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Education

- 2010 – Present **Ph.D. Candidate in Biology** – Degree expected in January 2018
University of New Mexico, Albuquerque, NM
Advisors: Drs. Joseph Cook & Jeremy Edwards
- 2006 **B.S. in Genetics, Cell Biology, and Development**
University of Minnesota – Twin Cities, Minneapolis, MN
Advisor: Dr. Patricia Tam

Professional Experience

- 2014 – Present **Research Assistant**, University of New Mexico, Albuquerque, NM
Department of Chemistry & Chemical Biology – Edwards Lab
- 2015 – Present **Consultant**, Sentieon Inc., Mountain View, CA
- 2017 **Co-Instructor**, University of New Mexico, Albuquerque, NM
Biology 519, Chemistry 587 – Genome Technologies & Bioinformatics
- 2016 **Co-Instructor**, University of New Mexico, Albuquerque, NM
Biology 519, Chemistry 587 – Transcriptome Technologies & Bioinformatics
- 2013 **Teaching Assistant**, University of New Mexico, Albuquerque, NM
Biology 202 – Genetics
- 2011 – 2013 **PiBBS Fellow**, University of New Mexico, Albuquerque, NM
Program in Interdisciplinary Biological & Biomedical Sciences
- 2010 – 2011 **Graduate Assistant**, University of New Mexico, Albuquerque, NM
Museum of Southwestern Biology – Division of Genomic Resources
- 2008 – 2010 **Research Associate II**, Institute for Systems Biology, Seattle, WA
Hood & Galas Labs
- 2006 – 2008 **Research Scientist Assistant**, University of Washington, Seattle, WA
Genome Sciences Department – MacCoss Lab
- 2004 – 2006 **Undergraduate Research**, University of Minnesota, Minneapolis, MN
Department of Medicine – Tam Lab

Research Interests

Molecular evolution, functional genomics, bioinformatics, transcriptomics, next-generation sequencing technologies, genome engineering, systems biology, epigenetics, phylogenomics.

