of Wageningen)
2020 – 2022	**Postdoctoral fellow** BSRC “Alexander Fleming” (Greece) Personally funded by the Hellenic State Scholarship Foundation
2019 – 2020	**Postdoctoral researcher** Benaki Phytopathological Institute (Greece)
2017 – 2018	**Postdoctoral researcher** Trinity College Dublin (Ireland) Advisor: Pr. Aoife McLysaght

Education

2013 – 2016	**PhD candidate, Doctoral School “Complexité du Vivant”** Université Pierre et Marie Curie (France) PhD advisors: Pr. Ingrid Lafontaine & Dr. Gilles Fischer
2011 – 2013	**Masters in Bioinformatics and Modelling**

Université Pierre et Marie Curie (France)
Research internship in Dr. Gilles Fischer's lab

2005-2011 **Undergraduate degree in Computer Science**
National University of Athens (Greece)

Research Output

Peer-reviewed publications (* denotes corresponding author):

- C. Casola, A. Owoyemi, **N. Vakirlis***. Degradation determinants are abundant in human noncanonical proteins. *BiorXiv* (2024). doi: 10.1101/2024.05.01.592071

- E. Caudal, V. Loegler, F. Dutreux, **N. Vakirlis**, E. Teyssonnière, C. Caradec, A. Friedrich, J. Hou, and J. Schacherer. Pan-transcriptome reveals a large accessory genome contribution to gene expression variation in yeast. *Nature Genetics* 56, 1278–1287 (2024). doi: 10.1038/s41588-024-01769-9

- **N. Vakirlis***, O. Acar, V. Cherupally & A.-R. Carvunis*. Ancestral Sequence Reconstruction as a tool to detect and study de novo gene emergence. *Genome Biology and Evolution* (2024) doi: 10.1093/gbe/evae151

- **N. Vakirlis*** & A. Kupczok*. Large-scale investigation of species-specific orphan genes in the human gut microbiome elucidates their evolutionary origins. *Genome Research.* **34**, 888–903 (2024), doi: 10.1101/gr.278977.124

- F.O. Gehlert, L. Nickel, **N. Vakirlis**, K. Hammerschmidt, H.I. Vargas Gebauer, C. Kießling, A. Kupczok, R.A. Schmitz, Active in vivo translocation of the Methanosarcina mazei Gö1 Casposon. *Nucleic Acids Research* gkad474 (2023) doi: 10.1093/nar/gkad474

- E. Tassios, C. Nikolaou*, & **N. Vakirlis***. Intergenic regions of Saccharomycotina yeasts are enriched in potential to encode transmembrane domains. *Molecular Biology and Evolution* msad059 (2023) doi:10.1093/molbev/msad059.

- **N. Vakirlis***, Z. Vance, Kate M. Duggan, A. McLysaght*, De novo birth of functional microproteins in the human lineage. *Cell Reports*, 41(12), (2022) doi: 10.1016/j.celrep.2022.111808

- A. Stavropoulou, E. Tassios, M. Kalyva, M. Georgoulopoulos, **N. Vakirlis**, I. Iliopoulos, C. Nikolaou. Distinct chromosomal "niches" in the genome of Saccharomyces cerevisiae provide the background for genomic innovation and shape the fate of gene duplicates. *NAR Genomics and Bioinformatics*. 4(4):lqac086, (2022) doi: 10.1093/nargab/lqac086

- Y. Gaafar, M. Westenberg, M. Botermans, K. László, K. de Jonghe, Y. Foucart, L. Ferretti, D. Kutnjak, A. Pecman, N. Mehle, J. Kreuze, G. Muller, **N. Vakirlis**, D. Beris, C. Varveri, H. Ziebell. Interlaboratory Comparison Study on Ribodepleted Total RNA High-Throughput

Sequencing for Plant Virus Diagnostics and Bioinformatic Competence. *Pathogens* 10, 1174 (2021). doi: 10.3390/pathogens10091174

- **N. Vakirlis**, A.-R. Carvunis, A. McLysaght, Synteny-based analyses indicate that sequence divergence is not the main source of orphan genes. *eLife*. **9**, e53500 (2020). doi: 10.7554/eLife.53500

