Clayton M. Small

Research Assistant Professor /

Data Science Graduate Program Coordinator

Data Science Initiative | University of Oregon | Eugene, OR 97403-5289

csmall@uoregon.edu | 979.255.4037

website: [h2omics.com](https://h2omics.com/) | @claymsmall

KEY CONTRIBUTIONS

- Partnered to establish stickleback as a gnotobiotic model for host-microbe interactions

- Led production and publication of the first reference genome for syngnathid fishes

- Developed graduate-level courses in applied bioinformatics and foundational statistics

- Led design of a new master’s program in data science at the University of Oregon

EDUCATION & TRAINING

2012- **Postdoctoral**

2017 University of Oregon – Eugene, OR

Advisor: William A. Cresko

2012 Ph.D., Zoology

Texas A&M University – College Station, TX

Genomic insights into sexual selection and the

evolution of reproductive genes in teleost fishes

Advisor: Adam G. Jones

2003 B.S., Zoology, cum laude

University of Idaho – Moscow, ID

Faculty Mentor: John A. Byers

PROFESSIONAL EXPERIENCE

2020- Research Assistant Professor / Graduate Program Coordinator

Present Data Science Initiative

Institute of Ecology and Evolution (Affiliate)

University of Oregon – Eugene, OR

2017- Research and Teaching Associate

2020 Knight Campus for Accelerating Science Impact and

Institute of Ecology and Evolution

University of Oregon – Eugene, OR

2005 Field and Laboratory Assistant

Texas A&M University – College Station, TX

2004 Field Research Technician

Washington Department of Fish and Wildlife

2003 Research Assistant, Barbados Sea Turtle Project

University of the West Indies, Cave Hill – Barbados

# GRANTS & AWARDS

2020- **National Science Foundation Rules of Life Collaborative**

2023 **Research:** “RoL: The evo-devo of male pregnancy and its effects

on the brood pouch microbiome,” Co-PI w/ W. Cresko and

A. Jones

2011 **National Science Foundation Doctoral Dissertation**

**Improvement Grant,** “A next-generation sequencing approach

to the evolution of malepregnancy transcriptomes in seahorses and pipefishes”

2011 **Roozbeh Arianpour Endowed Memorial Scholarship**

2010 **Texas A&M Graduate Student Council Travel Award**

2008 **Texas A&M EEB Graduate Student Travel Award**

2008 **American Museum of Natural History Lerner-Gray Fund for**

**Marine Research**, “Sexual selection and rate of reproductive

protein evolution in the male-pregnant syngnathid fishes”

2008 **Sigma Xi Grant in Aid of Research**, “Sexual selection and rate

of reproductive protein evolution in the male-pregnant

syngnathid fishes”

2007 **Texas A&M EEB Graduate Student Travel Award**

2002 **Sundquist Undergraduate Research Grant**,Department of

Biological Sciences, University of Idaho. “Sire mating success

and fawn postnatal growth rate in American pronghorn”

# PUBLICATIONS

**\****equal contributions*

**†** *high school / undergraduate student mentee*

Ramesh B, Small CM, Healey HM, Johnson B, Barker E, Currey MC, Bassham S, Myers M, Cresko WA, Jones AG. 2023. Improvements to the Gulf pipefish *Syngnathus scovelli* genome. *GigaByte* [10.46471/gigabyte.76](https://doi.org/10.46471/gigabyte.76).

Frantz SI, Small CM, Cresko WA, Singh ND. 2023. Ovarian transcriptional response to Wolbachia infection in *D. melanogaster* in the context of between-genotype variation in gene expression. *G3* [10.1093/g3journal/jkad047](https://doi.org/10.1093/g3journal/jkad047).

**\***Small CM, Healey HM, Currey MC, Beck EA, Catchen J, Lin ASP, Cresko WA, **\***Bassham S. 2022. Leafy and weedy seadragon genomes connect genic and repetitive DNA features to the extravagant biology of syngnathid fishes. [*PNAS* 119:e2119602119](https://doi.org/10.1073/pnas.2119602119) [(cover article)](https://www.pnas.org/toc/pnas/119/26).

