

Paul A. Maier, Ph.D.

Population Geneticist
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RESEARCH INTERESTS and BACKGROUND

I am an evolutionary biologist and population geneticist with extensive background in bioinformatics, seeking to empower people by unlocking the meaning of their DNA. My current research projects are establishing novel population genetic tools to estimate human ancestry, from hundreds of ancestral populations. I have broad interests in population genetics, genomics, herpetology, and evolutionary ecology. One of my research areas is the process of environmental adaptation, how it proceeds at the genomic level, and how it applies to species and population persistence. My Ph.D. research has unraveled ancient population history in Yosemite toads (*Anaxyrus canorus*), demonstrated adaptive differences in their larval development rates, and suggested that secondary contact zones could catalyze genetic adaptation to climate change. I was advised by Dr. Andrew Bohonak at the Department of Biology, San Diego State University, Dr. Amy Vandergast at the US Geological Survey, and Dr. Leonard Nunney at the Department of Ecology, Evolution and Organismal Biology, UC Riverside.

EDUCATION

San Diego State University, San Diego, California

University of California Riverside, Riverside, California

Ph.D. in Evolutionary Biology, 2018

GPA: 4.0

University of California Santa Barbara, Santa Barbara, California

B.S. in Aquatic Biology / Ecology and Evolution, 2008

GPA: 3.7

AWARDS and HONORS

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| 2017 – 2018 | Jordan D. Covin Memorial Scholarship (\$600) |
| 2017 – 2018 | ARCS Scholarship (\$7,500) |
| 2016 – 2017 | ARCS Scholarship (\$7,500) |
| 2015 – 2016 | ARCS Scholarship (\$7,500) |
| 2014 – 2015 | Jordan D. Covin Memorial Scholarship (\$900) |
| 2013 – 2014 | Harold & June Grant Memorial Scholarship (\$2,400) |
| 2012 – 2014 | USGS Conservation Genetics Assistantship (\$111,100) |
| 2012 – 2013 | Eugene Cota-Robles Fellowship (\$53,616; offer declined) |

MEMBERSHIPS

Society for the Study of Evolution
Society for Molecular Biology and Evolution
Phi Kappa Phi Honor Society
San Diego State Natural History Club

TEACHING EXPERIENCE

- 2017 – 2018 Teaching Associate: Organismal Biology, San Diego State University
2016 – 2017 Invited Guest Lecturer: Population Genetics, San Diego State, University
Designed workshop in population genomics for graduate students (see [here](#), and [here](#))
2016 – 2017 Teaching Associate: Herpetology, San Diego State University
2015 – 2016 Teaching Associate: Genetics & Evolution, San Diego State University
2014 – 2015 Teaching Associate: Genetics & Evolution, San Diego State University
2010 – 2014 Crew Lead: United States Geological Survey

** I have mentored 12 graduate and 6 undergraduate students **

EMPLOYMENT and RESEARCH EXPERIENCE

Population Geneticist, FamilyTreeDNA / Gene by Gene
Houston, Texas (Oct. 2018 – present)

- Researched and developed novel tools for estimating human population ancestry
- Invented novel method for joint global-local ancestry estimation (myOrigins 3.0)
- Invented age estimation method for largest human Y-DNA tree even constructed (>50,000 branches)
- Helped develop improved autosomal matching and relationship estimates, accounting for endogamy
- Used local ancestry methods to infer Sephardic origin for rare medical disease
- Invented novel method to infer local population origin for famous historical figure (using ancient DNA)
- Invented novel phylogenetic method for largest mtDNA tree ever constructed (>100,000 branches)
- Used phylogeographic and landscape genetic methods to track pre-historic human movement
- Used population genetic theory, machine learning, and hidden Markov models for DNA classification
- Employed expertise of Mendelian genetics, site frequency spectra, and other coalescent approaches
- Taught many employees and admins genetic concepts, and conducted several public interviews

Population Geneticist (Contractor), USDA El Dorado National Forest
Placerville, California (Jun. 2023 – present)