- **N. Vakirlis**, O. Acar, B. Hsu, N. Castilho Coelho, S. B. Van Oss, A. Wacholder, K. Medetgul-Ernar, R. W. Bowman, C. P. Hines, J. Iannotta, S. B. Parikh, A. McLysaght, C. J. Camacho, A. F. O'Donnell, T. Ideker, A.-R. Carvunis, De novo emergence of adaptive membrane proteins from thymine-rich genomic sequences. *Nature Communications*. **11**, 1–18 (2020). doi:10.1038/s41467-020-14500-z

- D. Beris, K. Kotsaridis, **N. Vakirlis**, A. Termentzi, I. Theologidis, B. Moury, N. Vassilakos, The plasma membrane Cation binding protein 1 affects accumulation of Potato virus Y in pepper both at the systemic level and in protoplasts. *Virus Research*, 197899 (2020). doi:10.1016/j.virusres.2020.197899

- **N. Vakirlis**, C. Monerawela, G. McManus, O. Ribeiro, A. McLysaght, T. James, U. Bond, Evolutionary journey and characterisation of a novel pan-gene associated with beer strains of Saccharomyces cerevisiae. *Yeast*. **36**, 425–437 (2019). doi:10.1002/yea.3391

- **N. Vakirlis**, A. S. Hebert, D. A. Opulente, G. Achaz, C. T. Hittinger, G. Fischer, J. J. Coon, I. Lafontaine, A Molecular Portrait of De Novo Genes in Yeasts. *Molecular Biology and Evolution*. **35**, 631–645 (2018). doi:10.1093/molbev/msx315

- **N. Vakirlis,** V. Sarilar, G. Drillon, A. Fleiss, N. Agier, J.-P. Meyniel, L. Blanpain, A. Carbone, H. Devillers, K. Dubois, A. Gillet-Markowska, S. Graziani, N. Huu-Vang, M. Poirel, C. Reisser, J. Schott, J. Schacherer, I. Lafontaine, B. Llorente, C. Neuvéglise, G. Fischer, Reconstruction of ancestral chromosome architecture and gene repertoire reveals principles of genome evolution in a model yeast genus. *Genome Research.* (2016), doi:10.1101/gr.204420.116

Book chapters:

- **N. Vakirlis**, A. McLysaght, Computational Prediction of de Novo Emerged Protein-Coding Genes, in *Computational Methods in Protein Evolution*, T. Sikosek, Ed. (Springer New York, New York, NY, (2019); *Methods in Molecular Biology*, pp. 63–81. doi:10.1007/978-1-4939-8736-8_4

Invited talks:

- Department of Cell Biology, Charles University, March 4, 2025 (Prague, Czech Rep.)
- EMBL-EBI, January 21, 2025 (Hinxton, UK)
- Vanderbilt University, Evolutionary Studies Initiative, November 10, 2023 (Nashville, TN, USA)
- Protein Evolution Meeting Münster, July 4, 2023 (Münster, Germany)
- University of Münster, Institute for Evolution and Biodiversity seminar, May 25, 2021 (Münster, Germany)

- Sorbonne Université, Laboratory of Computational and Quantitative Biology, February 6, 2020, (Paris, France)
- PRBB Computational Genomics Seminar series, January 16, 2020 (Barcelona, Spain)
- Institute of Research on Cancer and Ageing (IRCAN), April 3, 2019 (Nice, France)

Selected contributed talks:

