



Rémi Allio

Researcher, Centre de Biologie pour la Gestion des Populations
Montpellier, France

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Current position

Visiting researcher, EvoEco Lab, University of Toronto-Mississauga, ON, Canada. 2023-present
Principal Collaborator: Dr. Marc Johnson

Researcher, CBGP, Montpellier, France. 2022-present
Insect-plant interaction from a phylogenomic perspective.

Education

Post-doc, ISEM, University of Montpellier, France. 2021
Convergent evolution in myrmecophagous mammals.
Advisor: Dr. Frédéric Delsuc

Ph.D., ISEM, University of Montpellier, France 2017-2021
Phylogenomics and comparative genomics on myrmecophagous mammals.
Advisors: Drs. Frédéric Delsuc & Benoit Nabholz

M.Sc., University of Montpellier, France 2017
Evolutionary biology & ecology

B.Sc., University of Montpellier, France 2015
Ecology & biology of organisms

Research & Professional Experience

Graduate research project, Institute of Evolutionary Science 2017
of Montpellier, France
Advisors: Drs. Fabien Condamine & Benoit Nabholz
Thesis title: Study of the interaction between Papilionidae and their host plants in a macroevolutionary and genomic context

Graduate research project, Institute of Evolutionary Science 2016
of Montpellier, France
Advisor: Dr. Benoit Nabholz
Thesis title: Study of nuclear and mitochondrial mutation rates in animals

Undergraduate research project, Center for Functional Ecology and Evolution, 2015
Montpellier, France
Undergraduate project in experimental biology on chemical communication in mammals (manatee)
PI: Sylvia Campagna

Awards

“Best Graduate Student Paper Award” for *Molecular Biology & Evolution* 2017

Fundings

AS PRINCIPAL INVESTIGATOR

5. IB2024 - Travel support for international collaboration. 2024
INRAE, France. 6,000€
4. IB2024 - Research funding. 2024
INRAE, France. 30,000€
3. OVPR Internal Research Grant. 2023
University of Toronto-Mississauga, ON, Canada. 10,000CAD
2. IB2023 - Travel support for international collaboration. 2022
INRAE, France. 5,000€
1. Annual CBGP Internal call. 3,000€ 2022

AS A COLLABORATOR

2. **PolTroN**: Pollination Networks in the Tropics. 2022
CEMEB labex, France. 20,000€
1. **GENO_PEST**: GENOMics studies of the noctuid PEST genus *Spodoptera*. 2022
CEMEB labex, France. 18,855€

Publications

PEER-REVIEWED ARTICLES

11. **Allio, R.**, Delsuc, F., Belkhir, K., Douzery, E. J., Ranwez, V., & Scornavacca, C. (2024). OrthoMaM v12: a database of curated single-copy ortholog alignments and trees to study mammalian evolutionary genomics. *Nucleic Acids Research*, 52(D1), D529-D535. DOI: [10.1093/nar/gkad834](https://doi.org/10.1093/nar/gkad834)
10. Haran, J.*, Li, X.*, **Allio, R.***, Shin, S., Benoit, L., Oberprieler, R. G., Farrell, B. D., Brown, S. D. J., Leschen, R. A. B., Kergoat, G. J. & McKenna, D. D. (2023). Phylogenomics illuminates the phylogeny of flower weevils (Curculioninae) and reveals ten independent origins of brood-site pollination mutualism in true weevils. *Proceedings of the Royal Society B*, 290(2008), 20230889. DOI: [10.1098/rspb.2023.0889](https://doi.org/10.1098/rspb.2023.0889)
9. Heighton, S. P.*, **Allio, R.***, Murienne, J., Salmona, J., Meng, H., Scornavacca, C., Bastos, A.D.S., Njiokou, F., Pieterse, D.W., Tilak, M.-K., Luo, S.-J., Delsuc, F., & Gaubert, P. (2023). Pangolin genomes offer key insights and resources for the world’s most trafficked wild mammals. *Molecular Biology and Evolution*, Volume 40, Issue 10, October 2023, msad190. DOI: [10.1093/molbev/msad190](https://doi.org/10.1093/molbev/msad190)
8. Comte, A., Tricou, T., Tannier, E., Joseph, J., Siberchicot, A., Penel, S., **Allio, R.**, Delsuc, F., Dray, S., & de Vienne, D. M. (2023). PhylteR: efficient identification of outlier sequences in phylogenomic datasets. *Molecular Biology and Evolution*, Volume 40, Issue 11, November 2023, msad234. DOI: [10.1093/molbev/msad234](https://doi.org/10.1093/molbev/msad234)