- Developing hybrid panel for Yosemite toads (*Anaxyrus canorus*) and western toads (*Anaxyrus boreas*)
- Purpose of identifying extent and proportion of hybridization in questionable individuals
- Using methodologies and ddRADseq laboratory techniques developed from my dissertation

Joint Doctoral Research, Bohonak Lab, San Diego State University and UC Riverside
San Diego and Riverside, California (Aug. 2012 – July 2018)

Advisers: Andrew Bohonak (SDSU), Leonard Nunney (UCR), Amy Vandergast (USGS)

- Taught five semesters of university lab courses (Genetics & Evolution, Herpetology, Organismal Biology)
 - Highly positive student evaluations available upon request
- Population genomics of how the environment and climate mediate genetic structure and tadpole strategies in Yosemite toads (*Anaxyrus canorus*), major advisor: Dr. Andrew Bohonak
- Identified 1000s of single-copy nuclear SNPs, and a complete tadpole transcriptome
- Used spatial statistics, linear mixed modeling, and graph theory to describe Yosemite toad breeding meadow connectivity, and to predict future changes
- Identifying putatively adaptive markers in pure and admixed lineages of Yosemite toads
- Modeling the outcome of Yosemite toad inter-lineage admixture during climate change
- Research website: <http://www.mountainmanmaier.com/>
- Examples of programmatic outcomes:
 - <http://www.mountainmanmaier.com/software/>
 - <https://github.com/paulmaier/>

*Biologist GS-05/07 Lead, US Geological Survey
Oakhurst and San Diego, California (Feb. 2010 – Mar. 2017)*

Supervisors: Steve Ostoja, Amy Vandergast, Rob Klinger

- Surveyed and sampled animal (amphibians, reptiles, mammals) and plant populations across the western US, using various sampling, trapping and tagging methodologies (see “Technical Skills”)
- Lead for Yosemite toad (*Anaxyrus canorus*) fieldwork during 4 seasons:
 - Surveyed 185/224 (83%) toad meadows in Yosemite NP and 30/32 (94%) toad meadows in Kings Canyon NP (observed 107 adults, 800 subadults, 74,500 larvae, 26,200 eggs)
- Designed methodologies and protocols for meadow surveying, genetic sampling, Bd swabbing
- Trained and supervised activities of field crew, including navigation and gear management
- Managed tabular and spatial data, created summary reports, and contributed to analysis
- Contributed to other projects including Tamarisk biocontrol and Amargosa vole monitoring

*Director/Adviser of Science and GIS, The Biodiversity Group, 501(3)(c)
Ecuador (Jun. 2009 – 2016)*

Supervisor: Paul Hamilton

- Conducted research of lowland and mountainous amphibians and reptiles (2009/11/12/16)
- Identified hundreds of amphibian and reptiles species in western Ecuador
- Used transect protocol to develop model of species detectability by habitat
- Euthanized and preserved laboratory specimens and collected blood and liver samples
- Developed mission statement and pushed science and GIS initiatives into action

*Independent Contractor, Conservation Science
Mojave, California (September 2011)*

Supervisor: Bill Boarman

- Conducted visual encounter surveys for Mojave desert tortoises (*Gopherus agassizii*) in conjunction with federal requirements to mitigate installation of wind turbines

*Research Assistant, Florida International University
Costa Rica (Sept. – Dec. 2009)*

- Researched and collected data for amphibians, reptiles, and mammals using visual encounter, mark-recapture, and tagging methodologies
- Performed laboratory analyses to collect tissue, biomass, and nutrient data
- As lead biological technician, supervised data collection and photography

*Research Assistant, Institute for Conservation Research, San Diego Zoo
Dominica (Aug. – Sept. 2009)*

Supervisor: Chuck Knapp

- Conducted research on endangered Iguanas (*Iguana delicatissima*) to establish population data and identify a dispersal corridor into the island interior
- Tracked adult iguanas using telemetry and noosed adults for morphometric analysis
- Developed and supervised drift fence surveys to quantify hatchling abundance

