Rémi Allio

Researcher, Centre de Biologie pour la Gestion des Populations
INRAE, Montpellier, France
✉ remi.allio@inrae.fr RemiAllio RemiAllio.github.io

Current position

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

Visiting researcher, EvoEco Lab, University of Toronto-Missisauga, ON, Canada. 2023-2024
Principal Collaborator: Dr. Marc Johnson

Graduate research project, Institute of Evolutionary Science of Montpellier, France 2017
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 of Montpellier, France 2016
Advisor: Dr. Benoit Nabholz
Thesis title: Study of nuclear and mitochondrial mutation rates in animals

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

Professional Trainings & Certifications

Occupational First Aid Responder, INRAe, France	2025
PPE Inspector for Climbing Equipment, Hévéa, France	2024
Tree Climber & Tree Climber Rescuer, INRAe, France	2023, 2024

Awards

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

Fundings

As Principal Investigator

8. **NanoPoll** - Travel support for national collaboration (French Guiana).	2024
Station de recherche des Nouragues.	9,000€
CNRS, France.	
7. **POLLIDIV**: Origins and consequences of	2025-2029
brood-site pollination emergences	305,315€
in weevils' diversification.	
Agence Nationale de la Recherche (ANR), France.	
6. **EXPLORE#6** - Travel support for international collaboration (Costa Rica).	2024
Programme d'Excellence I-SITE,	17,000€
Université de Montpellier, France.	
5. **IB2024** - MomphiDiv project.	2024
Travel support for international collaboration (Canada).	6,000€
IB2024 - Mobility funding. INRAE, France.	
4. **WeBait**: Comparative genomics and Development	2024
of phylogenetic baits for weevils (Curculionidae).	30,000€
IB2024 - Research funding. INRAE, France.	
3. OVPR Internal Research Grant.	2023
University of Toronto-Mississauga	6,780€
Ontario, Canada.	
2. **IB2023** - MomphiDiv Project.	2022
Travel support for international collaboration (Canada).	5,000€
IB2023 - Mobility funding. INRAE, France.	
1. Annual CBGP Internal call.	2022
Montpellier, France.	3,000€

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

17. Haran, J., Zelvelder, B., Boupoya, C. A., Couvreur, T. L. P., Niangadouma, R., Benoit, L., Kergoat, G. J., Buatois, B., Dufäy, M., Kojima, H., & **Allio, R.** (2026). New species of Endaeus

Schoenherr, 1826 (Curculionidae: Curculioninae: Ochyromerini) associated with Annonaceae and Clusiaceae. *European Journal of Taxonomy*, 1039(1), 165–198. DOI: 10.5852/ejt.2026.1039.3185

16. Emerling, C. A., Teullet, S., **Allio, R.**, Gatesy, J., Springer, M. S. & Delsuc, F. (2026). Pseudogenes Document Protracted Parallel Regression of Oral Anatomy in Myrmecophagous Mammals. *Molecular Biology and Evolution*, msag009. DOI: 10.1093/molbev/msag009

15. Juvé, Y., Lutrat, C., Ha, A., Weyna, A., Lauroua, E., Afonso Silva, A. C., Roux, C., Schifani, E., Galkowski, C., Lebas, C., **Allio, R.**, Stoyanov, I., Galtier, N., Schlick-Steiner, B. C., Steiner, F. M., Baas, D., Kaufmann, B., & Romiguier, J. (2025). One mother for two species via obligate cross-species cloning in ants. *Nature*, 646, 372–377. DOI: 10.1038/s41586-025-09425-w

14. Battlay, P., Hendrickson, B. T., Mendez-Reneau, J. I., Santangelo, J. S., Albano, L. J., Wilson, J., Caizergues, A., [9 authors], **Allio, R.**, [35 authors] & Kooyers, N. J. (2025). Haploblocks contribute to parallel climate adaptation following global invasion of a cosmopolitan plant. *Nature Ecology & Evolution*, 1-15. DOI: 10.1038/s41559-025-02751-2

13. **Allio, R.***, Teullet, S.*, Lutgen, D.*, Magdeleine, A., Koual, R., Tilak, M. K., de Thoisy, B., Emerling, C.A., Lefebure, T., & Delsuc, F. (2025). Transcriptomic data reveal divergent paths of chitinase evolution underlying dietary convergence in anteaters and pangolins. *Genome Biology and Evolution*, evaf002. DOI: 10.1093/gbe/evaf002

12. Perrier, C., **Allio, R.**, Legeai, F., Gautier, M., Beneluz, F., Marande, W., Theron, A., Rodde, N., Herrera, M., Saune, L. and Parrinello, H. (2024). Transposable element accumulation drives genome size increase in Hylesia metabus (Lepidoptera: Saturniidae), an urticating moth species from South America. Journal of Heredity, esae069. DOI: 10.1093/jhered/esae069

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

10. Haran, J.*, Li, X.*, **Allio, R.***, Shin, S., Benoit, L., Oberprieler, R. G., Farell, 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

9. Heighton, S. P.*, **Allio, R.***, Murienne, J., Salmona, J., Meng, H., Scornavacca, C., Bastos, A.D.S., Njiokou, F., Pieterson, 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

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

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

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 phy-

logeny 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

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

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

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

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/syz030

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

PREPRINTS

1. 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

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

11. Zelvelder, B., Kergoat, G. Benoit, L., Tsuchida T., Haran, J. & **Allio. R**. (June 26-30th, 2024). The first example of extreme and independent host plant shifts mediated by parasitic plants in insects. Third Joint Congress on Evolutionary Biology 2024 (Montreal, Canada). [Oral communication]

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 1rst, 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 (Montpelllier). [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

Thibaud Glinez, Assistant Engineer. 2026
Weevil specimen curation, imaging, and identification key development.
Kéo Gengembre, Undergraduate student. 2025
Ochyromerini taxonomy.
Léo Laborieux, Graduate Student. 2024

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

Reviewing experience

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