Johnson BD, Anderson AP, Small CM, Rose E, Flanagan SP, Hendrickson-Rose C, Jones AG. 2022. The evolution of the testis transcriptome in pregnant male pipefishes and seahorses. [*Evolution* 76:2162-2180](https://doi.org/10.1111/evo.14579).

Petersen AM, Small CM, Yan Y, Wilson C, Bremiller RA, Buck LC, von Hippel FA, Cresko WA, Postlethwait JH. 2022. Evolution and developmental expression of the sodium iodide symporter (NIS, *slc5a5*) gene family: Implications for perchlorate toxicology. [*Evolutionary Applications* 15:1079-1098](https://doi.org/10.1111/eva.13424).

Beck EA, Healey HM, Small CM, Currey MC, Desvignes T, Cresko WA, Postlethwait JH. 2021. Advancing human disease research with fish evolutionary mutant models. [*Trends in Genetics* 38:22-44](https://doi.org/10.1016/j.tig.2021.07.002).

Beck EA,Currey M, Small CM, Cresko WA. 2020. QTL mapping of intestinal neutrophil variation in threespine stickleback reveals possible gene targets connecting intestinal inflammation and systemic health. [*G3* g3.119.400685](https://doi.org/10.1534/g3.119.400685).

Small CM,Currey M, Beck EA, Bassham S, Cresko WA. 2019. Highly reproducible 16S sequencing facilitates measurement of host genetic influences on the stickleback gut microbiome. [*mSystems* 4:e00331-19](https://doi.org/10.1128/mSystems.00331-19).

**\*†**Cytrynbaum EG, **\***Small CM, Kwon RY, Boaz H, Kent D, Yan Y, Knope ML, Bremiller RA, Desvignes T, Kimmel CB. 2019. Developmental tuning of mineralization drives morphological diversity of gill cover bones in sculpins and their relatives. [*Evolution Letters* 3:374-391](https://doi.org/10.1002/evl3.128).

Kimmel CB, Small CM, Knope ML. 2017. A rich diversity of opercle bone shape among teleost fishes. [*PLoS One* 12:e188888](https://doi.org/10.1371/journal.pone.0188888).

Small CM, Milligan-Myhre K, Bassham S, Guillemin K, Cresko WA. 2017. Host genotype and microbiota contribute asymmetrically to transcriptional variation in the threespine stickleback gut. [*Genome Biology and Evolution* 9:504-520](https://doi.org/10.1093/gbe/evx014).

**\***Small CM, **\***Bassham S, **\***Catchen J, Amores A, Fuiten AF, Brown RS, Jones AG, Cresko WA. 2016. The genome of the Gulf pipefish enables understanding of evolutionary innovations. [*Genome Biology* 17:258](https://doi.org/10.1186/s13059-016-1126-6).

Milligan-Myhre K, Small CM, Mittge EK, **†**Agarwal M, Cresko WA, Guillemin K. 2016. Innate immune responses to gut microbiota differ between threespine stickleback populations. [*Disease Models and Mechanisms* 9:187-198](https://doi.org/10.1242/dmm.021881).

Rose E, Small CM, **†**Saucedo HA, Harper C, Jones AG. 2014. Genetic evidence for monogamy in the dwarf seahorse, Hippocampus zosterae. [*Journal of Heredity* 105:828-833](https://doi.org/10.1093/jhered/esu050).

Small CM, Harlin-Cognato AD, Jones AG. 2013. Functional similarity and molecular divergence of a novel reproductive transcriptome in two male-pregnant Syngnathus pipefish species. [*Ecology and Evolution* 3:4092-4108](https://doi.org/10.1002/ece3.763).

Mobley KB, Small CM, Jones AG. 2011. Molecular insights into syngnathid biology: the genetics and genomics of pipefishes, seahorses, and seadragons. [*Journal of Fish Biology* 78:1624-1646](https://doi.org/10.1111/j.1095-8649.2011.02967.x).

Mobley KB, Small CM, Jue NK, Jones AG. 2010. Population structure of the dusky pipefish (*Syngnathus floridae*) from the Atlantic and Gulf of Mexico, as revealed by mitochondrial DNA and microsatellite analyses. [*Journal of Biogeography* 37:1363-1377](https://doi.org/10.1111/j.1365-2699.2010.02288.x).