*Research Assistant, Marine Science Institute, UC Santa Barbara
Clark County, Nevada (Nov. 2008 – Jun. 2009)*

Supervisors: Tom Dudley, Steve Ostoja

- Implemented recapture study on Mojave Desert amphibians, reptiles, and insects, to study effects of biocontrol beetle on invasive plants
- Identified Mojave desert plants using dichotomous keys and led teams to collect data on plant density, richness, and structure following experimental treatments

- Collected and analyzed soil samples for moisture, oxygen and nutrient content
- Managed, collated, and summarized data for dissemination to lead researchers

*Biological Science Technician GS-05, US Forest Service
Prather, California (Jun. – Oct. 2008)*

Supervisors: Stephanie Barnes, Rob Mason

- Acted as liaison, integrating resource management concerns (mitigating damage to Yosemite toads, *Anaxyrus canorus*) with several Sierra NF trail projects
- Assumed three simultaneous jobs: aquatic biologist, trail crew member, wilderness ranger
- As lead aquatic biologist, led crew decisions concerning impacts to high elevation amphibians, and surveyed construction sites for toad presence
- Enforced regulations amongst visitors, taught high elevation wilderness ethics to volunteer groups, and constructed trails using rock tools

*Biological Science Technician GS-04, US Forest Service
Shaver Lake, California (Jun. – Sept. 2006)*

Supervisors: Rob Grasso, Amy Lind

- Assisted study of livestock effects on Yosemite toads (*Anaxyrus canorus*) by surveying meadows and collecting population data
- Collected mark-recapture data (using VIE and PIT tags), Bd swabs, and morphometrics

TECHNICAL SKILLS

Analysis

Pop. Gen.: population delineation, demographic reconstruction, relationship prediction, simulations
 Phylogenetics: concatenated and coalescent approaches, TMRCA dating, ancestral state reconstruction
 Bioinformatics: many pipelines, including: PLINK, GATK, STACKS, PyRAD, Bioconductor
 Machine learning: support vector machines, random forests, neural networks, hidden Markov models
 Statistics: GLM/GLiM/GAM, mixed models, gravity models, time series, Bayesian methods (e.g. ABC)
 GIS: geospatial modeling, kriging, network analysis, cartography, database creation and maintenance

Software

Platforms: Macintosh OS X, Microsoft Windows XP/Vista/7/8, Linux
 Microsoft: Word, Excel, Access, Powerpoint
 GIS: ESRI ArcGIS, QGIS
 Statistics: R, SAS, SYSTAT, Canoco, JMP, Primer
 Programming: R, Python, Unix/Linux, C, C++, Java, Perl
 Image Editing: Adobe Photoshop, Lightroom, Illustrator

Laboratory

Extraction: Qiagen (DNA and RNA), 96-well plates (DNA)
 Electrophoresis: gel visualization and excision
 PCR: basic, touchdown, gradient, emulsion
 Quantification: Bioanalyzer, Qubit, Nanodrop
 Cleanup: AMPure XP, Serapure, Qiagen column purification
 Library Prep: digestion/ligation, Pippin Prep, MID combinatorial barcoding, cDNA synthesis
 Sequencing: Roche 454 Titanium Jr., Illumina HiSeq 2500 (ddRAD and RNAseq library prep)

Wildlife Biology

Amphibian: surveys (visual encounter, call, time constraint, coverboard)
Reptile: noosing, telemetry, surveys (visual encounter, time constraint, burrow, quadrat)
Small mammal: Sherman trapping, ear tagging
Avian: surveys (call, point count, nest search)
Fish: seining, gill netting
Insect: pitfall trapping, sweep netting, stick and light trap, UV lamp moth surveys
Plant: point intercept, Nudds board, quadrat
Misc.: radio telemetry, PIT tagging, VIE tagging, radio collars, dichotomous keys

Other

Mountaineering: backpacking, cross-country navigation, glacier travel, basic climbing, WFR
Photography: wildlife macro-photography and videography
Teaching: presenter for both youth and professional audiences
Spanish: intermediate fluency both written and spoken
Driving: experienced with manual transmissions and 4WD
Flying: pilot of single engine land airplanes, C-150/152/172s

