Diego Ortega-Del Vecchyo

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Academic Appointments

Junio 2018 –	**Assistant Professor** Group Leader, Computational Population Genetics Group National Autonomous University of Mexico International Laboratory for Human Genome Research

Education

Junio 2016	**Ph.D. in Bioinformatics** University of California, Los Angeles Co-advised by John Novembre and Kirk Lohmueller
Junio 2009	**Bachelor in Genomic Sciences** National Autonomous University of Mexico Advised by Joost van Heerwaarden

Postdoctoral positions

2016 –2018	**Postdoctoral Fellow** Integrative Biology Department University of California, Berkeley Advised by Montgomery Slatkin

Publications

Peer-reviewed Research Papers
(*Authors contributed equally)
(+corresponding author o authors)
(& Student working in my group)

1. Brandt DYC+, Huber CD+, Chiang CWK+, **Ortega-Del Vecchyo D**+. The Promise of Inferring the Past using the Ancestral Recombination Graph. *Genome Biology and Evolution*. 2024.

2. Fang LL, Peede D, **Ortega-Del Vecchyo D**, McTavish EJ+, Huerta-Sanchez E+. Leveraging shared ancestral variation to detect local introgression. *PLoS Genetics*. 2024. 20 (1): e1010155. doi: https://doi.org/10.1371/journal.pgen.1010155

3. Izarraras-Gomez A&+, **Ortega-Del Vecchyo D**+. Ancient DNA uncovers past migrations in California. *Nature*. 2023. doi: 10.1038/d41586-023-03503-7

4. Medina-Munoz SG, **Ortega-Del Vecchyo D**, Cruz-Hervert LP, Ferreyra-Reyes L, Garcia-Garcia L, Moreno-Estrada A+, Ragsdale A+. Demographic Modeling of Admixed Latin American Populations from Whole Genomes. *American Journal of Human Genetics*. 2023. 110(10):1804-1816. doi: 10.1016/j.ajhg.2023.08.015

5. Buck R, **Ortega-Del Vecchyo D**, Gehring C, Michelson R, Flores-Renteria D, Klein B, Whipple AV, Flores-Rentería L+. Sequential hybridization may have facilitated ecological transitions in the Southwestern pinyon pine syngameon. *New Phytologist*. 2023. 237 (6): 2435-2449. doi: 10.1111/nph.18543

6. Figueroa-Corona L+, Moreno-Letelier A, **Ortega-Del Vecchyo D**, Peláez P, Gernandt DS, Eguiarte LE, Wegrzyn J, Piñero D. Changes in demography and geographic distribution in the weeping pinyon pine (*Pinus pinceana*) during the Pleistocene. *Ecology and Evolution*. 2022. 12(10):e9369. doi: 10.1002/ece3.9369

7. **Ortega-Del Vecchyo D**, Berg J, Sohail M+. Editorial: Genetic Architecture and Evolution of Complex Traits and Diseases in Diverse Human Populations, *Frontiers in Genetics*. 2022. 13:869056.

8. **Ortega-Del Vecchyo D+**, Lohmueller KE, Novembre J+. Haplotype-based inference of the distribution of fitness effects, *Genetics*. 2022, 220(4), iyac002.

9. Jiménez-Kaufmann A, Chong AY, Cortés A, Quinto-Cortés CD, Fernandez-Valverde SL, Ferreyra-Reyes L, Cruz-Hervert LP, Medina-Muñoz SG, Sohail M, Palma-Martinez MDJ, Delgado-Sánchez G, Mongua-Rodríguez N, Mentzer AJ, Hill AVS, Moreno-Macías H, Huerta-Chagoya A, Aguilar-Salinas CA, Torres M, Kim HL, Kalsi N, Schuster SC, Tusié-Luna T, **Ortega-Del Vecchyo D**, García-García L+ and Moreno-Estrada A+. Imputation Performance in Latin American Populations: Improving Rare Variants Representation With the Inclusion of Native American Genomes. *Frontiers in Genetics*. 2022. 12:719791.

