**Maéva A. TECHER**

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**EDUCATION**

**2012-2015 Ph.D. in Population Genetics and Ecology**

University of Reunion Island, France

Thesis: Genetic diversity, structure and admixture of native and introduced honey bee populations in the South West Indian Ocean islands.

**2010-2012 Master of Sciences in Biodiversity and Tropical Ecosystems**

University of Reunion Island, France

**2007-2010 Bachelor of Sciences in Biology of Organisms and Populations**

University of Reunion Island, France

**RESEARCH EXPERIENCE**

**2021-present** **Postdoctoral Research Associate**

**Texas A&M University and NSF-BII Behavioral Plasticity Research Institute, USA**

Co-Advisors: Pr. Hojun Song, Pr. Spencer Behmer and Pr. Gregory Sword

* Leading and generating a high temporal resolution and tissue-specific transcriptomic data during locust phase change for *Schistocerca gregaria*
* Built, tracked, and co-organized the rearing and maintenance of locusts and grasshoppers in crowded and isolated conditions in quarantine
* Plays an integral role in the organization of BPRI genome team that produced five new high-quality and chromosome-length locust genomes (largest ~8.5 Gb)
* Collaborate and produce samples for BPRI interdisciplinary experts (neurobiology, transcriptomics, single-cell genetics, behavior, nutrition, microbiome, functional genetics, ecology and evolution)
* Analysing population genetics data for Orthoptera (GBS-type)

**2016-2021** **Postdoctoral Scholar and Research Fellow (from 2019)**

**Okinawa Institute of Science and Technology, Japan**

Advisor: Pr. Alexander S. Mikheyev

* Developed new method to extract DNA/RNA from single low input arthropod material for Illumina and PacBio next-generation sequencing
* Created the largest worldwide collection to retrace the invasive routes of the honey bee parasitic Varroa mite (56 countries spanning over 30 years)
* Developed a bioinformatics pipeline for population genomics for analysing large sequencing datasets generated in-house (> 1500 whole genomes)
* Selected, designed, and validated a new targeted genotyping by 10k SNP sequencing
* Collaborative work in *Varroa* pedigree and linkage map analysis

*This work resulted in two publications in Communications Biology and Trends in Parasitology, one in Molecular Ecology and two other manuscripts are in preparation.*

**2012-2015 PhD Graduate Student**

**University of Reunion Island, France**

Supervisors: Bernard Reynaud, Hélène Delatte & Johanna Clémencet

* Collected and extracted DNA from > 3,000 honey bee individuals from the South West Indian Ocean islands and mainland native areas (Europe and Africa)
* Performed various molecular methods using mtDNA and microsatellites genotyping
* Retraced the colonization and admixture levels of native and invasive honey bee subspecies populations in insular systems using population genetics

*This work resulted in 6 publications including in BMC Genetics, PLoS One and Genome Biology and Evolution.*

**GRANTS AND AWARDS**

**2023 Postgraduate poster award** for Life on a Dynamic Planet Symposium (Texas A&M University, U.S.A)

**2020 OIST internal grant for co-organizing an international Mini Symposia** (2.5 million JPY)

**2019 KAKENHI Grant** for Japan Society for the Promotion of Sciencefellow (1.2 million JPY)

**2019 JSPS Postdoctoral Standard Fellowship** (Joint call between CNRS – JSPS P19723)

**2013-2014 *Agreenium* Fellow Travel Grants** (Toulouse and Bordeaux**,** France)

**2012-2015 Ph.D. Fellowship** from the Science and Technology Reunion Island Doctoral School

**2009 Travel award to the Darwin Conference 2009** at Cambridge, England

(winner of the 6th edition of the Rosalind Franklin Challenge, University of La Réunion)

**2009 Expo sciences Reunion Travel award** to the Eskom Expo for Young Scientists

(University of Pretoria, South Africa)

**PUBLICATIONS**

*Peer-reviewed*

[1] **Techer, M. A.,** Roberts, J. M. K., Cartwright, R. A., & Mikheyev, A. S. (2022). The first steps toward a global pandemic: Reconstructing the demographic history of parasite host switches in its native range. Molecular Ecology, 31(5), 1358–1374.

[2]Hasegawa, N., **Techer, M. A.,** & Mikheyev, A. S. (2020). A toolkit for studying Varroa genomics and transcriptomics: Preservation, extraction, and sequencing library preparation. BMC Genomics, 22(1), 54.

[3]Galataud, J., Delatte, H., **Techer, M. A.,** Simiand, C., Sookar, P., Reynaud, B., & Clémencet, J. European meets African honeybees (*Apis mellifera L*.) in the tropics: morphological changes related to genetics in Mauritius Island (South-West Indian Ocean), PLOS One.