7. Coiro, M., **Allio, R.**, Mazet, N., Seyfullah, L. J., & Condamine, F. L. (2023). Reconciling fossils with phylogenies reveals the origin and macroevolutionary processes explaining the global cycad biodiversity. *New Phytologist*. DOI: [10.1111/nph.19010](https://doi.org/10.1111/nph.19010)
6. Condamine, F. L., **Allio, R.**, Reboud, E. L., Dupuis, J. R., Toussaint, E. F., Mazet, N., Hu S.-J., Lewis D.S., Kunte K., Cotton A. M., & Sperling, F. A. (2023). A comprehensive phylogeny and revised taxonomy illuminate the origin and diversification of the global radiation of Papilio (Lepidoptera: Papilionidae). *Molecular Phylogenetics and Evolution*, 183, 107758. DOI: [10.1016/j.ympev.2023.107758](https://doi.org/10.1016/j.ympev.2023.107758)
5. **Allio R.**, Tilak M. K., Scornavacca C., Avenant N. L., Corre E., Nabholz B., & Delsuc F. (2021). High-quality carnivore genomes from roadkill samples enable species delimitation in aardwolf and bat-eared fox. *eLife*, 10, e63167. DOI: [10.7554/eLife.63167](https://doi.org/10.7554/eLife.63167)
4. **Allio R.**, Nabholz B., Wanke S., Chomicki G., Pérez-Escobar O. A., Cotton A. M., Clamens A.-L., Kergoat G. J., Sperling F. A. H. & Condamine F. L. (2020). Genome-wide macroevolutionary signatures of key innovations in butterflies colonizing new host plants. *Nature communications*, 12(1), 354. DOI: [10.1038/s41467-020-20507-3](https://doi.org/10.1038/s41467-020-20507-3)
3. **Allio, R.**, Schomaker-Bastos, A., Romiguier, J., Prosdocimi, F., Nabholz, B., & Delsuc, F. (2020). MitoFinder: Efficient automated large-scale extraction of mitogenomic data in target enrichment phylogenomics. *Molecular Ecology Resources*, 20(4), 892-905. DOI: [10.1111/1755-0998.13160](https://doi.org/10.1111/1755-0998.13160)
2. **Allio, R.**, Scornavacca, C., Nabholz, B., Clamens, A. L., Sperling, F. A., & Condamine, F. L. (2020). Whole genome shotgun phylogenomics resolves the pattern and timing of swallowtail butterfly evolution. *Systematic Biology*, 69(1), 38-60. DOI: [10.1093/sysbio/syzo30](https://doi.org/10.1093/sysbio/syzo30)
1. **Allio, R.**, Donega, S., Galtier, N., & Nabholz, B. (2017). Large variation in the ratio of mitochondrial to nuclear mutation rate across animals: implications for genetic diversity and the use of mitochondrial DNA as a molecular marker. *Molecular biology and evolution*, 34(11), 2762-2772. DOI: [10.1093/molbev/msx197](https://doi.org/10.1093/molbev/msx197)

PREPRINTS

2. Zelvelder, B., Kergoat, G. J., Benoit, L., Tsuchida, T., Haran, J., & **Allio, R.** (2024). The first example of extreme and independent host plant shifts mediated by parasitic plants in insects. *bioRxiv*, 2024-04. DOI: [10.1101/2024.04.03.587887](https://doi.org/10.1101/2024.04.03.587887)
1. **Allio, R.**, Teullet, S., Lutgen, D., Magdeleine, A., Koual, R., Tilak, M. K., de Thoisy, B., Emerling, C.A., Lefebure, T., & Delsuc, F. (2022). Comparative transcriptomics reveals divergent paths of chitinase evolution underlying dietary convergence in ant-eating mammals. *bioRxiv*, 2022-11. DOI: [10.1101/2022.11.29.518312](https://doi.org/10.1101/2022.11.29.518312)

Programming and protocols

2. **MitoFinder**: a pipeline to assemble mitochondrial genomes and annotate mitochondrial genes from trimmed read sequencing data. [Github project](#)
1. Tilak, M. K., **Allio, R.**, & Delsuc, F. (2020). An optimized protocol for sequencing mammalian roadkill tissues with Oxford Nanopore Technology (ONT). [Protocol.io page](#)