10. Sohail M+*, Izarraras-Gomez A*&, **Ortega-Del Vecchyo D**+. Populations, traits and their spatial structure in humans, *Genome Biology and Evolution*. 2021. 13(12):evab272.

11. Silva P+, Galaverni M, **Ortega-Del Vecchyo D**, Fan Z, Caniglia R, Fabbri E, Randi E, Wayne R, Godinho R+. Genomic evidence for the Old divergence of Southern European Wolf populations. *Proceedings of the Royal Society B*, 2020, 287:20201206.
12. Adrion JR*, Cole CB*, Dukler N*, Galloway JG*, Gladstein AL*, Gower G*, Kyriazis C*, Ragsdale AP*, Tsambos G*, Baumdicker F, Carlson J, Cartwright RA, Durvasula A, Gronau I, Kim BY, McKenzie P, Messer PW, Noskova E, **Ortega-Del Vecchyo D**, Racimo F, Struck TJ, Gravel S, Gutenkunst RN, Lohmueller KE, Ralph PL, Schrider DR, Siepel A, Kelleher J+, Kern AD+. A community-maintained standard library of population genetic models. *eLife*:e54967.
13. **Ortega-Del Vecchyo D**, Slatkin M+. Fst between archaic and present-day samples. *Heredity*, 2019. 122:711-718.
14. **Ortega-Del Vecchyo D+**, Piñero D, Jardón-Barbolla L, van Heerwaarden J+. Appropriate homoplasy metrics in linked SSRs to predict an underestimation of demographic expansion times. *BMC Evolutionary Biology*. 2017. 17:213.
15. vonHoldt, B+, Fan Z, **Ortega-Del Vecchyo D**, Wayne R. *EPAS1* variants in high altitude Tibetan wolves were selectively introgressed into highland dogs. *PeerJ*. 2017. 5:e3522.
16. **Ortega-Del Vecchyo D**, Marsden CD, Lohmueller K+. PReFerSim: Fast simulation of demography and selection under the Poisson Random Field model. *Bioinformatics*. 2016. 32 (22):3516-3518.
17. Robinson, JA, **Ortega-Del Vecchyo D**, Fan Z, Kim BY, vonHoldt BM, Marsden CD, Lohmueller KE*, Wayne RK*+. Genomic flatlining in the endangered island fox. *Current Biology*. 2016. 26: 1-7.
18. Fan Z*, Silva PM*, Gronau I, Wang S, Armero AS, Schweizer RM, Ramirez O, Pollinger J, Galaverni M, **Ortega-Del Vecchyo D**, Du L, Zhang W, Zhang Z, Xing J, Vilà C, Marques-Bonet T, Godinho R, Yue B+, Wayne RK+. Worldwide patterns of genomic variation and admixture in gray wolves. *Genome Research*. 2016. 26: 163-173.
19. Freedman AH+, Schweizer RM, **Ortega-Del Vecchyo D**, Han E, Davis BW, Gronau I, Silva PM, Galaverni M, Fan Z, Marx P, Lorente-Galdos B, Ramirez O, Hormozdiari F, Alkan C, Vilà C, Squire K, Geffen E, Kusak J, Boyko AR, Parker HG, Lee C, Tadigotla V, Siepel A, Bustamante CD, Harkins TT, Nelson SF, Marques-Bonet T, Ostrander EA, Wayne RK, Novembre J. Demographically-based evaluation of genomic regions under selection in domestic dogs. *PLoS genetics*. 2016; 10(1):e1004016.
20. Marsden CD*, **Ortega-Del Vecchyo D***, O'Brien D, Taylor JF, Ramirez O, Vilà C, Marques-Bonet T, Schnabel RD, Wayne RK, Lohmueller KE+. Bottlenecks and selective sweeps during domestication have increased deleterious genetic variation in dogs. *Proceedings of the National Academy of Sciences*. 2016; 113(1):152-157.
21. Sidore C*, Busonero F*, Maschio A*, Porcu E*, Naitza S*, Zoledziewska M, Mulas A, Pistis G, Steri M, Danjou F, Kwong A, **Ortega-Del Vecchyo D**, Chiang CWK, Bragg-Gresham J, Pitzalis M, Nagaraja R, Tarrier B, Brennan C, Uzzau S, Fuchsberger C, Atzeni R, Reinier F, Berutti R, Huang J, Timpson NJ, Toniolo D, Gasparini P, Malerba G, Dedoussis G, Zeggini E, Soranzo N, Jones C, Lyons R, Angius A, Kang HM, Novembre J, Sanna S*+, Schlessinger D*+, Cucca F*+, Abecasis GR*+. Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers. *Nature Genetics*. 2015; 47(11):1272-1281.