Publications

1. **J.A. Weber***, J. Kim*, O. Jung*, J.H. Jeon, H. Lee, S. Jho, Y.S. Cho, D.S. Kim, W. Paek, S. Kim, H. Lee, S. Lee, J.S. Edwards, J.A. Cook, J. An, J. Bhak. Whole genome sequencing of the endangered long-tailed goral (*Naemorhedus caudatus*) reveals adaptive evolution and potentially significant conservation implications. *Submitted*. ***Contributed equally**
2. H.M. Kim*, N. Lee*, **J.A. Weber***, S.G. Park, Y.S. Cho, Y. Bhak, N. Lee, Y. Jeon, S. Jeon, Y.J. Jo, S. Woo, K. Shin, O. Chung, J.C. Ryu, H.S. Yim, J.H. Lee, J.S. Edwards, A. Manica, J. Bhak, J. Yum. The jellyfish genome sheds light on the early evolution of active predation. *Submitted*. ***Contributed equally**
3. J. Kim*, **J.A. Weber***, S. Jho*, J. Jang, J.H. Jun, Y.S. Cho, H.M. Kim, H. Kim, Y. Kim, O. Chung, C. Kim, H.J. Lee, B. Kim, K. Han, S. Lee, I.S. Koh, K. Chae, J.S. Edwards, J. Bhak. KoVariome: Korean National Standard Reference Variome database of whole genomes with SNV, Indel, CNV, and SV analyses. *In Review*. ***Contributed equally**
4. H.J. Lee, O. Chung, Y.S. Cho, S. Jho, J.H. Jun, J. Kim, **J.A. Weber**, J.S. Edwards, J. Lim, W.K. Paek, J. Bhak. A whole genome analysis of the red-crowned crane provides insight into avian longevity. *In Review*.
5. S. Kim, Y.S. Cho, H.M. Kim, O. Chung, H. Kim, S. Jho, H. Seomun, J. Kim, W.Y. Bang, C. Kim, J. An, C.H. Bae, Y. Bhak, S. Jeon, H. Yoon, Y. Kim, J. Jun, H. Lee, S. Cho, O. Uphyrkina, A. Kostyria, J. Goodrich, D. Miquelle, M. Roelke, J. Lewis, A. Yurchenko, A. Bankevich, J. Cho, S. Lee, J.S. Edwards, **J.A. Weber**, J. Cook, S. Kim, H. Lee, A. Manica, I. Lee, S.J. O'Brien, J. Bhak, J.H. Yeo. Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly. *Genome Biology* 17:211 (2016).
6. B.S. McLean, K.C. Bell, J.L. Dunnum, A. Abrahamson, J.P. Colella, E.R. Deardorff, **J.A. Weber**, A.K. Jones, F. Salazar-Miralles, J.A. Cook. Natural history collections-based research: progress, promise, and best practices. *Journal of Mammalogy* 97(1):287–29 (2016).
7. O. Chung, S. Jin, Y.S. Cho, J. Lim, H. Kim, S. Jho, H. Kim, J. Jun, H. Lee, A. Chon, J. Ko, J.S. Edwards, **J.A. Weber**, K. Han, S.J. O'Brien, A. Manica, J. Bhak, W.K. Paek. The first whole genome and transcriptome of the cinereous vulture reveals adaptation in the gastric and immune defense systems and possible convergent evolution between the Old and New World vultures. *Genome Biology* 16(1):1-11 (2015).
8. C.R. Tyler, **J.A. Weber**, M. Labrecque, J.M. Hessinger, J.S. Edwards, A.M. Allan. ChIP-Seq analysis of the adult male mouse brain after developmental exposure to arsenic. *Data in Brief* 5:248-54 (2015).
9. Y. Ogasawara, N. Torrez-Martinez, A.D. Aragon, B.J. Yackley, **J.A. Weber**, A. Sundararajan, T. Ramaraj, J.S. Edwards, C.E. Melancon. High-quality draft genome sequence of *Actinobacterium Kibdelosporangium* sp. MJ126-NF4, producer of type II polyketide azicemicins, using Illumina and PacBio technologies. *Genome Announcements* 3(2):e00114-15 (2015).
10. **J.A. Weber**, D.H. Baxter, S. Zhang, D.Y. Huang, K.H. Huang, M.J. Lee, D.J. Galas, K. Wang. The microRNA spectrum in 12 body fluids. *Clinical Chemistry* 56(11):1733-41 (2010).
11. K. Wang, S. Zhang, **J.A. Weber**, D. Baxter, D.J. Galas. Export of microRNAs and microRNA-protective protein by mammalian cells. *Nucleic Acids Research* 38(20): 7248-59 (2010).

See <https://scholar.google.com/citations?hl=en&user=IMBahUcAAAAJ> for current publications and citations.

Non-Refereed Publications:

1. D.N. Freed, R. Aldana, **J.A. Weber**, J.S. Edwards. The Sentieon Genomics Tools – A fast and accurate solution to variant calling from next-generation sequence data. *bioRxiv* doi:10.1101/115717 (2017).
2. **J.A. Weber**, R. Aldana, B.D. Gallagher, J.S. Edwards. Sentieon DNA pipeline for variant detection - Software-only solution, over 20x faster than GATK 3.3 with identical results. *PeerJ PrePrints* 4:e1672v2 (2016).

3. K. Wang, S. Zhang, **J.A. Weber**, D. Baxter, D.J. Galas. Mammalian cells in culture actively export specific microRNAs. *Nature Precedings* hdl:10101/npre.2009.3718.1 (2010).

Manuscripts In Preparation:

1. **J.A. Weber**, O. Chung, Y.S. Cho, H. Kim, Y. Kim, J. Mudge, J.A. Cook, J.L. Kelley, J. Bhak, C.C. Witt, J.S. Edwards. Whole genome comparisons among hummingbirds reveal targets of natural selection during repeated high-altitude colonization.
2. **J.A. Weber**, J.L. Dunnum, K.C. Bell, Y.S. Cho, J. Bhak, J.L. Kelley, J.S. Edwards, J.A. Cook. Comparative genomics analyses reveal independently evolved high-altitude adaptations in three species of wild cavies.

