

## Nikolaos Vakirlis, PhD

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### Research experience

**Junior Investigator, Institute for Fundamental Biomedical Research, BSRC “Alexander Fleming”, (Greece)**

*1/10/2022- (ongoing)*

Group Leader, Evolutionary Genomics Lab ([link](#))

**Postdoctoral research fellow, Institute for General Microbiology, Christian-Albrechts University of Kiel (Germany)**

*1/7/2021-31/8/2022*

In collaboration with Anne Kupczok (University of Wageningen)

**Postdoctoral research fellow, Christoforos Nikolaou lab, BSRC “Alexander Fleming” (Greece)**

*1/2/2020- 30/6/2022*

Personally funded by the Hellenic State Scholarship Foundation (IKY).

**Postdoctoral researcher, Department of Phytopathology, Benaki Phytopathological Institute (Greece)**

*7/1/2019-31/3/2020*

**Postdoctoral research fellow, Aoife McLysaght Lab, Trinity College Dublin (Ireland)**

*16/1/2017-31/12/2018*

**PhD candidate, Gilles Fischer Lab, Université Pierre et Marie Curie (France)**

*1/10/2013-31/09/2016*

PhD advisors: Drs. Ingrid Lafontaine & Gilles Fischer

**MSc research intern, Gilles Fischer Lab, Université Pierre et Marie Curie (France)**

*1/3/2013-10/9/2013*

Advisors: Drs. Ingrid Lafontaine & Gilles Fischer

## Research Output

### **Peer-reviewed publications:**

- 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](https://doi.org/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. Georgouloupoulos, **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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/10.1002/yea.3391)

- **N. Vakirlis**, A. S. Hebert, D. A. Oplente, G. Achaz, C. T. Hittinger, G. Fischer, J. J. Coon, I. Lafontaine, A Molecular Portrait of De Novo Genes in Yeasts. *Mol Biol Evol*. **35**, 631–645 (2018). doi:[10.1093/molbev/msx315](https://doi.org/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 Res.* (2016), doi:[10.1101/gr.204420.116](https://doi.org/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](https://doi.org/10.1007/978-1-4939-8736-8_4)

### **Invited talks:**

- Institute for Evolution and Biodiversity seminar, May 25, 2021: *Towards a complete understanding of the origins of genetic novelty*, University of Münster, Münster, Germany
- LCQB seminar, February 6, 2020: *Unravelling the mystery of orphan genes to understand the origins of genetic novelty*, Laboratory of Computational and Quantitative Biology, Sorbonne Université, Paris, France
- PRBB Computational Genomics Seminar, January 16, 2020: *Unravelling the mystery of orphan genes to understand the origins of genetic novelty*, PRBB, Barcelona, Spain
- IRCAN seminar, April 3, 2019: *Novel genes "from scratch" in the human genome*, IRCAN, Nice, France

### **Organisation of international conferences:**

- Co-organizer of *SMBE Satellite Meeting on De novo gene birth*, September 2023 (forthcoming), College Station, Texas, US
- Co-organizer of the symposium “Origins, Evolution and Function of Novel Genes”, SMBE 2019, Manchester, UK

### **Selected conference talks as presenting author:**

- Oral presentation: “Evolutionary origins of orphan genes from prokaryotes of the human gut”, EMBO meeting Mechanisms in Ecology and Evolution, 2022, EMBL, Heidelberg, Germany
- Oral presentation: “Evolutionary origins of the *S. cerevisiae* pan-transcriptome”, 14<sup>th</sup> International Conference “Levures, Modèles et Outils”, 2021, Strasbourg, France