22. Zoledziewska M*, Sidore C*, Chiang CWK*, Sanna S*, Steri M, Busonero F, Marcus JH, Marongiu M, Maschio A, **Ortega-Del Vecchyo D**, Floris M, Meloni A, Delitala A, Concas MP, Murgia F, Biino G, Vaccargiu S, Nagaraja R, Lohmueller KE, Zeggini E, Understanding T, Scientific S, Uzzau S, Jones C, Lyons R, Angius A, Abecasis GR*+, Novembre J*+, Schlessinger D*+, Cucca F*+. Height-reducing variants and selection for short stature in Sardinia. *Nature Genetics*. 2015; 47(11):1352-1356.

23. Freedman AH, Gronau I, Schweizer RM, **Ortega-Del Vecchyo D**, Han E, Silva PM, Galaverni M, Fan Z, Marx P, Lorente-Galdos B, Beale H, Ramirez O, Hormozdiari F, Alkan C, Vilà C, Squire K, Geffen E, Kusak J, Boyko AR, Parker HG, Lee C, Tadigotla V, Wilton A, Siepel A, Bustamante CD, Harkins TT, Nelson SF, Ostrander EA, Marques-Bonet T, Wayne RK+, Novembre J+. Genome sequencing highlights the dynamic early history of dogs. *PLoS genetics*. 2014; 10(1):e1004016.

24. Flores-Rentería L+, Wegier A, **Ortega-Del Vecchyo D**, Ortíz-Medrano A, Piñero D, Whipple A V., Molina-Freaner F, Domínguez CA. Genetic, morphological, geographical and ecological approaches reveal phylogenetic relationships in complex groups, an example of recently diverged pinyon pine species (Subsection Cembroides). *Molecular Phylogenetics and Evolution*. 2013; 69(3):940-949.

25. Chi EC, Zhou H, Chen GK, Chi EC, **Ortega-Del Vecchyo D**, Lange K+. Genotype imputation via matrix completion Genotype Imputation via Matrix Completion. *Genome Research*. 2013; 23:509-518.

26. van Heerwaarden J+, **Ortega-Del Vecchyo D**, Alvarez-Buylla ER, Bellon MR. New genes in traditional seed systems: diffusion, detectability and persistence of transgenes in a maize metapopulation. *PLoS one*. 2012; 7(10):e46123.

Preprints:

1. Fan C, Cahoon JL, Dinh BL, **Ortega-Del Vecchyo D**, Huber CD, Edge MD, Mancuso N, Chiang CWK. A likelihood-based framework for demographic inference from genealogical tres. *BioRxiv*. doi: 10.1101/2023.10.10.561787

2. Peede D, **Ortega-Del Vecchyo D+**, Huerta-Sanchez E+. The Utility of Ancestral and Derived Allele Sharing for Genome-Wide Inferences of Introgression. BioRxiv. 2022. doi: https://doi.org/10.1101/2022.12.02.518851

Grants awarded

2019 – 2022	**UC MEXUS-CONACYT Collaborative Grant Award** UC Mexus & CONACyT Ref. CN 19-29 “Análisis del impacto de la demografía y la selección natural utilizando muestras del presente y del pasado” Co-Pis: D. Ortega-Del Vecchyo y Rasmus Nielsen Amount: $22,200 USD
2019 – 2021	**Programa de Apoyo a Proyectos de Investigación e Innovación Tecnológica** National Autonomous University of Mexico. Ref. IA200620 “Temporal analysis of the impact of natural selection on new alleles” PI: D. Ortega-Del Vecchyo