TRAINING and CERTIFICATIONS

2016 *Wilderness First Responder Re-Certificate*, Wilderness Medical Institute
2015 *Private Pilot License*, Riverside Flight Academy
2013 *Next Generation Data Analysis with R*, Institute for Integrative Genome Biology
2013 *Wilderness First Responder Re-Certificate*, Wilderness Medical Associates
2013 *Workshop in Conservation Genomics*, UCLA La Kretz Center for California Conservation Science
2013 *Genomics Data Analysis Workshop*, USGS San Diego Field Station
2013 *eDNA Workshop*, Amphibian Population Task Force
2012 *Spatial Statistics Workshop*, USGS Western Ecological Research Center
2010 *Wilderness First Responder Certificate*, Wilderness Medical Associates
2001 *Black Belt*, West Coast Taekwondo

PROFESSIONAL ACTIVITIES

2017 – present *Ad Hoc Reviewer*:
Evolution, Heredity, Molecular Ecology, Conservation Genetics, Nature Scientific Reports,
Molecular Biology and Evolution, Herpetological Conservation and Biology
2017 – 2018 *Ad Hoc Reviewer*, Panel for Student Success Fee, San Diego State University
2017 – 2018 Student Job Search Committee for “Quantitative Biology Faculty,” San Diego State University
2016 – 2017 *President*, San Diego State Natural History Club, San Diego State University
2015 – 2016 *Co-Organizer*, R Workshop for Graduate Students, San Diego State University
2015 – 2016 *Field Event Organizer*, SDSU Natural History Club, San Diego State University
2013 – 2014 *Chair*, Student Job Search Committee for “Genomics Faculty,” San Diego State University

OTHER ACTIVITIES

2015 – 2018 *Private Pilot*, Riverside Flight School and Plus One Flyers Club
2004 – 2008 *Collegiate Rower*, UC Santa Barbara Rowing Club
2001 – present *Distance Runner*, 2nd place in Lake Tahoe Marathon and other awards
2001 – present *Wildlife Photographer*, several 1st place awards
1997 – present *Percussionist*, advanced musical experience across many genres

PRESENTATIONS

Maier P.A. (2023). A taste of population genetics: the sampler platter (invited tech talk). Presentation to Gene by Gene Ltd. Laboratory, Houston, TX.

Maier P.A., Vandergast A.G., Bohonak A.J. (2023). Ten years of evolutionary research on the Yosemite toad (*Anaxyrus canorus*): what can the past and present tell us about their future? Presentation to Amphibian Population Task Force (APTF), Sebastopol Community Cultural Center, Sebastopol, CA.
<https://doi.org/10.6084/m9.figshare.23304287.v1>

Vandergast A.G., Wood D.A., **Maier P.A.** (2022). Applying genetics to inform the three Rs (resiliency, redundancy, and representation) for conservation of California's rich diversity of herpetofauna. American Society of Ichthyologists and Herpetologists Conference. Spokane, WA.

Maier P.A. (2022). Unraveling your population history with myOrigins 3.0. Presentation to East Coast Genetic Genealogy Conference, Baltimore, MD.

Maier P.A., Vilar M.G., Estes, R.J. (2022). mtDNA Academy. Presentation to East Coast Genetic Genealogy Conference, Baltimore, MD.