[4]Traynor, KS., Mondet, F., de Miranda, J. R., **Techer, M. A\*.**, Kowallik, V., Oddie, MAY., Chantawannakul, P., & McAfee, A. (2020). Varroa destructor: A Complex Parasite, Crippling Honey Bees Worldwide. Trends in Parasitology, 36(7), 592–606.

\* *Data mining and creation of species haplotype distribution interactive map resource* [*https://mikheyevlab.github.io/varroa-mtDNA-world-distrib/*](https://mikheyevlab.github.io/varroa-mtDNA-world-distrib/)

[5] Dukku, U. H., **Techer, M. A.,** & Vincent, S. N. (2020). A country-wide survey of Varroa destructor, an ectoparasitic mite of honey bees, in Nigeria: a preliminary report. Journal of Apicultural Research, 59(1), 59–62.

[6] **Techer, M. A.,** Rane, R. V., Grau, M. L., Roberts, J. M. K., Sullivan, S. T., Liachko, I., Childers, A. K., Evans, J. D., & Mikheyev, A. S. (2019). Divergent evolutionary trajectories following speciation in two ectoparasitic honey bee mites. Communications Biology, 2(1), 357.

[7] Wragg, D., **Techer, M. A.,** Canale-Tabet, K., Basso, B., Bidanel, J.-P., Labarthe, E., Bouchez, O., Le Conte, Y., Clémencet, J., Delatte, H., & Vignal, A. (2018). Autosomal and Mitochondrial Adaptation Following Admixture: A Case Study on the Honeybees of Reunion Island. Genome Biology and Evolution, 10(1), 220–238.

[8] **Techer, M. A.,** Clémencet, J., Simiand, C., Turpin, P., Garnery, L., Reynaud, B., & Delatte, H. (2017). Genetic diversity and differentiation among insular honey bee populations in the southwest Indian Ocean likely reflect old geographical isolation and modern introductions. PLOS One, 12(12), e0189234.

[9] **Techer, M. A.**, Clémencet, J., Simiand, C., Preeaduth, S., Azali, H. A., Reynaud, B., & Hélène, D. (2017). Large-scale mitochondrial DNA analysis of native honey bee *Apis mellifera* populations reveals a new African subgroup private to the South West Indian Ocean islands. BMC Genetics, 18(1), 53.

[10] **Techer, M. A.,** Clémencet, J., Simiand, C., Portlouis, G., Reynaud, B., & Delatte, H. (2016). Genetic diversity of the honeybee (*Apis mellifera L.*) populations in the Seychelles archipelago. Insect Conservation and Diversity / Royal Entomological Society of London, 9(1), 13–26.

[11] Rasolofoarivao, H., Clémencet, J., **Techer, M. A.,** Ravaomanarivo, L. H. R., Reynaud, B., & Delatte, H. (2015). Genetic diversity of the endemic honeybee: *Apis mellifera unicolor* (Hymenoptera: Apidae) in Madagascar. Apidologie, 46(6), 735–747.

[12] **Techer, M. A.,** Clémencet, J., Turpin, P., Volbert, N., Reynaud, B., & Delatte, H. (2015). Genetic characterization of the honeybee (*Apis mellifera*) population of Rodrigues Island, based on microsatellite and mitochondrial DNA. Apidologie, 46(4), 445–454.

**SKILLS AND COMPETENCES**

*Bioinformatics skills:*

**Classical population genetics analysis** using microsatellites genotyping and mitochondrial sequencing.

**Whole genome sequencing** and **transcriptomics** **analysis** (quality check, reads mapping, variant calling for population genomics analysis).

**Reference genome** and **large** **SRA set submission** with NCBI and DDBJ.

Model-based inference of demographic history using DIYABC and fastsimcoal2.

**Data science analysis and reproducibility** with Snakemake, unix-shell, R, markdown, and GitHub.

Spatial data mapping using QGis and R.

Graphical illustration editing using Microsoft Office Package, Adobe Aura & Illustrator, Gimp, Inkscape. Certified “Effective Visual Communication” workshop by Seyens Ltd.

*Strong wet laboratory skills:*

**DNA/RNA** **extraction** **and quantification** routinely acquired from diverse tissues and preservation.

**NGS libraries preparation with low input gDNA** for HiSeq4000 and NovaSeq6000 Illumina platforms.

Proficient in targeted methods for mtDNA barcoding by RFLP or Sanger sequencing, microsatellites genotyping and SNP genotyping-by-sequencing (from design to validation).

*Fieldwork:*

**Experience of *in vitro* or semi-artificial rearing of various arthropods** (notably honey bees, varroa mites, Schistocerca grasshoppers, stick insects).

**Experience in experimental** **beekeeping**.

**Insect field collection and sorting**. Recording and direct observations of interactions among indigenous plants and animals-visitors, flora diversity inventory in quadrat (insular and tropical regions).

Measuring morphological traits in non-destructive (arthropods) and destructive (angiosperms) using binocular/microscopy material mounted with a camera.