	Amount: $324,952 MXN
2022 – 2023	**Programa de Apoyo a Proyectos de Investigación e Innovación Tecnológica** National Autonomous University of Mexico. Ref. IA206222 “New methods to study the evolution of alleles under natural selection using genealogical trees” PI: D. Ortega-Del Vecchyo Amount: $388,612 MXN
2023	**SMBE 2023 regional meeting** Society for Molecular Biology and Evolution “SMBE Mexico Population Genomics meeting 6” Co-PI: D. Ortega-Del Vecchyo Amount: $25,000 USD
2023 -	**National Institutes of Health - R01** National Institutes of Health “A genome-wide genealogical framework for statistical and population genetic analysis” Co-PI: D. Ortega-Del Vecchyo Monto asignado: $195,300 USD
2023 –	**Programa de Apoyo a Proyectos de Investigación e Innovación Tecnológica** National Autonomous University of Mexico. Ref. IN215524 “Inferencia espaciotemporal del impacto de la selección natural actuando en variantes genéticas y su aplicación para analizar la evolución de fenotipos” PI: D. Ortega-Del Vecchyo Expected amount: $500,000 MXN

Awards

2007-2009	**SEP-CONACYT scholarship** Funded my studies in the lab of Dr. Daniel Piñero with Dr. Joost Van Heerwaarden.
2010-2015	**UC MEXUS fellowship** Funded my doctoral studies
2011	**Evolutionary Quantitative Genetics workshop travel award, NESCENT** Travel award to attend the ‘Evolutionary Quantitative Genetics’ course on NESCent, Durham, North Carolina.
2015	**Graduate Programs In Bioscience Fellowship Incentive Program Fellowship** $3,000 USD award to fund my doctoral studies
2015-2016	**UCLA Dissertation Year Fellowship** Award to fund my last year of research as a doctoral student.

2018	**Readers' choice: The best of Heredity 2018** My paper published on Heredity was one of the most accessed and cited articles on *Heredity* (see https://www.nature.com/collections/cgggfjjdej/).
2022	**Featured article, Genetics** My paper was highlighted on the april 2022 issue of *Genetics*.

Conference Presentations

Oral presentations

2015	Society for Molecular Biology and Evolution, Vienna
2015	Probabilistic Modeling in Genomics at CSHL, Long Island
2015	Mexico Population Genetics Meeting, Querétaro
2016	Southern California Evolutionary Genetics and Genomics meeting
2017	Horizons in Genomic Sciences, Cancún
2018	SMBE satellite meeting "Modern Methods for Ancient DNA", Providence
2018	Foro Nacional de Biología y Probabilidad, Cuernavaca
2018	Horizons in Genomic Sciences, Cancún
2018	Biomatesis, Querétaro
2019	Mexico Population Genetics Meeting, Mexico City
2019	Evolution Meeting, Providence RI
2019	Mexican Veterinary Oncologist Association, Mexico City
2022	Horizons in Genomic Sciences, Cancún
2023	Molecular Evolution in Small Populations, SMBE meeting, Princeton
2023	Simposio Internacional del 20 aniversario de la LCG, Cuernavaca
2023	Primer Encuentro de Genómica en la UNAM, Cuernavaca
2024	Horizons in Genomic Sciences, Mexico City

Poster presentations

2010	Western Evolutionary Biology Meeting, UC Irvine
2011	UCLA Bioinformatics Retreat
2011	American Genetic Association Annual Symposium, Guanajuato
2012	UCLA Bioinformatics Retreat
2012	American Society of Human Genetics, San Francisco
2013	Society for Molecular Biology and Evolution, Chicago
2013	American Society of Human Genetics, Boston
2014	Society for Molecular Biology and Evolution, San Juan
2014	Midwest PopGen Meeting, Chicago
2014	American Society of Human Genetics, San Diego
2017	Society for Molecular Biology and Evolution, Austin
2022	American Society of Human Genetics, Los Angeles

