

# Clayton M. Small

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## KEY CONTRIBUTIONS

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- 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 statistics
- Led launch of a new master's program in data science at the University of Oregon

## EDUCATION & TRAINING

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- 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

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- 2020-      **Research Assistant Professor / Graduate Program Coordinator**  
Present    Data Science Department  
            Institute of Ecology and Evolution (Affiliate)  
            University of Oregon – Eugene, OR

- 2017-  
2020      **Research and Teaching Associate**  
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**

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- 2020-  
2023      **National Science Foundation Rules of Life Collaborative  
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 male pregnancy transcriptomes in seahorses  
and pipefishes”
- 2011      **Roosbeh 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**

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*\*equal contributions*

*† high school / undergraduate student mentee*

\*Small CM, \*Beck EA, Currey MC, Tavalire HF, Bassham S, Cresko WA. 2023. Host genomic variation shapes gut microbiome diversity in threespine stickleback fish. *mBio* [e00219-23](#).

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](#).

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](#).

\*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 \(cover article\)](#).

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](#).

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](#).

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](#).

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](#).

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](#).

\*†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](#).

Kimmel CB, Small CM, Knope ML. 2017. A rich diversity of opercle bone shape among teleost fishes. [PLoS One 12:e188888](#).

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](#).

\*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](#).

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](#).

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](#).

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](#).

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](#).

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](#).

Jones AG, Small CM, Paczolt KA, Ratterman NL. 2010. A practical guide to methods of parentage analysis. [\*Molecular Ecology Resources\* 10:6-30](#).

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](#).

## **SUBMITTED/DRAFT MANUSCRIPTS**

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

## **TEACHING**

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2015, \***Instructor**, BI 610 (Advanced Biological Statistics) University  
2023 of Oregon, Fall Term

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

- 2021 Statistics) University of Oregon, Spring Term  
Course gitbook: [https://uo-biostats.github.io/Found\\_Stat/](https://uo-biostats.github.io/Found_Stat/)
- 2014-  
2019 **\*Course Developer and Instructor**, BI 623 (Advanced Topics in Genomic Analysis) University of Oregon, Summer Term
- 2017-  
2018 **\*Co-Course Developer and Instructor**, BI 624 (Genomics Research Lab) 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-  
2011 **Teaching Assistant**, BIOL 111 (Introductory Biology) 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

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- 2015-  
2019 **Primary Mentor**, high school/undergraduate research assistant (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-  
2010 **Primary Mentor**, UBM undergraduate biology/math research 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"

## INVITED CONFERENCE TALKS

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4<sup>th</sup> International Fish Microbiota Workshop. Wageningen, Netherlands. September 6, 2023. Host genomic variation shapes gut microbiome diversity in threespine stickleback fish. C. M. Small, E. A. Beck, M. C. Currey, H. F. Tavalire, S. Bassham, and W. A. Cresko.

2<sup>nd</sup> 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.

7<sup>th</sup> 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 threespine 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

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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.

## **CONTRIBUTED PAPER PRESENTATIONS**

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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)

1<sup>st</sup> 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)

## SERVICE

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**NSF Consultant:** Invited participant in BIO Directorate's scoping session, "LIFE: Leveraging Innovations From Evolution," Aug. 14-16, 2023.

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

**Academic administration:** Member, Strategic Implementation Team, School of Computer and Data Sciences. University of Oregon, 2023.

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

**Symposium organization:** 8<sup>th</sup> annual Ecological Integration Symposium. "Interdisciplinary Approaches to Biodiversity: From Speciation to Extinction." Texas A&M University, April 20<sup>th</sup>-21<sup>st</sup>, 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**

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- 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