Maier P.A. (2022). Innovator (invited session): the tree of mankind age estimates. Presentation to RootsTech International Conference, Salt Lake City, UT.
<https://www.youtube.com/watch?v=jjkL8PWAewk>

Maier P.A. (2022). The Million Mito Project: growing the tree of womankind. Presentation to RootsTech International Conference, Salt Lake City, UT.
<https://www.youtube.com/watch?v=cpctoeKbOKw>

Maier P.A., Vilar M.G., Estes, R.J. (2021). Everything you wanted to know about mitochondrial DNA. Presentation to Genealogical Forum of Oregon. Portland, OR.
<https://www.youtube.com/watch?v=UZ7wl5I0K7s>

Maier P.A. (2021). Family Finder's myOrigins 3.0 explained – Part 1 (overview). Presentation to support product launch and white paper. Houston, TX.
<https://www.youtube.com/watch?v=VnzTeCQ3Hd8>

Maier P.A. (2021). Family Finder's myOrigins 3.0 explained – Part 2 (methodology). Presentation to support product launch and white paper. Houston, TX.
<https://www.youtube.com/watch?v=suDc4CPJsII>

- Maier P.A.** (2021). Family Finder's myOrigins 3.0 explained – Part 3 (why do I have ...). Presentation to support Product launch and white paper. Houston, TX.
<https://www.youtube.com/watch?v=MfcNPUS6ldE>
- Maier P.A.** (2020). A taste of population genetics: the sampler platter. Presentation to RootsTech International Conference, Salt Lake City, UT.
<https://doi.org/10.6084/m9.figshare.11920899.v1>
- Maier P.A.** (2019). A taste of population genetics: the sampler platter. Presentation to 14th International Conference on Genetic Genealogy, Houston, TX.
- Maier P.A.** (2018). Evolutionary past, present, and future of the Yosemite toad (*Anaxyrus canorus*): a total evidence approach to delineating conservation units. Exit Seminar, San Diego State University, San Diego, CA.
- Maier P.A., Bohonak A.J.** (2017). Historical Isolation and Future Adaptation of an Endemic Toad. Presentation to Southwest Herpfest 2017, University of California Riverside, Riverside, CA.
- Maier P.A., Vandergast A.G., Ostojia S.M., Aguilar A., Bohonak A.J.** (2016). Historical isolation and future adaptation: using evolutionary genomics to conserve the Yosemite toad. Presentation to Student Research Symposium (SRS), San Diego State University, San Diego, CA.
- Maier P.A., Vandergast A.G., Ostojia S.M., Aguilar A., Bohonak A.J.** (2016). Historical isolation and future adaptation: using evolutionary genomics to conserve the Yosemite toad. Presentation to Amphibian Population Task Force (APTF), University of California Davis, Davis, CA.
- Maier P.A., Ostojia S.M., Vandergast A.G., Aguilar A., Bohonak A.J.** (2015). Influence of landscape heterogeneity on genomic diversity and adaptation in the Yosemite toad (*Anaxyrus canorus*). Presentation to Amphibian Population Task Force (APTF), Pepperdine University, Malibu, CA.
- Maier P.A., Ostojia S.M., Vandergast A.G., Aguilar A., Bohonak A.J.** (2014). Influences of habitat variation and geography on genomic diversity in the Yosemite toad. Graduate seminar "lunch bunch" presentation, University of California Riverside, Riverside, CA.
- Maier P.A., Ostojia S.M., Vandergast A.G., Aguilar A., Bohonak A.J.** (2014). Influences of habitat variation and geography on genomic diversity in the Yosemite toad. Invited presentation for special genomics session, 21st Annual Wildlife Society Meeting, Pittsburgh, PA.
- Maier P.A.** (2014). Evolutionary biology and conservation in the Sierra Nevada. Presentation for the Research Experience for Undergraduates (REU) program, Sierra Nevada Research Institute, Wawona, CA.
- Maier P.A.** (2013). The tiptoeing toad and tropics untold. Presentation for the San Diego Natural History Club, San Diego State University, San Diego, CA.
- Maier P.A.** (2012). Evolutionary genomics I: adaptation in sticklebacks. Seminar in Evolutionary Biology, San Diego State University, San Diego, CA.
- Maier P.A.** (2010). Wilderness ethics. classroom session presented at the USGS Initiation Days for field crew education, Sierra Nevada Research Institute, Wawona, CA.

Maier P.A. (2010). Natural history of the Yosemite toad. Classroom session presented at the USGS Initiation Days for field crew education, Sierra Nevada Research Institute, Wawona, CA.