Jones AG, Small CM, Paczolt KA, Ratterman NL. 2010. A practical guide to methods of parentage analysis. [*Molecular Ecology Resources* 10:6-30](https://doi.org/10.1111/j.1755-0998.2009.02778.x).

Small CM, Carney GE, Mo Q, Vannucci M, Jones AG. 2009. A microarray analysis of sex- and gonad-biased gene expression in the zebrafish: evidence for masculinization of the transcriptome. [*BMC Genomics* 10:579](https://doi.org/10.1186/1471-2164-10-579).

**SUBMITTED/DRAFT MANUSCRIPTS**

\*Small CM, \*Beck EA, Currey MC, Tavalire HF, Bassham S, Cresko WA. 2022. Host genomic variation shapes gut microbiome diversity in threespine stickleback fish. In revision at *mBio*. [bioRxiv preprint available](https://doi.org/10.1101/2022.11.14.516485).

Small CM and Jones AG. Sexual selection is not a pervasive driver of male pregnancy protein evolution in syngnathid fishes.

**TEACHING**

2020- \***Course Developer and** **Instructor**, BI 610 (Foundational

2021 Statistics) University of Oregon, Spring Term

Course gitbook: <https://uo-biostats.github.io/Found_Stat/>

2014- \***Course Developer and** **Instructor**, BI 623 (Advanced Topics in

2019 Genomic Analysis) University of Oregon, Summer Term

2017- \***Co-Course Developer and** **Instructor**, BI 624 (Genomics

2018 Research Lab) University of Oregon, Fall Term

2015 \***Instructor**, BI 610 (Advanced Biological Statistics) University of Oregon, Fall Term

2013 **Co-Instructor**, BI 610 (Advanced Biological Statistics)

University of Oregon, Fall Term (co-taught with W. A. Cresko)

2005-**Teaching Assistant**,BIOL 111 (Introductory Biology)

2011 Texas A&M University, laboratory instructor for 2 semesters

**Teaching Assistant**,BIOL 214 (Genes, Ecology, and Evolution)

Texas A&M University, teaching assistant, 4 semesters

**Teaching Assistant**, BIOL 107 (Introduction to Zoology)

Texas A&M University, laboratory instructor, 3 semesters

**Teaching** **Assistant**, BIOL 466 (Principles of Evolution)

Texas A&M University, teaching assistant, 3 semesters

*\* instructor of record for graduate-level course*

**RESEARCH MENTORING**

2015- **Primary Mentor,** high school/undergraduate research assistant

2019 (mentee Eli Cytrynbaum), Kimmel Lab, University of Oregon

2013 **Primary Mentor,** SPUR/AORTA undergraduate research program, University of Oregon, Summer Term (mentee Shamariah Hale)

2007- **Primary Mentor,** UBM undergraduate biology/math research

2010 program, Texas A&M University, (mentee Danielle Schroeder)

2009- **Primary Mentor,** Undergraduate research thesis project

2012 Texas A&M University, (mentee Hector Saucedo)

Thesis: “Characterizing the mating system of the opossum pipefish, *Microphis* *brachyurus* *lineatus*, using polymorphic microsatellite markers”

# CONTRIBUTED PAPER PRESENTATIONS

Society for the Study of Evolution, Portland, Oregon, June 25, 2017. The Gulf pipefish genome enriches our understanding of an evolutionary innovation. C. M. Small, S. Bassham, J. Catchen, A. Amores, A. Fuiten, A. G. Jones, and W. A. Cresko. (talk)

SyngBio 2017, Tampa, Florida, May 15, 2017. The Gulf pipefish reference genome facilitates genetic study of derived morphologies and an evolutionary novelty. C. M. Small, S. Bassham, J. Catchen, A. Amores, A. Fuiten, A. G. Jones, and W. A. Cresko. (talk)

NIGMS National Centers for Systems Biology Annual Meeting, Albuquerque, New Mexico, July 9-10, 2015. Gnotobiotic threespine stickleback provide insights into host genotype-by-environment interactions and the gastrointestinal transcriptome. C. M. Small, K. Milligan-Myhre, K. Guillemin, and W. A. Cresko. (talk and poster)

