

# *Ana Y. Morales-Arce*

Istituto Zooprofilattico Sperimentale delle Venezie

🏠 Verona, Italy

✉ [amorales@izsvenezie.it](mailto:amorales@izsvenezie.it)

🌐 [aymorales-arce.com](http://aymorales-arce.com)

## PROFESSIONAL APPOINTMENTS

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- Present-2024 Research fellow, Istituto Zooprofilattico Sperimentale delle Venezie, IT
- 2023-2020 Postdoctoral Researcher at Institute of Ecology and Evolution, University of Bern, CH & Instituto Gulbenkian de Ciência, Oeiras, PT  
(*Supervised by:* Claudia Bank and Maria João Amorim)
- 2020-2018 Postdoctoral Fellow, Center for Evolution and Medicine (CEM), Arizona State University, USA  
(*Supervised by:* Jeffrey D. Jensen and Anne C. Stone)

## EDUCATION

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- 2017-2012 Ph.D. Archaeology, University of Calgary, Canada  
Thesis: Ancient mitochondrial DNA in Mesoamerica and its borderlands. The cases of Paquimé (A.D. 1200-1450), Greater Nicoya (A.D. 800-1250) and Central Mexico (A.D. 900-1519).
- 2010-2006 M.Sc. Anthropology, University of Costa Rica  
Thesis: Genetic variation associated with lactose intolerance in Amerindians of Lower Central America and the related potential health problems.
- 2004 -2000 B.Sc. Biotechnology Engineering, Instituto Tecnológico de Costa Rica (TEC)  
Thesis: Genetic variation of squirrel monkeys (*Saimiri oerstedii*). Implications for conservation.

## RESEARCH INTERESTS

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Population genetics, computational modeling, pathogens evolution, ancient DNA.

## PUBLICATIONS

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- 2022 Claudia Bank, Mark A. Schmitz, **Morales-Arce AY**. Evolutionary models predict potential mechanisms of escape from mutational meltdown. *Front. Virol.* 2:886655.
- 2022 Susanna Sabin, **Morales-Arce AY**, Susanne P. Pfeifer, and Jeffrey D. Jensen. Comparative population genomics of *Mycobacterium canettii* and *Mycobacterium tuberculosis*. *G3 Genes|Genomes|Genetics*, 12 (5): jkac055.
- 2022 **Morales-Arce AY**, Johri P, Jensen JD. Inferring the distribution of fitness effects in influenza A virus and human cytomegalovirus. *Heredity.* 128: 79–87.
- 2021 Songül Alpaslan-Roodenberg, David Anthony, Hiba Babiker, Eszter Bánffy, Thomas Booth, Patricia Capone, Arati Deshpande-Mukherjee, Stefanie Eisenmann, Lars Fehren-Schmitz, Michael Frachetti, Ricardo Fujita, Catherine J. Frieman, Qiaomei Fu, Henry Louis Gates Jr., Victoria Gibbon, Wolfgang Haak, Mateja Hajdinjak, Kerstin P. Hofmann, Brian Holguin, Takeshi Inomata, Hideaki Kanzawa-Kiriyama, William Keegan, Janet Kelso, Johannes Krause, Ganesan Kumaresan, Chapurukha Kusimba,

