WALID MAWASS, PH.D.

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ACADEMIC APPOINTMENTS

Postdoctoral Scholar, University of Chicago 2023-present
Human Genetics department

Postdoctoral Research Associate, University of Arizona 2021-2023
Ecology and Evolutionary Biology Department

EDUCATION

PhD Université du Québec à Trois-Rivières (UQTR), Canada September 2023

MS Université du Québec à Trois-Rivières (UQTR), Canada December 2017
(*Accepted into Ph.D. program through fast-track option)*

BS Lebanese University – Faculty of Sciences II, Lebanon August 2014
Life Sciences (Ecology and Biodiversity option)

RESEARCH EXPERIENCE

University of Chicago, USA 2023-present
Postdoctoral Scholar
Advisor: Dr. Jeremy Berg

- Characterize the limitations of principal component analysis (PCA) in mitigating population stratification in large-scale genetic analysis studies across massive biobanks and meta-analyses.
- Formulate analytical frameworks (Rial et al., Zhou et al.) using moment equations and allele frequency spectra to evaluate linked selection, stabilizing selection, and disease-variant evolution.
- Evaluate empirical bias in polygenic risk scores (PGS) selection tests and Genome-Wide Association Studies (GWAS) summary statistics due to residual ancestry stratification within ancestry-diverse panels.
- Assessment of the role of linked selection in shaping genetic diversity patterns in mammalian species by employing empirical measurements from wild monitored populations, while accounting for recombination and functional target sizes using genomic data.

University of Arizona, USA 2021-2023
Postdoctoral Research Associate
Advisor: Dr. Joanna Masel

- Evaluated an analytical model designed to investigate the role of beneficial mutation shortage in determining the long-term evolutionary dynamics of small populations
- Developed C-based forward-time simulators and HPC pipelines to track long-term mutational dynamics and fitness trajectories assuming a finite genome with recombination and linkage blocks.
- Quantified the impacts of mutational load and weak epistasis on long-term population health and fitness under equilibrium dynamics.

Université du Québec à Trois-Rivières, Canada 2016-2021

Graduate Research Assistant
Advisor: Dr. Emmanuel Milot

- Processed and analyzed massive retrospective human genealogies comprising millions of individual records to model long-term inheritance of complex phenotypic traits.
- Applied linear mixed-effects models and variance partitioning to isolate additive genetic variance from complex environmental variation in longitudinal human cohorts.
- Assessed the sensitivity of quantitative genetic parameter estimates to variability in pedigree quality and model specification.

PUBLICATIONS (TOTAL: 11)

Peer-Reviewed & Accepted

1. Mawass, W., and Milot, E., 2025, Assessing the impact of pedigree attributes on the validity of quantitative genetic parameter estimates; *Journal of Evolutionary Biology,* 38 (4), 439–456. doi: https://doi.org/10.1093/jeb/voaf010
2. Mawass, W., Mayer, F.M. and Milot, E., 2022. Genotype-by-environment interactions modulate the rate of microevolution in reproductive timing in humans. *Evolution*, *76*(7), 1391-1405. doi: https://doi.org/10.1111/evo.14504
3. Mawass, W., Hernández, U., Matheson, J., Berg, J. J., and Masel, J., Extinction vortices are driven more by a shortage of beneficial mutations than by deleterious mutation accumulation. *Proc Biol Sci 1 June 2026; 293 (2072): 20260600*. doi: https://doi.org/10.1098/rspb.2026.0600

Preprints (Under Review)

4. Mawass, W., and Milot, E., Contrasting evolutionary outcomes in a human life history trait which is heritable and under consistent unbiased directional selection, *bioRxiv*, 2025.10.13.682154. doi: https://doi.org/10.1101/2025.10.13.682154
5. Blanc, J, Mawass, W., and Berg, J. J., Quantifying the susceptibility of polygenic scores to ancestry stratification, *bioRxiv*, 2025.12.04.692430. doi: https://doi.org/10.64898/2025.12.04.692430

Manuscripts in Preparation

6. **Mawass, W.** "Empirically reported heritable fitness variance predicts severe depletion of neutral diversity in wild populations" (*in prep; advanced manuscript provided upon request*)
7. **Mawass, W.**, Blanc, J., Sherif, A. and Berg, J. J., "Evaluating bias in polygenic score associations due to imperfect control of population stratification" (*in prep; advanced manuscript provided upon request)*
8. Hernández, U., **Mawass, W.**, Matheson, J., and Masel, J., "Rare variants drive high variance in human ancestral fitness at mutation-selection-drift balance" (*in prep*)
9. Marcelle, M., Hernández, U., **Mawass, W.**, Gutenkust, R and Masel, J., "High deleterious mutation rate distorts site frequency spectrum in mammals and leads to erroneous inference of demographic expansions" (*in prep*)
10. Rial, K, **Mawass, W.**, and Berg, J. J., "Information about the derived orientation of disease risk-increasing variants provides power to detect signals of directional selection on diseases" (*in prep*)
11. Zhou, S., **Mawass, W.**, Hayward, L. and Berg, J. J., "Linked neutral diversity under stabilizing selection: a two-locus moments mode" (*in prep*)