Maier P.A. (2010). Camouflage. Assembly presented at the Ellis Elementary School for an upcoming educational unit, Ellis Elementary School, Sunnyvale, CA.

POSTERS

Warshauer E., **Maier P.A.**, Runfeldt G., Fuentes I., Escámez M.J., Valinotto L., et al. Sephardic ancestry in Recessive Dystrophic Epidermolysis Bullosa individuals carrying the prevalent c.6527insc mutation. European Society for Dermatological Research conference, Amsterdam, Netherlands.

Maier P.A., Bohonak A.J., Vandergast A.G. (2017). Historical isolation and future adaptation: using conservation genomics to conserve the Yosemite toad, ARCS Scientist of the Year Dinner, San Diego, CA.

Maier P.A., Bohonak A.J., Vandergast A.G. (2016). Historical isolation and future adaptation: using conservation genomics to conserve the Yosemite toad, ARCS Scientist of the Year Dinner, San Diego, CA.

Rosso A., **Maier P.A.**, Ostojia S.M., Aguilar A. (2012). Conservation genetics of Yosemite toads in Sequoia Kings National Park, University of California Merced, Merced, CA.

PUBLICATIONS

Maier P.A., Vandergast A.G., Bohonak A.J. Yosemite toad (*Anaxyrus canorus*) transcriptome reveals interplay between speciation genes and adaptive introgression. *Molecular Ecology*. In review.

Warshauer E., **Maier P.A.**, Runfeldt G., Fuentes I., Escámez M.J., Valinotto L., Natale M., Manzur G., Illera N., García M., del Río M., Mencia Á., Larcher F., Hellenthal G., Brown A., Consuegra L., Rivera C., Nogueiro I., Tang J., Oro A., Marinkovich P., Palisson F., Titeux M., Hovnanian A., Sprecher E., Skorecki K., Norris D., Bruckner A., Kogut I., Bilousova G., Roop D. Sephardic ancestry in Recessive Dystrophic Epidermolysis Bullosa individuals carrying the prevalent c.6527insc mutation. *Am J Hum Genet*. In review.

Lee S.R., Ostojia S.M., **Maier P.A.**, Matchett J.R., Knapp R.A., McKenny H., Brooks M.L., Danielle N., Berlow E.L. Distribution and spatiotemporal variation of Yosemite toad populations across Sierra Nevada national parks. (2023). *Herpetological Conservation and Biology*. In review.

Begg T.J.A., Schmidt A., Kocher A., Larmuseau H.H.D., Runfeldt G., **Maier P.A.**, Wilson J.D., Barquera R., Maj C., Szolek A., Sager M., Clayton S., Peltzer A., Hui R., Ronge J., Reiter E., Freund C., Burri M., Aron F., Tiliakou A., Osborn J., Behar D., Boecker M., Brandt G., Cleynen I., Strassburg C., Prüfer K., Kühnert D., Meredith W.R., Noethen M.M., Attenborough R.D., Kivisild D., Krause J. (2023). Genomic analyses of hair from Ludwig van Beethoven. *Current Biology*, 33, 1–17. <https://doi.org/10.1016/j.cub.2023.02.041>

Maier P.A., Vandergast A.G., Bohonak A.J. (2023). Using landscape genomics to delineate future adaptive potential for climate change in the Yosemite toad (*Anaxyrus canorus*). *Evolutionary Applications*, 16(1), 74–97. <https://doi.org/10.1111/eva.13511>