- Sibel Kusimba, Carles Lalueza-Fox, Bastien Llamas, Scott MacEachern, Swapan Mallick, Hirofumi Matsumura, Janet Monge, **Morales-Arce AY**, Giedre Motuzaite Matuzeviciute, Veena Mushrif-Tripathy, Nathan Nakatsuka, Rodrigo Nores, Christine Ogola, Mercedes Okumura, Nick Patterson, Ron Pinhasi, S.P.R. Prasad, Mary E. Prendergast, Jose Luis Punzo, David Reich, Rikai Sawafuji, Elizabeth Sawchuk, Stephan Schiffels, Jakob Sedig, Svetlana Shnaider, Kendra Sirak, Pontus Skoglund, Viviane Slon, Meradeth Snow, Marie Soressi, Matthew Spriggs, Philipp W. Stockhammer, Anna Szécsényi-Nagy, K. Thangaraj, Vera Tiesler, Ray Tobler, Chuan-Chao Wang, Christina Warinner, Surangi Yasawardene, Muhammad Zahir. Ethics of DNA Research on Human Remains: Five Globally Applicable Guidelines. *Nature*, 599: 41-46.
- 2020 **Morales-Arce AY**, Sabin SJ, Stone AC, Jensen JD. The population genomics of within-host *Mycobacterium tuberculosis*. *Heredity*, 126(1):1-9.
- 2020 **Morales-Arce AY**, Harris RB, Stone AC, Jensen JD. Evaluating the contributions of purifying selection and progeny-skew in dictating within-host *Mycobacterium tuberculosis* evolution. *Evolution*, 74-5: 992-1001.
- 2019 **Morales-Arce AY**, McCafferty G, Hand J, Schmill N, McGrath K, Speller C. Ancient mitochondrial DNA and population dynamics in Postclassic Central Mexico: Cholula (A.D. 900-1350) and Tlatelolco (A.D. 1325-1521). *Archaeological and Anthropological Sciences*, 11: 3459-3475.
- 2017 **Morales-Arce AY**, Hofman CA, Duggan AT, Benfer AK, Katzenberg MA, McCafferty G, Warinner C. Successful reconstruction of whole mitochondrial genomes from ancient Central America and Mexico. *Scientific Reports*. 7(1):18100.
- 2017 **Morales-Arce AY**, Snow MH, Kelley JH, Katzenberg MA. Ancient mitochondrial DNA and ancestry of Paquimé inhabitants, Casas Grandes (1200-1450 A.D.). *American Journal of Physical Anthropology*, 163: 616-626.
- 2015 **Morales-Arce AY**. Ancient DNA studies in Mesoamerica: major contributions and limitations. *Proceedings of the Annual Chacmool Archaeological Conference* 47: 139-148.
- 2014 McCafferty G, Carrol G, Manion J, **Morales-Arce AY**, Smekal M. Huesos Nicaragua: Creación de un Laboratorio de Bio-Arqueología en la Universidad Nacional/ Bones Nicaragua: Creation of a Bio-Archaeology Laboratory in the National University. *Mi Museo y Vos* 29: 13-16.
- 2012 **Morales-Arce AY**, Alvarado Rojas S, Calvo Brenes M, Contreras Rojas J, Raventós Vorst H. Un acercamiento al contenido cultural de los delirios de personas con esquizofrenia de Costa Rica/ Cultural content of delusions in people with schizophrenia from Costa Rica. *Cuadernos de Antropología*, 22.
- 2012 **Morales-Arce AY**. Lactose Intolerance in Indigenous Groups of Lower Central America. Genetic variation and its potential health problem. LAP LAMBERT Academic Publishing, Saarbrücken, Germany. 84p.

## BOOK CHAPTERS

- 2022 **Morales-Arce AY**, Smith-Guzmán NE. Human genetic diversity through time in Central America: Current advances and future directions. In: Roberto Herrera, Yahaira Núñez-Cortés, and Geoffrey McCafferty, editors. *The Cultural Mosaic of Central*

America: Diverse Archaeologies of the Archaeology of Diversity. Salt Lake City, UT:  
University of Utah Press. In review.

## RESEARCH & FIELDWORK EXPERIENCE

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### Research fellow

- Present-February 2024 Istituto Zooprofilattico Sperimentale delle Venezie, SCT1-Verona, Italy
- Conducting molecular diagnostics of mycoplasma, paratuberculosis and avian influenza
  - Conducting Mycoplasma genetics research using NGS technologies

### Post-doctorate Research

- June 2023-July 2021 Institute of Ecology and Evolution, University of Bern, Switzerland
- Conducted computational modeling, bioinformatic analysis, and genomics to understand patterns and genomic signatures in *in-vitro* Influenza A viral populations in presence of mutagenic drugs
  - Used of R, Julia, Linux, and Python for data analysis and models
  - Processed data to visualize the results and conduct statistical analysis
  - Prepared and presented data at lab meetings and represented the project at conferences
- June 2021-July 2020 Gulbenkian Science Institute, Oeiras, Portugal
- Designed and conducted influenza A virus infection experiments in a BSL2 laboratory
  - Collaborated with the cell biologist, virologist, and molecular biologist team to establish experimental evolution protocols in the influenza A virus
  - Conducted site-directed mutagenesis, reverse genetics, viral growth curves, viral RNA counts and counted PFU using plaque assays
  - Extracted RNA using a diversity of methods and quantified RNA, i.e., nanodrop, qubit, and qPCR
  - Cultured different types of cell lines, i.e., MDCK and 293T, and infected them under different drug conditions (viral passages)
  - Conducted Illumina sequencing to obtain whole genome data
  - Ordered reagents and budgeted the experiments
  - Wrote reports and presented results weekly in the lab and collaborators meetings
- June 2020-July 2018 Center for Evolution and Medicine, Arizona State University, USA
- Extracted DNA from tuberculosis patient's samples and sequenced
  - Analyzed time-sampled population genetics data and Bayesian computation modeling of evolutionary forces in within-host *Mycobacterium tuberculosis*.
  - Used R, SLiM, and Linux for computational modelling
  - Prepared data, from raw results to Bayesian statistical analysis, and visualized it using R packages

