



# Rémi Allio

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

✉ [remi.allio@inrae.fr](mailto:remi.allio@inrae.fr)  [RemiAllio](#)  [RemiAllio.github.io](#)

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## 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-Mississauga, ON, Canada. 2023-2024  
Principal Collaborator: Dr. Marc Johnson

**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

## 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 <i>Molecular Biology &amp; Evolution</i>	2017
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## Fundings

### AS PRINCIPAL INVESTIGATOR

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

### AS A COLLABORATOR

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

## Publications

### PEER-REVIEWED ARTICLES

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*, evafo02. DOI: [10.1093/gbe/evafo02](https://doi.org/10.1093/gbe/evafo02)

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](https://doi.org/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](https://doi.org/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](https://doi.org/10.1098/rspb.2023.0889)

9. Heighton, S. P.\*, **Allio, R.\***, Muriienne, 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/syz030](https://doi.org/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](https://doi.org/10.1093/molbev/msx197)

#### PREPRINTS

3. 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. (2024). Structural variants underlie parallel adaptation following global invasion. *bioRxiv*, 2024-07. DOI: [10.1101/2024.07.09.602765](https://doi.org/10.1101/2024.07.09.602765)
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

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 1<sup>st</sup>, 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*

<b>Teaching Assistant</b> (12h), Evolutionary Biology	2018-2019
<b>Teaching Assistant</b> (12h), Evolutionary Biology	2017-2018

### SUPERVISORY EXPERIENCE

<b>Léo Laborieux</b> , Graduate Student. Host plant shifts and the emergence of new pest insects: the case the weevil genus <i>Phlyctinus</i> .	2024
<b>Tom Rigaud</b> , Undergraduate student. South african weevils taxonomy.	2024
<b>Benjamin Zelvelder</b> , 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
<b>Benjamin Zelvelder</b> , Graduate Student. Study of the evolution of weevil-plant-parasitic plant interactions using a phylogenomic approach.	2023
<b>Léo Laborieux</b> , Graduate Student. Host plant shifts and the emergence of new pest insects: the case the weevil genus <i>Phlyctinus</i> .	2023

<b>Sophie Teullet</b> , Graduate Student. Molecular evolution of chitinase genes in myrmecophagous mammals.	2020
<b>Mathilde Barthe</b> , Graduate Student. Convergent molecular evolution in the genomes of myrmecophagous carnivores.	2019
<b>Dave Lutgen</b> , 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