*Languages:*

French and Creole (mother tongue), English (fluent), Japanese (intermediate), and Spanish (novice).

*Communication:*

Highly-skilled in visual communication using Slides PowerPoint, cartoon and 8-Bit artwork.

*Networking:*

Building from scratch a worldwide research collection for Varroa mites (contacting, creating MTA and import documents, shipments, processing samples in respect of the Convention on Biological Diversity).

**STUDENT MENTORING**

**2022 Alexis Acoff, MSc student,** Southern Illinois University Edwardsville

**2021-2022 Alyssa Canova, Ph.D. student,** Texas A&M University

 **Vivian Peralta Santana, Ph.D. student,** Texas A&M University

**Christopher Brennan, Ph.D. student,** Texas A&M University

**Audélia Mechti, Ph.D. student,** Texas A&M University

**Danielle Sherry, undergraduate**, Texas A&M University

**2020 Nonno HASEGAWA, Ph.D. student,** OIST

**2019 Elroy KWAN-AU, Honour student**, ANU Canberra, hosted at OIST

**2015 Julien GALATAUD, MSc student**, University of La Réunion.

*Leaderships and management Skills for Postdoc course certified with hfp consulting in 2019.*

**ORAL PRESENTATIONS**

*Selected invited talks*

**2020** Invited speaker at the honey bee genomics workshop session at the 28th Plant and Animal Genome Conference (PAG XXVIII) at San Diego, California, USA.

**2020** Invited speaker at the COLOSS (Prevention of honey bee Colony LOSSes) Asia Conference 2020 in Chiang Mai, Thailand.

**2019** Invited speaker at the OIST Science Festival 2019, Okinawa, Japan. <https://www.oist.jp/science-festival-2019>

**2019** Invited speaker at ANU Canberra, Australia.

**2018** Invited speaker by the EcoEncontros at the University of Sao Paulo, Brazil.

**2017** Invited speaker by OIST Communication Section to the Science Trip to Miyako High School, Miyako-jima.

*Selected International conferences talks*

**2018 Techer, M. A.**, Roberts, J.K and Mikheyev, A. S. Tracking genomics footprints of successful host switches in honey bee Varroa mites. Eurbee 8, Ghent, Belgium.

**2018 Techer, M. A.**, Roberts, J.K and Mikheyev, A. S. At the origin of a global invasion: the honeybee parasite that keeps on jumping. IUSSI2018, Guaruja, Brazil.

**2016 Techer, M. A.**, Clémencet, J., Simiand, C., Reynaud, B., Delatte\*, H. Genetic diversity and structure of *A. mellifera* in the South West Indian Ocean islands. Eurbee 7, Cluj-Napoca, Romania.

**2014 Techer, M. A.**, Clémencet, J., Simiand, C., Turpin, P., Reynaud, B. & Delatte, H. 2014. Unraveling the mysteries of honeybee in the Mascarene Islands. IUSSI2015, Cairns, Australia.

**POPULAR SCIENCE AND OUTREACH COLLABORATION**

**2019 Honey and Coral Project.** Collaboration for prevention of red soil erosionbetween the Ecology and Evolution and Onna Village Office, Agricultural Section, Okinawa.

[www.oist.jp/news-center/news/2019/9/6/honeybees-help-save-okinawan-coral](http://www.oist.jp/news-center/news/2019/9/6/honeybees-help-save-okinawan-coral)

**2019 Guest at WonderLabs podcast** (Apple: [apple.co/2KP4pWl](https://apple.co/2KP4pWl), Google: [bit.ly/2StEUuX](https://bit.ly/2StEUuX))

**2018 Speaker at the 3rd Nerd Nite Okinawa.**

**2016-2019 OIST Science Festival**.Lead organizer of the booth“The wonderful world of honeybees” and creator of the “EcoEvo Quest” video game (.ppt support).

**2017** Teacher at **Onna/OIST Children’s school of Science.**

**OTHER EXPERIENCES**

**2021** Jury at the Graduate Student Forum of Entomology at Texas A&M University

**2020-2021** Co-organizer of the “Honey bee health in a changing world” and “COLOSS Asia” at OIST in March 2021 and website developer <https://honeybeehealth2021.github.io/>

**2020** Jury member of “My Research in 200s”, OIST.

**2017-2019** Member of the Internal Seminar Series organizing committee, OIST.

**2017** Volunteer at theTEDxOIST**,** Okinawa.

**2015** Volunteer at the IAEA research *Tephritidae* meeting**,** La Réunion.

**2014-2016** Ph.D. student delegate at the UMR PVBMT and 3P Laboratory.

Reviewer at Apidologie, BioMed Research International, PeerJ, JAS, Entomological Science, Insects, Experimental and Applied Acarology, Molecular Ecology.

<https://publons.com/researcher/3098984/maeva-techer>

**REFERENCES**

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