Seminars

2008	Instituto de Ecología, UNAM
2013	UCLA Bioinformatics Retreat
2016	UCLA QCBio Friday Research Lunch Series
2018	Center for Theoretical Evolutionary Genomics, UC Berkeley
2018	Laboratorio Nacional de Genómica para la Biodiversidad
2020	Instituto de Ecología, UNAM
2020	Seminario Virtual para BioScienceApp.
2020	San Diego State University, Virtual Seminar
2021	Facultad de Ciencias, UNAM, Seminario Virtual
2022	University of Southern California
2022	University of California, Los Angeles
2022	Brown University
2022	Pennsylvania State University
2023	Instituto de Matemáticas, UNAM Juriquilla

Teaching

2007-2008	Population Genetics. Center for Genomic Sciences, UNAM. Teaching assistant. Three courses, 1 semester each (64 hours per semester).
2013	Genetics. University of California, Los Angeles. Teaching Assistant. 1 trimester (44 hours).
2018	Biotechnology Seminar. UNAM, Campus Juriquilla. 1 semester (40 hours).
2019	Introduction to Bioinformatics. UNAM, Campus Juriquilla. 1 semester (64 hours).
2020	Genomics of domestication. UNAM, Biological Sciences graduate program. 1 class (2 hours).
2019-2023	Evolution. UNAM, Campus Juriquilla. 3 courses, 1 semester each (40 hours per course).
2019,2023	Genomics. UNAM, Campus Morelos. Bachelor in Genomic Sciences. 2 classes (2 hours per course).
2020	Phylogenetics. UNAM, Campus Juriquilla. 2 weeks (16 hours).

Students mentored

Graduated students

2014-2015	Amy Chow. Bachelor student at University of California, Los Angeles; afterwards she became a masters student in mechanical engineering at San Diego State University.
2021-2023	Héctor Alessandro López Hernández. Masters degree in the Biological Sciences Program at the National Autonomous University of Mexico.
2020-	Valeria Alejandra Añorve Garibay. Bachelor in Genomic Sciences at the National Autonomous University of Mexico.

Students currently working on a graduate program in my group

2019-	Liliana Chavaje Ávila. Masters student in Mathematical Engineering at the Autonomous University of Querétaro. Her dissertation defense is scheduled by February 2024.
2023-	Héctor Alessandro López Hernández. PhD degree in the Biological Sciences Program at the National Autonomous University of Mexico.
2020-	Alan Raymundo Izarraras Gómez. PhD student in the Biomedical Sciences Program at the National Autonomous University of Mexico. He became a PhD candidate on 2022.

Student Committee Service

2019	Alan Vladimir Godínez Plascencia. Bachelor degree in Genomic Sciences, UNAM.
2019	Jesús Abraham Avelar Rivas. PhD Student in Plant Biotechnology. LANGEBIO.
2020-2021	Andrés Jiménez Kaufmann. Masters student in Integrative Biology. LANGEBIO.
2020	Daniela Orozco Pérez. Bachelor degree in Genomic Sciences. UNAM.
2020	Jorge Luis Cuamatzi Flores. PhD student in Biological Sciences. Autonomous University of Querétaro.
2020-	Alan Vladimir Godínez Plascencia. PhD student in Biomedical Sciences, UNAM.
2020	Jazeps Medina Tretmanis. Bachelor degree in Computer Sciences, UNAM.
2021	Rebeca Olvera León. Bachelor degree in Technology, UNAM.