Scientific Communications

10. Zelvelder, B., Haran, J., Benoit, L., Kergoat, G., & **Allio R.** (June 21-25th, 2023). Can parasitic plants act as a facilitating bridge for insects host plant shifts? *Evolution* 2023 (Albuquerque, New Mexico, USA). [Oral communication]
9. **Allio R.** (December 1st, 2022). speaker: Population genomics, phylogenomics, diversity analysis. Reflections, assessment and perspectives of the Bioinformatics activities within the "Agriculture, Environment, Biodiversity" cluster. Agropolis international (Montpellier, France) [Invited speaker]
8. **Allio R.** (November 30th, 2021). Phylogenomic et comparative genomics: Study adaptation from a macroevolution perspective. Centre de Biologie pour la Gestion des Populations (Montpellier). [Invited speaker]
7. **Allio R.**, Tilak M.-K., Scornavacca, C., Avenant N.L., Corre E., Nabholz B. & Delsuc F. (October 5-9th, 2020). Genomics from roadkill enable species delimitation in aardwolf and bat-eared fox. *Biodiversity Genomics 2020* (Institut Sanger, UK). [Virtual talk]
6. **Allio R.**, Tilak M.-K., Avenant N.L., Corre E., Nabholz B. & Delsuc F. (February 4-5th, 2020). Roadkill genomics: high quality mammalian genomes from hybrid assembly of short Illumina reads and MinION long reads. *Rencontres ALPHY : Génomique Evolutive, Bioinformatique, Alignement et Phylogénie* (Lyon, France). [Oral communication]
5. **Allio R.**, Tilak, M.-K., Magdeleine, A., Nabholz, B., & Delsuc, F. (February 3rd, 2020). How roadkill can become a valuable resource for genome-wide analyses. *Laboratoire d'Ecologie des Hydrosystèmes Naturels et Anthropisés* (Lyon, France). [Invited speaker]
4. **Allio R.**, Romiguier J., Nabholz B. & Delsuc F. (July 21-25th, 2019). Extracting complementary mitogenomic data from target enrichment experiments: a case study with 501 ant UCE libraries. *Annual Meeting of the Society for Molecular Biology and Evolution* (Manchester, UK). [Poster]
3. **Allio R.**, Romiguier J., Nabholz B. & Delsuc F. (February 7-8th, 2019). In search of mitochondrial DNA from Ultra Conserved Elements sequencing data. *ALPHY: Bioinformatics and Evolutionary Genomics* (Paris, France). [Oral communication]
2. **Allio R.**, Koual R., Tilak M.-K., Avenant N.L., Nabholz B. & Delsuc F. (October 16-17th, 2018). Testing the hypothesis of allopatric speciation through biogeographical disjunction in three species of African carnivores. *9th Annual Oppenheimer De Beers Research Conference* (Johannesburg, Afrique du Sud). [Poster]
1. **Allio R.**, Koual R., Tilak M.-K., Avenant N.L., Nabholz B. & Delsuc F. (August 19-22th, 2018). Testing the hypothesis of allopatric speciation through biogeographical disjunction in three species of African carnivores (aardwolf, bat-eared fox, and black-backed jackal). *2nd Joint Congress in Evolutionary Biology* (Montpellier, France). [Poster]

Teaching & Supervisory Experience

TEACHING

University of Montpellier, France

Teaching Assistant (12h), Evolutionary Biology

2018-2019

Teaching Assistant (12h), Evolutionary Biology

2017-2018

SUPERVISORY EXPERIENCE

Tom Rigaud , Undergraduate student. South african weevils taxonomy.	2024
Benjamin Zelvelde r, PhD candidate. Phylogenomics of weevils brood-site pollinators in the tropics: towards an understanding of the specialization factors of pollination systems in rainforests.	2023-present
Benjamin Zelvelde r, Graduate Student. Study of the evolution of weevil-plant-parasitic plant interactions using a phylogenomic approach.	2023
Léo Laborieux , Graduate Student. Host plant shifts and the emergence of new pest insects: the case the weevil genus <i>Phlyctinus</i> .	2023
Sophie Teullet , Graduate Student. Molecular evolution of chitinase genes in myrmecophagous mammals.	2020
Mathilde Barthe , Graduate Student. Convergent molecular evolution in the genomes of myrmecophagous carnivores.	2019
Dave Lutgen , Graduate Student. Comparative transcriptomics of salivary glands in placental mammals.	2019

Reviewing experience

Systematic Biology, Systematic Entomology, Molecular Phylogenetics & Evolution, Molecular Ecology, Molecular Ecology Resources, Bioinformatics, Zoologica Scripta, Zoological Research, Wellcome Open Research, PeerJ