SCHOLARSHIPS/AWARDS

- University of Chicago BSD CAP travel award
- Excellence award from CPCS-BCM
- 1st prize award in departmental poster competition

CONFERENCE PRESENTATIONS (12 AS ORAL & 12 AS POSTER)

Selected Oral Presentations

- SMTPB Conference at NITMB 2025
- Mid-West Population Genetics Conference 2024
- U of Chicago BSD Postdoctoral Symposium 2024
- Arizona Postdoctoral Research Conference 2023
- Evolution Conference 2021, 2022, 2023, 2025
- SMBE 2021
- SQEBC 2018
- AGA President's Symposium 2018, 2020

Selected Poster Presentations

- Mid-West Population Genetics Conference 2025, 2026
- Evolution Conference 2025
- ProbGen 2025, 2026
- PEQG 2022, 2026
- Journées Généalogie et Génétique 2017, 2019
- Sixth EvoDemoSoc Annual Meeting 2019
- SQEBC 2017

TEACHING EXPERIENCE

- Preceptor, ECOL 419/519 – Introduction to Modeling in Biology Spring 2021
  University of Arizona
  - Taught upper-level undergraduate and graduate students mathematical modeling, reading and interrogating scientific literature, and computational simulation methods using R, Python and Mathematica.
- Co-Lead instructor, ECOL 599 – Independent Study on Theoretical and Empirical Population Genetics 2021-2023
  University of Arizona
  - Co-designed syllabus and led weekly discussion-based seminars on foundational and contemporary population genetics papers, ranging from the theoretical to the empirical.
- Guest Lecturer, GNT 1007 – Molecular Genetics, Spring 2019
  Université du Québec à Trois-Rivières (UQTR)
  - Delivered interactive lectures to undergraduate biology majors on quantitative trait inheritance, gene-environment interactions, and variance partitioning approaches.

STUDENT MENTORSHIP & ADVISING

Direct Student Research Mentorship

- **Undergraduate Computer Science Researcher** (University of Arizona, Summer 2022): Mentored an undergraduate student in translating complex theoretical population genetics (Wright-Fisher vs. Moran processes, effective population size) into C-based forward-time simulation algorithms.
- **STAR Lab Research Mentor** (University of Arizona, 2022–2023): Guided undergraduate trainees through hands-on biology projects, from hypothesis generation and literature search to experimental design and implementation.

- **UChicago Computational Biology Outreach (COMBO) Mentor** (2024): Mentored high school students from underrepresented backgrounds in Python programming, statistical genetics fundamentals, and data analysis.
- **UChicago Berg Lab** (2026): Mentored a research trainee of a mathematics background on a method development project, providing guidance and teaching by engaging weekly with materials, such as papers, presentations and technical issues.

Academic Advising & Evaluation

- **Grand Award Judge, SARSEF Regional Science and Engineering Fair** (2023): Evaluated high school and middle school research projects in biology and data science.
- **Evaluator for Master's & Doctoral Poster Competitions** (UQTR, 2019): Reviewed and scored graduate research presentations, providing structured feedback on scientific rigor and delivery.
- **Student Representative, Executive Committee for Cellular & Molecular Biology** (UQTR, 2019–2021): Contributed to program reforms and development of curriculum courses and their respective frameworks.

LEADERSHIP, SERVICE & OUTREACH

Outreach and Service

- GSA ECLP alumni mentorship program 2025
- Grand award judge at the 2023 SARSEF fair 2023
- STAR Lab research mentor 2022-2023
- Chair/moderator 2021
- UQTR outreach program 2019
- Instructor for local scientific outreach program 2013

Conference Organization

- WAMBAM 2017
- Journées Généalogie et Génétique 2017
- SQEBC 2018

Leadership

- GSA Early Career Leadership Program member 2023-2025
  Co-Chair of GSA Community and Membership Engagement (CME)
- EEB Committee for Community, Anti-Racism, and Equity (CARE) 2022-2023
  Postdoc member
- AEBCM (student association at UQTR) 2018-2021
  Executive committee member serving as VP for Scientific Affairs

COMPUTER & STATISTICAL SKILLS

- **Programming Languages:** Python (NumPy, SciPy, pandas, scikit-learn), R, SQL, C, Unix Shell, Wolfram/Mathematica.
- **Methodologies:** Genome-Wide Association Studies (GWAS), Polygenic Risk Score (PGS) Evaluation, Random Matrix Theory, Mixed-Effects / Multilevel Modeling, Population Stratification Correction, High-Dimensional Variance Partitioning.
- **Environments & Workflows:** High-Performance Computing (HPC), Snakemake, Git/GitHub, RStudio, Jupyter.

SCHOLARLY MEMBERSHIPS

- American Society of Human Genetics (ASHG)
- Genetics Society of America (GSA)
- Society for Molecular Biology and Evolution (SMBE)

- Society for the Study of Evolution (SSE)
- Society for Modeling and Theory in Population Biology (SMTPB)
- American Genetic Association (AGA)
- National Postdoctoral Association

LANGUAGES (TOTAL: 3)

- **Arabic**: Native Language
- **English**: Full Professional Proficiency
- **French**: Native Language