2020-2022	Santiago Gerardo Medina Muñoz. Masters student in Integrative Biology. LANGEBIO.
2020-2022	Ram González Buenfil. Masters student in Integrative Biology. LANGEBIO.
2022-	María José Palma Martínez. PhD student in Biomedical Sciences. UNAM.
2022-	Santiago Gerardo Medina Muñoz. PhD student in Integrative Biology. LANGEBIO.
2022-	Ram González Buenfil. PhD student in Integrative Biology. LANGEBIO.
2022	Laura Alicia Figueroa Corona. PhD student in Biological Sciences. UNAM.
2022	Ali Berenice Posada Reyes. PhD student in Biomedical Sciences. UNAM.
2022-	María José Palma Martínez. PhD student in Biomedical Sciences. UNAM.
2022-	Santiago Gerardo Medina Muñoz. PhD student in Integrative Biology. LANGEBIO.
2022-	Ram González Buenfil. PhD student in Integrative Biology. LANGEBIO.
2022-	David Peede. PhD student in Ecology, Evolution and Organismal Biology, Brown University
2023	Fernanda Renee García Flores. Bachelor degree in Genomic Sciences. UNAM.
2023	Iván Eduardo Sedeño Jiménez. Bachelor degree in Technology. UNAM.
2023-	Isabela Midori Watanabe. PhD student in Biomedical Sciences. UNAM.
2023-	Carolina Castañeda García. PhD student in Biomedical Sciences. UNAM.
2023-	Viridiana Villa Islas. PhD student in Biomedical Sciences. UNAM.
2023-	Sofía Vieyra Sánchez. Masters student in Integrative Biology. LANGEBIO.
2024	Emmanuel Hernández Sánchez. Bachelor degree in Genomic Sciences. UNAM.

Professional service

2016-	Reviewer for more than 30 papers in various academic such as: American Journal of Human Genetics, Nature, Molecular Biology and Evolution, eLife y PLoS Genetics (My activity can be reviewed in https://publons.com/researcher/3164540/diego-ortega-del-vecchyo/).
2020-	Academic editor for *Frontiers in Genetics.*
2020	Organizing committee of the conference 'ISCB-LA SoIBIO BioNetMX Symposium on Bioinformatics'.
2020	Organizing committee of the conference 'MexPopGen5'.
2020-	Organizing committee of the conference 'SMBE 2024' that will be done in Puerto Vallarta, México.
2021	Hiring Professor committee, UNAM Campus Juriquilla
2022	Organizing committee of the symposium "GS4: Using Ancestral Recombination Graphs (ARGs) to Infer Evolutionary Processes"
2022-	Faculty representative. UPEID Council.
2022-	Recommender (editor equivalent) for *Peer Community in Evolutionary Biology.*
2023	Organizing committee "Días académicos LIIGH", UNAM Campus Juriquilla.
2023-	Organizing committee of the 'MexPopGen6' meeting
2023-	Academic editor for the journal *Genome Biology and Evolution.*
2023-	Faculty representative – Academic committee of the Bachelor in Genomic Sciences undergraduate program. UNAM Campus Juriquilla.
2023	Member of the admission subcommittee "Genetics, Genomics and Bioinformatics" Biomedical Sciences Graduate Program (Semester 2024-I).

Science Outreach

2012	Founder and collaborator of the organization Más Ciencia por México, A.C. I wrote blog posts for the general public on Genomic Sciences Research.
2020-	I did YouTube videos where I explained different concepts on Population Genetics.
2020-	Interview with TV UNAM about Rosalind Franklin's work (https://www.youtube.com/watch?v=5_bJGpcwxxU)

2020	Interview for Ciencia UNAM (https://ciencia.unam.mx/leer/1054/posible-contacto-entre-polinesios-y-americanos-antes-de-colon)
2021	Interview for The Scientist (https://offers.the-scientist.com/uncovering-ancient-residual-dna-multisponsored-ebook)
2022	Interview for Nature (https://www.nature.com/articles/d41586-022-01551-z)
2023	Interview for Corriente Alterna
2023	Interview for Gaceta UNAM (https://www.gaceta.unam.mx/el-pangenoma-humano-un-modelo-mas-diverso/)
2023	Participation on the Querétaro 2023 Science Fairl at the CECEQ “Gómez Morín”
2023	Participation on the Open Doors event from ENES Juriquilla 2023.
2023	Paper for Gaceta UNAM Juriquilla (https://www.campusjuriquilla.unam.mx:8080/?page_id=26057)