- Oral presentation: “Unravelling the mystery of orphan genes to understand the origins of genetic novelty”, ISCBacademy Webinar, August 24 2020, <https://iscb.swoogo.com/iscbacademy-11-vakirlis>
- Oral presentation: “Synteny based analyses indicate that sequence divergence is not the main source of orphan genes”, eLife Online Research Talks, Tuesday April 7 2020, <https://www.youtube.com/watch?v=PQpp29ebtR4&t=2319s>
- Oral presentation: “Synteny based analyses indicate that sequence divergence is not the main source of orphan genes”, SMBE 2020, Québec City, Canada (CANCELLED DUE TO COVID-19)
- Oral presentation, "Synteny based analyses indicate that sequence divergence is not the main source of orphan genes", 14<sup>th</sup> Conference of the Hellenic Society for Computational Biology and Bioinformatics (HSCBB19), Patras, Greece, 2019
- Oral presentation, "Mechanism and Impact of De Novo Gene Emergence Across 15 Yeast Genomes", 28th International Conference on Yeast Genetics and Molecular Biology (ICYGMB), Prague, Czech Republic, 2017
- Oral presentation, “De novo genes in yeasts”, Young Researchers in Life Sciences (YRLS), Pasteur Institute, Paris, 2016

## Funding

- Two-year independent funding by the Hellenic Foundation of Research and Innovation (HFRI/EΛIΔEK), 120.000 euros, ORIGAMI: Studying the origin of genes *de novo* in yeast using population and functional genomics approaches.
- Two-year postdoctoral research fellowship by the Hellenic State Scholarship Foundation (IKY): “Investigating *de novo* gene emergence across the entire budding yeast subphylum”, 1/2/2020-2022, in affiliation with BSRC Alexander Fleming
- Three-year PhD fellowship by the Doctoral School “Complexité du Vivant” of Université Pierre et Marie Curie (Paris 6): “Relationships between protein-coding genes’ evolutionary rates and chromosome dynamics in yeast”, 2013-2016

## Awards and distinctions

- Young Investigator Travel and Registration Award, SMBE 2019, Manchester.
- European Union’s Seal of Excellence for the 2019 MSCA postdoctoral fellowship proposal ORIGAMI.

## Teaching

Module organizer and full-time teaching responsibilities for course “Health Information Systems and Technology”, UK Level 6, 15 credit course validated by Open University UK, Deree, The American College of Greece (2023)

Total of 188 teaching hours of 1<sup>st</sup> and 2<sup>nd</sup> year Computer Science undergraduate workshops and courses. Supervision of bi-disciplinary semester-long research projects, UPMC (Paris 6) (2013-2016)

## Supervision, mentoring and popularization of science

- Co-supervision of Master’s thesis of Dimitris Nakos, “Understanding the evolutionary origins and trajectories of human microproteins”, National University of Athens (2023)
- Co-supervision of Master’s thesis of Jori de Leuw, “Classification of the evolutionary origin of orphan genes using machine learning approaches”, Wageningen University and Research (2023)
- Co-supervision of Master’s thesis of Emilios Tassios, “A large-scale study of the evolution of genomic novelty in budding yeasts”, University of Crete (2022)
- Supervision of undergraduate thesis of Kate Marie Duggan, “Evolution ‘from scratch’ of micro-proteins unique to the human lineage”, Trinity College Dublin (2021)
- Member of the PhD committee of William Blevins, University Pompeu-Fabra (2020)
- Undergraduate mentor at SBE Annual Meeting 2019
- Participation in “Pint of Science Greece” popular science event with oral presentation “Where did the genes that help make your beer (and every other gene) come from?” (2018)

## Reviewing activities

I am a Review Editor for Frontiers in Genetics. I have peer-reviewed for many journals including Nature Ecology and Evolution, ELife, Genome Research, PLoS Biology, Molecular Biology and Evolution, Genome Biology and Evolution and Bioinformatics.

## Education

**PhD (Diplôme de Docteur): Complexité du Vivant (Complexity of the Living World)**

*2013-2016 (UPMC, France)*

**Spring school of theoretical informatics**

*2014 (France)*

**MSc in Bioinformatics and Modelling**

*2011-2013 (UPMC, France)*

**BSc in Computer Science**

*2005-2011 (University of Athens, Greece)*

**Graduation with Honours**

*2004-2005 (St. Joseph Greek-French high-school, Greece)*

[Languages](#)

Greek, English, French (trilingual)