- Applied bayesian computational approaches and modelling for human cytomegalovirus (HCMV) sampled patient data and *in-vitro* influenza A virus
- Inferred genomic patterns of fitness effects in within-host HCMV and Influenza A virus
- Presented and debated results at conferences

### **PhD Researcher**

Sep 2012 – Aug 2017 Ancient DNA Lab, Dept. of Archaeology, University of Calgary

- Applied several novel DNA extraction and sequencing techniques to successfully recover DNA from ancient human remains to determine ancestry and sex
- Managed and conducted experiments in molecular biology laboratories and in a world-class 6-room ISO-6 clean room for ancient DNA research
- Collaborated with a team of researchers to develop novel molecular techniques for extraction of ancient DNA from low-quantity and highly degraded human skeletal samples
- Conducted PCR techniques and Sanger DNA sequencing to target ancestry and sex information from 106 ancient skeletal remains (teeth, hand, feet, and rib bones)
- Prepared Illumina sequencing libraries and conducted in-solution DNA enrichment to sequence in Illumina HiSeq v2 2x100 bp chemistry, leading to whole recovery of mitogenomes
- Used bioinformatics pipelines optimized (BWA, leeHom, Schmutzi) for ancient DNA analysis, resulting in the recovery of whole genome information from low quantity DNA samples
- Analyzed DNA sequences' quality and verified alignments using Genious, Phylotree and Haplogrep software.
- Applied biostatistical analysis on large data sets for publications (i.e. Principal Component Analysis, variance measurements, DNA sequence Networks, Fst, Bayesian analysis)
- Validated DNA analyses by replicating results in subsamples and with partner laboratories that minimized risk of contamination of results
- Effectively communicated research results across subject fields with publications, and in interdisciplinary conference proceedings suitable for a broad audience
- Prepared reports and wrote operational procedures for experiments and equipment to facilitate the flow of work and management of equipment for other researchers and students

### **Other fieldwork**

2014

**Research Assistant**, UNAM, Nicaragua

- Assisted Dr. McCafferty on the successful creation of a Bio-Archaeology Laboratory in the National University.

- 2014      **Research Assistant**, Museo de las Culturas del Norte, Casas Grandes, INAH-Chihuahua, Mexico
- Assisted the study directed by Dr. Anne Katzenberg (University of Calgary), collecting archaeological human remains in the Casas Grandes, Paquimé.
- 2004      **Research Assistant**, School of Biology, University of Costa Rica, Costa Rica
- Assisted in fieldwork collecting primate blood samples in Manuel Antonio National Park, extraction of DNA and data analysis. Project: Genetic diversity of monkeys in Costa Rica, directed by Dr. Gustavo Gutierrez.

### TEACHING EXPERIENCE

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- 2022      **Teaching Assistant**, University of Bern  
*Statistics for Biology (Spring term)*
- Enrollment: 70 students
- 2020      **Original lectures contribution**, Arizona State University  
*Advanced evolutionary medicine (online class)*
- Enrollment: 30 students
- 2017      **Instructor of Record**, University of Calgary  
*Introduction to Primatology and Human Evolution (ANTH 201, Winter 2017)*
- Enrollment: 200 students
- 2016-2013      **Teaching Assistant**, University of Calgary  
*Ethnographic Survey of Latin America (2013)*  
*Archaeology & Popular Culture -Frauds, Myths & Mysteries (2015)*  
*Introduction to Archaeology (2015)*
- Enrollment: 2 laboratories of 20 students each
- Head Graduate Teaching Assistant: Introduction to Physical Anthropology (2014-16)*
- Enrollment: 8 laboratories of 22 students each
- 2012-2011      **Instructor of Record**, University of Costa Rica  
*Molecular Basis of Human Phylogeny (2012)*
- Enrollment: 20 students
- Principles of Population Genetics (2011)*
- Enrollment: 30 students
- Biological Anthropology (2011)*
- Enrollment: 30 - 40 students