- Warshauer E.M., **Maier P.**, Fuentes I., Runfeldt G., Escámez M., Valinotto L., Brown A., Palisson F., Hovnanian A., Roop D. (2022). Sephardic ancestry in Recessive Dystrophic Epidermolysis Bullosa individuals carrying the prevalent c.6527insC mutation [abstract]. *Journal of Investigative Dermatology*, 142(12), S232. <https://doi.org/10.1016/j.jid.2022.09.316>
- Maier P.A.**, Vandergast A.G., Ostojia S.M., Aguilar A., Bohonak A.J. (2022). Landscape genetics of a sub-alpine toad: Climate change predicted to induce upward range shifts via asymmetrical migration corridors. *Heredity*, 129(5), 257–272. <https://doi.org/10.1038/s41437-022-00561-x>
- Maier P.A.**, Runfeldt G., Estes R.J., Vilar M.G. (2022). African mitochondrial haplogroup L7: A 100,000-year-old maternal human lineage discovered through reassessment and new sequencing. *Scientific Report*, 12(1), 10747. <https://doi.org/10.1038/s41598-022-13856-0>
- Maier P.A.**, Vandergast A.G., Ostojia S.M., Aguilar A., Bohonak A.J. (2022). Gene pool boundaries for the Yosemite toad (*Anaxyrus canorus*) reveal asymmetrical migration within meadow neighborhoods. *Frontiers in Conservation Science*, 3, 1–14. <https://doi.org/10.3389/fcsc.2022.851676>
- Maier P.A.**, Hu R., Runfeldt G., Giniebra D., Frichot E. (2021). myOrigins 3.0: Combining global and local methods for determining population ancestry. FamilyTreeDNA White Paper 2021-08-18. <https://doi.org/10.13140/RG.2.2.30398.00328>
- Hu R., **Maier P.A.**, Runfeldt G., Estes R., Rocha E., Walker A., Baur P., Ty L. (2021). Family Finder Matching 5.0: Matching algorithm and relationship estimation. FamilyTreeDNA White Paper 2021-08-18. <https://doi.org/10.13140/RG.2.2.13620.78720>
- Warshauer E., Brown A., Fuentes I., Shortt J., Gignoux C., Montinaro F., Metspalu M., Youssefian L., Vahidnezhad H., Jacków J., Christiano A.M., Uitto J., Fajardo-Ramírez Ó.R., Salas-Alanis J.C., McGrath J.A., Consuegra L., Rivera C., **Maier P.A.**, Runfeldt G., Behar D.M., Skorecki K., Sprecher E., Palisson F., Norris D.A., Bruckner A.L., Kogut I., Bilousova G., Roop D.R. (2021). Ancestral patterns of Recessive Dystrophic Epidermolysis Bullosa mutations in Hispanic populations suggest Sephardic ancestry. *American Journal of Medical Genetics Part A*, 185(11), 3390–3400. <http://doi.org/10.1002/ajmg.a.62456>
- Lindauer A.L., **Maier P.A.**, Voyles J. (2020). Daily fluctuating temperatures decrease growth and reproduction rate of a lethal amphibian fungal pathogen in culture. *BMC Ecology*, 20(18), 1–9. <https://doi.org/10.1186/s12898-020-00286-7>
- Jia K.-H., Zhao W., **Maier P.A.**, Hu X.-G., Jin Y., Zhaou S.-S., Jiao S.-Q., El-Kassaby Y.A., Wang T., Wang X.-R., Mao J.-F. (2020). Landscape genomics predicts climate change vulnerability for forest tree: a case from a wide-spread conifer tree, *Platycladus orientalis*. *Evolutionary Applications*, 13(4), 665–676. <https://www.doi.org/10.1111/eva.12891>
- Maier P.A.**, Vandergast A.G., Ostojia S.M., Aguilar A., Bohonak A.J. (2019). Pleistocene glacial cycles drove lineage diversification and fusion in the Yosemite toad (*Anaxyrus canorus*). *Evolution*, 73(12), 2476–2496. <https://www.doi.org/10.1111/evo.13868>
- Maier P.A.** (2019) *Anaxyrus canorus* (Yosemite toad) larval diet. *Herpetological Review*, 50(1), 111–112. https://www.researchgate.net/publication/334973844_Anaxyrus_canorus_Yosemite_Toad_Larval_diet
- Maier P.A.** (2018). *Anaxyrus canorus* (Yosemite toad) breeding behavior. *Herpetological Review*, 49(4), 727–728. https://www.researchgate.net/publication/334973673_Anaxyrus_canorus_Yosemite_Toad_Breeding_behavior
- ** You can view the observation here: <https://youtu.be/EspmwdPasBE> **

