

Federico López-Osorio

Bioinformatics | Genomics

+00 000 0000000
0000-0001-7654-7967

f*****@gmail.com
federico-lopez-osorio-a46b5754

flopezo

zOAvFzMAAAAJ
@flopezos

Summary

I am a biologist with expertise in bioinformatics, genomic analysis, and modern techniques to visualise data. My scientific research focuses on discovering the genetic features underlying traits of interest in insects and other organisms. I integrate genome-wide data using reproducible workflows and communicate findings to the scientific community, the general public, and stakeholders.

Experience

Marie Skłodowska-Curie Actions Fellow

Queen Mary University of London

2019 – 2022 London, UK

- Analysed population genomic data to understand the origin of a social supergene in ants
- Co-authored a responsive mode research grant proposal successfully funded by the Biotechnology and Biological Sciences Research Council (BBSRC) (ref. BB/T015683/1)
- Published research papers in high-impact journals
- Actively participated in research projects of graduate students and contributed to their mentoring

Postdoctoral researcher

Queen Mary University of London

2018 – 2019 London, UK

- Analysed hundreds of RNA-seq samples of bees to investigate the effects of exposure to various insecticides
- Wrote shell and R scripts to identify differentially expressed genes and visualise results
- Disseminated findings in poster format at an international conference
- Assisted graduate students in their research projects

Gerstner Scholars Program (Biology) Fellow

American Museum of Natural History

2016 – 2018 New York, NY, USA

- Designed, managed, and developed a comparative genomics study of social wasps
- Collected field samples and sequenced genomes and transcriptomes of wasp species
- Developed bioinformatics workflows for *de novo* assembly of genomes and transcriptomes, annotating genomes, finding differentially expressed genes, orthology inference, and phylogenomics
- Presented findings in talks at international conferences
- Wrote progress and final reports

Education

Ph.D. in Biology

University of Vermont

Aug. 2010 – May 2016

Dissertation: Phylogenetics and molecular evolution of highly eusocial wasps

B.Sc. in Biology

Universidad Industrial de Santander

2009

Skills

Bioinformatics

- Analysis of high-throughput genomic data
- Quality control of genome-scale assays
- Genome and transcriptome assembly, including non-model organisms
- Structural and functional genome annotation
- Orthology inference and phylogenomics
- Differential gene expression and transcript usage (RNA-seq)
- Variant calling and analysis
- Metagenome assembly and taxonomic profiling

Data Analysis

- Data visualisation (e.g., ggplot2)
- Linear models (e.g., GLM, GLMM)
- Data normalisation and transformation
- Unsupervised learning (e.g., PCA)
- Experimental design
- Effective reporting with aesthetic appeal

Programming

- R, Tidyverse, Shiny
- Shell scripting
- Unix systems, high-performance computing
- git, GitHub
- LaTeX, R Markdown, Quarto
- Workflow management (e.g., Snakemake)
- Package management (e.g., Conda)
- Python

Languages

English (fluent) | Spanish (native)

Journal Articles

- Witwicka, A., **López-Osorio, F.**, Patterson, V., & Wurm, Y. (2023). Expression of subunits of an insecticide target receptor varies across tissues, life stages, castes, and species of social bees. *Molecular Ecology*, 32(5), 1034–1044. doi:10.1111/mec.16811
- Stolle, E., Pracana, R., **López-Osorio, F.**, Priebe, M. K., Hernández, G. L., Castillo-Carrillo, C., ... Wurm, Y. (2022). Recurring adaptive introgression of a supergene variant that determines social organization. *Nature Communications*, 13(1), 1180. doi:10.1038/s41467-022-28806-7
- **López-Osorio, F.**, & Wurm, Y. (2020). Healthy pollinators: Evaluating pesticides with molecular medicine approaches. *Trends in Ecology & Evolution*, 35(5), 380–383. doi:10.1016/j.tree.2019.12.012
- Loope, K. J., **López-Osorio, F.**, & Dvořák, L. (2017). Convergent reversion to single mating in a wasp social parasite. *The American Naturalist*, 189(6), E138–E151. doi:10.1086/691405
- **López-Osorio, F.**, Pickett, K. M., Carpenter, J. M., Ballif, B. A., & Agnarsson, I. (2017). Phylogenomic analysis of yellowjackets and hornets (Hymenoptera: Vespidae, Vespinae). *Molecular Phylogenetics and Evolution*, 107, 10–15. doi:10.1016/j.ympev.2016.10.006
- Perrard, A., **López-Osorio, F.**, & Carpenter, J. M. (2016). Phylogeny, landmark analysis and the use of wing venation to study the evolution of social wasps (Hymenoptera: Vespidae: Vespinae). *Cladistics*, 32(4), 406–425. doi:10.1111/cla.12138
- **López-Osorio, F.**, Perrard, A., Pickett, K. M., Carpenter, J. M., & Agnarsson, I. (2015). Phylogenetic tests reject Emery's rule in the evolution of social parasitism in yellowjackets and hornets (Hymenoptera: Vespidae, Vespinae). *Royal Society Open Science*, 2(9), 150159. doi:10.1098/rsos.150159
- **López-Osorio, F.**, Pickett, K. M., Carpenter, J. M., Ballif, B. A., & Agnarsson, I. (2014). Phylogenetic relationships of yellowjackets inferred from nine loci (Hymenoptera: Vespidae, Vespinae, *Vespula* and *Dolichovespula*). *Molecular Phylogenetics and Evolution*, 73, 190–201. doi:10.1016/j.ympev.2014.01.007

Book Chapters

- Lopez-Osorio, F. (2021). *Emery's Rule* (C. K. Starr, Ed.). doi:10.1007/978-3-030-28102-1_42
-