### WORK EXPERIENCE

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- 2012-2004      Research Assistant and Laboratory Technician, Genetics Laboratory, School of Biology, University of Costa Rica

- Carried out genetic techniques and protocols for multiple faculty members, coordinated research activities and grant applications, was accountable for budgets and development of new methodologies and experimental techniques.

July 2012-August 2011, with Prof. Henriette Raventós-Vorst, Center for Molecular Biology, School of Biology, University of Costa Rica

- Investigated susceptibility genes for schizophrenia in Costa Rica. Screened several genetic (molecular) markers associated to OPO using the genetic analyzer ABI Prism 3130

July 2011- July 2009 with Prof. Jorge Azofeifa Navas, School of Biology, University of Costa Rica

- Genetic variation in modern groups of Lower Central America. Ancient DNA laboratory design and training on contamination issues in archaeological sites.
- Haplotypic variation around the region of the lactase gene (LCT, 2q21) in Costa Rica.

June 2009- May 2004 with Prof. Ramiro Barrantes, School of Biology, University of Costa Rica

- History and genetic structure of Costa Rica: molecular, demographic and social perspective.
- Mitochondrial DNA and Y chromosome analysis in Costa Rica.
- Haplotypic variation of TP53 locus in Amerindians of Lower Central America. Sequencing and genotyping DNA in 3130 and 310 genetic analyzers.

2004-2003 Biotechnology Department, Technological Institute of Costa Rica (TEC), Costa Rica

- Carried out sampling in the forest and DNA extraction as well as molecular analysis.

November 2003- June 2003 with Prof. Olman Murillo

- Genetic variability of Jaúl (*Alnus acuminata*) in Costa Rica.

July 2003- March 2003, Computer technician at LAIMI (Microprocessor Laboratory of the Technological Institute of Costa Rica)

## **SCHOLARSHIPS, GRANTS AND AWARDS**

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2020-2018	Research Fellowship, CEM. Arizona State University. USD 140 000.
2017-2012	Wadsworth International Fellowship. The Wenner Gren Foundation. USD 70 000.
2016	Shelley Saunders PhD Research Award. The Canadian Association for Physical Anthropology. CAD 800.
2016	Martha Biggar Anders Memorial Award. University of Calgary. CAD 2200.
2016	Faculty of Graduate Studies Travel Award. University of Calgary. CAD 500.
2016	Professional Development Grant. GSA. University of Calgary. CAD 750.
2015	Dissertation Research Grant. University of Calgary. CAD 1500.
2015	Grants-in-Aid of Research Program. Sigma Xi. USD 600.

## **ACADEMIC ACTIVITIES**

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2022	Reviewer for the National Science Foundation, USA.
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- 2023 -2017 Reviewer for the Journals *PCIBiol*, *Plos One*, *Scientific Reports*, *Molecular Biology and Evolution*, *Genome Biology and Evolution*, *Frontiers in Ecology and Evolution*, *Molecular Ecology Resources*, *PCIEvolBiol*.
- 2017-2016 Student Awards Committee Member. Graduate Student Association. University of Calgary.
- 2017-2014 Assistant /Language Editor position in Open Archaeology.