1st Joint Congress on Evolutionary Biology, Ottawa, Canada, July 8, 2012. The evolution of male pregnancy genes among pipefish and seahorse lineages with diverse mating systems. C. M. Small, A. Harlin-Cognato, and A. G. Jones. (talk)

Society for the Study of Evolution, Portland, Oregon, June 28, 2010. Evolution of the male pregnancy transcriptome in pipefish: A 454 sequencing approach. C. M. Small, A. Harlin-Cognato, A. G. Jones. (talk)

Society for the Study of Evolution, Minneapolis, Minnesota, June 19, 2008. Sex- and gonad-biased gene expression in *Danio rerio* revealed by microarray analyses. C. M. Small, G. E. Carney, Q. Mo, M. Vannucci, A. G. Jones. (talk)

Society for Molecular Biology and Evolution, Halifax, Nova Scotia, Canada, June 25, 2007. Sexual selection at genomic and molecular levels: Expression patterns and evolution of reproductive protein-coding genes in *Danio rerio*. C. M. Small, A. G. Jones, and G. E. Carney. (poster)

Society for the Study of Evolution, Stony Brook, New York, June 24, 2006. Identifying gonad-specific transcripts in *Danio rerio* using microarrays: Groundwork for the study of reproductive molecular evolution in fishes. C. M. Small, Q. Mo., G. E. Carney, and A. G. Jones. (poster)

# INVITED CONFERENCE TALKS

2nd International Fish Microbiota Workshop. Eugene, Oregon. September 3, 2019. Highly reproducible 16S sequencing facilitates measurement of host genetic influences on the stickleback gut microbiome. C. M. Small, M. Currey, E. A. Beck, S. Bassham, and W. A. Cresko.

META Center Symposium on Host-Microbe Systems Biology. Eugene, Oregon. August 6, 2016. Host genotype, the microbiota, and their interaction contribute to transcriptional variation of the gut in larval threespine stickleback. C. M. Small, K. Milligan-Myhre, K. Guillemin, and W. A. Cresko.

7th Aquatic Animal Models of Human Disease Conference. Austin, Texas. December 13-18, 2015. Microbiota and host genotype interact to influence the gastrointestinal transcriptome of gnotobiotic threepine stickleback. C. M. Small, K. Milligan-Myhre, K. Guillemin, and W. A. Cresko.

EVO-WIBO. Port Townsend, Washington. April 26, 2014. Transcriptomic insights into the evolution of male pregnancy. C. M. Small, W. A. Cresko, and A. G. Jones.

**INVITED SEMINARS**

Host genetics, evolutionary innovations, and host-microbe interactions in marine fishes. Texas A&M University - Corpus Christi, April 3, 2023.

Genomic resources enable the study of adaptation in pipefishes and their relatives. University of Tampa, November 18, 2016.

Genomic resource development for the study of adaptation in non-model fishes. University of San Francisco, April 19, 2016.

Selection in relation to sex and the genomics of male pregnancy in pipefish and seahorses. Texas A&M University, November 8, 2011.

Evolutionary insights into reproductive transcriptomes: examples from non-model teleost fishes. University of Oregon. August 12, 2011.

# SERVICE

**Graduate program coordination:** Coordinator of planning and curriculum development for the new Data Science Master’s Program. University of Oregon, 2020-2022.

**Academic administration:** Member, search committee for Career Instructor in the undergraduate Data Science Program. University of Oregon, 2021.

Member, undergraduate Data Science Program planning committee. University of Oregon, 2019.

**Symposium organization:** 8th annual Ecological Integration Symposium. “Interdisciplinary Approaches to Biodiversity: From Speciation to Extinction.” Texas A&M University, April 20th-21st, 2007. (Co-organizer)

**Academic Journal Peer Review:** *Behavioral Ecology*, *Ecology and Evolution*, *Gene*, *Molecular Biology and Evolution, Molecular Ecology*, *Molecular Ecology Resources*, *mSystems, Nature Communications, Nature Ecology and Evolution*.

# HONORARY AND PROFESSIONAL SOCIETIES

- AAAS/Science Program for Excellence in Science (Sponsored in 2019)

- National Society of Collegiate Scholars

- Phi Sigma Biological Sciences Honors Society (Beta Eta Chapter)

- Society for the Study of Evolution