Selected Presentations

1. Sequencing, Finishing, and Analysis in the Future Meeting, 12th Annual Meeting, Santa Fe, NM, 2017. *Whole genome comparisons of montane hummingbirds reveal targets of natural selection during independent high-altitude colonizations.*
2. American Society of Mammalogists, 96th Annual Meeting, Minneapolis, MN, 2016. *The molecular basis of high-elevation adaptation in wild cavies.*
3. Society for the Study of Evolution, Annual Meeting, Austin, TX, 2016. *The molecular evolution of high-altitude adaptation in Andean hummingbirds.*
4. University of New Mexico Department of Biology, Albuquerque, NM, 2014. *Genomic signatures of high-altitude adaptation in an Andean hummingbird.*
5. Society for Molecular Biology and Evolution Annual Conference, Chicago, IL, 2013. *The molecular basis of high-altitude adaptation in a hummingbird (Oreotrochilus melanogaster).*
6. National Institute of Biomedical Imaging and Bioengineering Training Grantees Meeting, Bethesda, MD, 2012. *A whole genome assembly of the Black-breasted Hillstar (Oreotrochilus melanogaster).*
7. New Mexico Bioinformatics Symposium, Santa Fe, NM, 2012. *The molecular evolution of high-altitude adaptation in guinea pigs.*
8. New Mexico Bioinformatics Symposium, Santa Fe, NM, 2011. *Mammalian cells in culture actively export specific microRNAs.*
9. Institute for Systems Biology 7th Annual International Symposium, Systems Biology and Engineering, Seattle, WA, 2010. *A global survey of microRNA in human body fluids.*
10. Institute for Systems Biology Annual Retreat, Port Angeles, WA, 2009. *Extracellular microRNA – a new class of biomarker.*
11. Institute for Systems Biology 6th Annual International Symposium, Seattle, WA, 2009. *MicroRNA in Human Body Fluids.*

Grants

- Lynn Hertel Memorial Scholarship, 2016. *The timing and genetic consequences of guinea pig domestication.*
- Society for the Study of Evolution Travel Grant, 2016. *The molecular evolution of high-altitude adaptation in Andean hummingbirds.*
- Donald Caughran Memorial Scholarship, 2016.
- Alvin R. and Caroline G. Grove Summer Research Scholarship, 2016.

- NM-INBRE Sequencing & Bioinformatics Pilot Award, 2015. *A genomic perspective on molecular adaptation to hypoxia.*
- American Society of Mammalogists Grant-in-Aid of Research, 2015. *Molecular evolution of high-altitude adaptation in wild cavies.*
- Society for the Study of Evolution Travel Grant, 2015. *Genomic signatures of high-altitude adaptation in an Andean hummingbird.*
- Gaudin Scholarship, 2015. *Molecular evolution of high-altitude adaptation in the Andes.*
- Graduate Research Allocations Committee Research Grant, 2015.
- Gaudin Scholarship, 2013. *The molecular basis of high-elevation adaptation in the Andes.*
- Graduate Research Allocations Committee Research Grant, 2015.
- Gaudin Scholarship, 2012. *The molecular basis of high-elevation adaptation in guinea pigs.*
- Program for Interdisciplinary Biological and Biomedical Sciences Graduate Fellowship, 2011.
- Graduate Research Allocations Committee Research Grant, 2011.

Professional Activities & Service

- Reviewer for *BMC Evolutionary Biology*.
- Mentor to 1 post-baccalaureate student, 4 undergraduate students, and 1 high school student.
- Professional Memberships: Society for Molecular Biology and Evolution, Society for the Study of Evolution, American Society of Mammalogists.

Teaching Experience

- Co-Instructor – Biology 519, Chemistry 587: Genome Technologies & Bioinformatics.
- Co-Instructor – Biology 519, Chemistry 587: Transcriptome Technologies & Bioinformatics.
- Guest Lecturer – Chemistry 587: Genome Technologies & Bioinformatics.
- Teaching Assistant – Biology 202: Genetics.

Field Experience

- Museum of Southwestern Biology (MSB) Mammal Division mammal surveys across NM. 2011 – Present
- Joint MSB Mammal Division/Gorgas Memorial Institute infectious disease monitoring and mammal survey in Darién Province, Panama. 2015

Citizenship

- United States citizen.