- “Classifying the evolutionary origins of orphan genes using machine learning”, legend 2024, FORTH (Herakleion, Greece)
- “Ancestral Sequence Reconstruction as a tool to detect and study de novo gene emergence”, SMBE Satellite Meeting on De novo gene birth, 2023 (College Station, US)
- “De novo birth of functional microproteins in the human lineage”, Microproteins meeting 2023 (Helsingør, Denmark)
- “Evolutionary origins of orphan genes from prokaryotes of the human gut”, EMBO meeting Mechanisms in Ecology and Evolution, 2022, EMBL (Heidelberg, Germany)
- “Evolutionary origins of the *S. cerevisiae* pan-transcriptome”, 14th International Conference “Levures, Modèles et Outils”, 2021 (Strasbourg, France)
- “Unravelling the mystery of orphan genes to understand the origins of genetic novelty”, ISCBacademy Webinar, 2020, https://iscb.swoogo.com/iscbacademy-11-vakirlis
- "Mechanism and Impact of De Novo Gene Emergence Across 15 Yeast Genomes", 28th International Conference on Yeast Genetics and Molecular Biology (ICYGMB), 2017 (Prague, Czech Republic)
- “De novo genes in yeasts”, Young Researchers in Life Sciences (YRLS), Pasteur Institute, 2016 (Paris, France)

Competitive Funding

2024	Four-year G4 grant by Pasteur Institute in Paris (400,000€): “Understanding the evolutionary origins and dynamics of antimicrobial peptides as a path toward wiser applications”
2022	Two-year independent funding by the Hellenic Foundation of Research and Innovation (120.000€). ORIGAMI: Studying the origin of genes *de novo* in yeast using population and functional genomics approaches.
2020	Two-year postdoctoral research fellowship by the Hellenic State Scholarship Foundation (26.000€): “Investigating *de novo* gene emergence across the entire budding yeast subphylum”, in affiliation with BSRC “Alexander Fleming”
2013	Three-year PhD fellowship by the Doctoral School “Complexité du Vivant” of Université Pierre et Marie Curie: “Relationships between protein-coding genes’ evolutionary rates and chromosome dynamics in yeast”

Awards and distinctions

- Young Investigator Travel and Registration Award, SMBE 2019

- European Union's Seal of Excellence for the 2019 MSCA postdoctoral fellowship proposal ORIGAMI.

Organization of international conferences

- Main organizer of EMBO Early Career Lecture Course "Evolutionary and Comparative Genomics", November 2024, Nafplion, Greece

- Co-organizer of SMBE Satellite Meeting on De novo gene birth, November 2023, College Station, Texas, US

- Co-organizer of the symposium "Origins, Evolution and Function of Novel Genes", SMBE 2019, Manchester, UK

Teaching

2023 – 2024	Part-time faculty, Deree, The American College of Greece. Module leader and instructor for course "Health Information Systems and Technology", UK Level 6, 15-credit course validated by The Open University UK.
2013 - 2016	Total of 188 teaching hours of 1st and 2nd year Computer Science undergraduate workshops and courses. Supervision of bi-disciplinary semester-long research projects. Université Pierre et Marie Curie.

Reviewing activities

I have served as a guest editor for the journal Genome Biology and Evolution, for the special issue "De novo gene evolution".
I have peer-reviewed for various journals including PLoS Biology, Nature Ecology and Evolution, ELife, Genome Research, PLoS Genetics, Molecular Biology and Evolution, Genome Biology and Evolution, Bioinformatics and Nature Communications.

Supervision, mentoring and popularization of science

- Member of the Board of the Hellenic Evolutionary Society (2022 - 2027)
- Participation in “Pint of Science Greece” popular science event (2023)
- PhD co-supervisor, Emilios Tassios, University of Ioannina-BSRC Fleming (2023)
- MSc thesis co-supervisor, Felipe Perez, Wageningen University and Research (2024)
- MSc thesis co-supervisor, Dimitris Nakos, National University of Athens (2023)
- MSc thesis co-supervisor, Jori de Leuw, Wageningen University and Research (2023)
- MSc thesis co-supervisor, Emilios Tassios, University of Crete (2022)
- Undergraduate thesis supervisor, Kate Marie Duggan, Trinity College Dublin (2021)
- Member of the PhD defense committee of Claire Patiou, University of Lille (2025)
- Member of the PhD defense committee of William Blevins, University Pompeu-Fabra (2020)
- Undergraduate mentor at SMBE Annual Meeting 2019
- Participation in “Pint of Science Greece” popular science event (2018)

Languages

I have native speaker fluency in Greek, French and English.