## CONFERENCE PRESENTATIONS

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- August 2023 Genetic background dependent evolutionary response to mutagenic drug exposure in influenza A virus. Congreso Mesoamericano de Ecología y Evolución. Ciudad de Guatemala. GUAT.
- August 2022 Bridging experiments and simulations to study the effect of mutagenic drugs on influenza A virus populations. European Society for Evolutionary Biology (ESEB). Prague, CZE.
- June 2022 Evolution and phylogeny. SIBdays. Biel, CH. Session's co-chair.
- March 2022 Mutagenic drugs consistently induce rapid mutational meltdown across several strains of laboratory-passed influenza A virus. Biology22, Basel, CH.
- April 2020 The population genetics of within-host *Mycobacterium tuberculosis*. American Association of Physical Anthropologists. Los Angeles, CA, USA
- July 2019 The population genetics of within-host drug resistance in *Mycobacterium tuberculosis*. Society for Molecular Biology and Evolution (SMBE). Manchester, UK.
- April 2019 The population genetics of within-host *Mycobacterium tuberculosis*. The Evolutionary Genetics of Infectious Disease, Carleton University, ON, CA.
- April 2019 Greater Nicoya from an ancient molecular perspective. Society for American Archaeology 84th Annual Meeting (SAA), Albuquerque, NM, USA.
- November 2017 Ancient Mesoamerican groups and their multiple faces: From Cholula and Tlatelolco to an ancient genetic landscape in Central Mexico and beyond. 50th Chacmool Conference, Calgary, AB, CA. *Session organizer and presenter*.
- May 2016 Infant sex determination and ancient mtDNA among offerings dedicated to Ehécatl-Quetzalcóatl in Tlatelolco (1325-1521 AD). 49th Annual Meeting of the Canadian Archaeological Association (CAA), Whitehorse, Yukon, CA.
- April 2016 Ancient mitochondrial DNA of Pre-Columbian populations inhabiting Greater Nicoya during the Sapoá period (A.D. 800-1350). Latin American Research Center, Graduate Student Symposium (LARC), Calgary, AB, CA.
- April 2016 Ancient mitochondrial DNA and pre-Columbian inhabitants ancestry at Paquimé, Casas Grandes. SAA, Orlando, FL, USA.
- February 2016 Ancient mitochondrial DNA of Pre-Columbian populations inhabiting Greater Nicoya during the Sapoá period (A.D. 800-1350). 6<sup>th</sup> Annual Interdisciplinary Archaeology Research Conference (UCLA), Los Angeles, CA, USA.
- November 2015 Ancient mitochondrial DNA approach to explore pre-Columbian inhabitants' ancestry at Paquimé, Casas Grandes, 48th Chacmool Conference, Calgary, AB, CA.
- April 2015 Exploring the ancient mitochondrial DNA of pre-Columbian populations inhabiting Central Mexico during the postclassic period (A.D. 900-1521). SAA, San Francisco, CA, USA.

- April 2015 Ancient Mitochondrial DNA of Precolumbian Populations inhabiting Greater Nicoya during the Sapoá Period (800-1350 AD). *Methods in Ecology and Evolution: Next Generation Ecology and Evolution*, Calgary, AB, CA.
- November 2014 Ancient DNA in Mesoamerica: limitations and contributions. 47th Chacmool Conference. Calgary, AB, CA.
- April 2014 Bioarchaeological approaches to the site La Cascabel in Bahía Culebra, Costa Rica (800-1350 AD). SAA, Austin, TX, USA.
- February 2011 Genetic variability of lactose intolerance in Amerindians of lower Central America. Central American Congress of Anthropology, Tegucigalpa, Honduras.
- November 2010 Haplotypic variation of lactose intolerance in Costa Rica. Nutrition and Health Congress. San José, CR.
- December 2009 Haplotypic variation around the region of the lactase gene (LCT, 2q21) in Amerindians of Costa Rica. Darwin200 Celebration International Symposium, Alajuela, CR.

## LANGUAGES

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Spanish: Native speaker

English: Fluent comprehension, reading, writing, and speaking

Italian: Fluent comprehension, reading, writing and speaking

## REFERENCES

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Prof. Claudia Bank – *Postdoctoral Supervisor*

Universität Bern. E-mail: Claudia.bank@unibe.ch

Prof. Maria Joao Amorim – *Postdoctoral Supervisor*

Instituto Gulbenkian de Ciência. E-mail: mjamorim@igc.gulbenkian.pt

Prof. Jeffrey Jensen – *Postdoctoral Supervisor*

School of Life Sciences. Arizona State University. E-mail: Jeffrey.D.Jensen@asu.edu

Prof. Anne Stone – *Postdoctoral Supervisor*

School of Human Evolution and Social Change. Arizona State University. E-mail: acstone@asu.edu

Prof. Geoffrey McCafferty - *PhD Supervisor*

Archaeology and Anthropology Department. University of Calgary. E-mail: mccafer@ucalgary.ca