Maier P.A. (2018). Evolutionary past, present, and future of the Yosemite toad (*Anaxyrus canorus*): a total evidence approach to delineating conservation units. Ph.D. dissertation. University of California Riverside, and San Diego State University, San Diego, CA. <https://escholarship.org/uc/item/7jf3x4kg>

[Introduction](#)

[Chapter 1: Pleistocene Glacial Cycles Drove Lineage Diversification and Fusion](#)

[Chapter 2: Genomic Geography: Islands and Rivers of Divergence at Secondary Contact Zones](#)

[Chapter 3: A Novel Genetic Network Model Estimates Environmentally Mediated Migration](#)

[Chapter 4: Predicting The Unknown: Conservation Units for Evolutionary Potential](#)

[Conclusion](#)

Maier P.A., Ostojia S.M., Aguilar A., Bohonak A.J. (2016). Conservation genomics of the Yosemite toad: implications of deep divergence and limitations to meadow connectivity. USGS Cooperator's Report to the National Park Service. San Diego State University, San Diego, CA.
<http://dx.doi.org/10.13140/RG.2.2.10270.41281>

Klinger R., Cleaver M., Anderson S., **Maier P.**, Clark J. (2015). Implications of scale-independent habitat specialization on persistence of a rare small mammal. *Global Ecology and Conservation*, 3, 100–114.
<http://dx.doi.org/10.1016/j.gecco.2014.10.003>

Klinger R., Cleaver M., Anderson S., **Maier P.**, Clark J. (2013). Short-term population dynamics, demography, and habitat selection by the Amargosa vole. USGS Final Report to the Bureau of Land Management. USGS Bishop Field Station, Bishop, CA.

MANUSCRIPTS IN PREPARATION

Maier P.A. Larval development evolution among pure and admixed lineages of *Anaxyrus canorus*. *In prep.*

YOSEMITE TOAD EXPERIENCE

I have spent approximately 3,240 hours conducting research on Yosemite toads in meadows throughout their distribution in Yosemite and Kings Canyon NP, and also Sierra NF, Stanislaus NF, Inyo NF, and Humboldt-Toiyabe NF. This includes 8 field seasons in the years 2006, 2008, 2010–14, and 2016. My participation in 2006 and 2008 was through the US Forest Service, during which time I handled approximately 50 adult toads, 200 subadults, and counted 10,000 larvae. I performed morphometric analysis on adults, swabbed them for Bd, sexed them, and installed PIT tags. I injected all metamorphs and older subadults with visible implant elastomer (VIE) tags. I visited approximately 50 toad meadows in the national forests. In 2010–14 my participation was through the US Geological Survey, where I led a census of all toad meadows in Kings Canyon and Yosemite NP. I visited 185/224 (83%) toad meadows in Yosemite NP and 30/32 (94%) toad meadows in Kings Canyon NP. During this time I observed 107 adults, 800 subadults, 74,500 larvae, 26,200 eggs. Of these, I swabbed approximately 25 adults and 100 subadults for Bd and clipped ~1 mm² tail tissue from 2300 tadpoles for genetic analysis. In 2016, I observed 24 adult toads, 3,500 subadults, 41,500 tadpoles, and 15,000 eggs. I handled 1,455 tadpoles and 1,024 metamorphs for morphometric analysis. **In total, I have observed (and handled) 181 (50) adult toads, 4,500 (1,224) subadults, 126,000 (3,755) tadpoles, and 41,200 eggs. To my knowledge, none of these animals have been killed or harmed.** I have previously been authorized to handle Yosemite toads under a 10a1a permit.

OTHER RELEVANT AMPHIBIAN EXPERIENCE

I have observed or handled many other species of amphibian, including 60 species in the US, and 190 species overall, includes the countries of Ecuador, Costa Rica, Belize, Dominica, and Mexico. This includes captive husbandry and specimen preservation.

REFERENCES

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