

SHELLY A. TRIGG, Ph.D.

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Gloucester Marine Genomics Institute, 417 Main Street, Gloucester, MA 01930

SUMMARY OF QUALIFICATIONS

- Systems Biologist/Genomicist with 11+ years of experience and an established record of scientific contribution to the fields of plant and marine animal genomics
- Experienced in developing and optimizing innovative assays using a broad range of approaches and techniques to investigate molecular pathways underlying organism health
- Experienced in written and oral communication to various audiences through technical reports, peer reviewed scientific journal articles, public presentations, and community outreach
- Demonstrated abilities to collaborate and take leadership through team and project management, and volunteer activities with government agencies, tribal organizations, commercial fisheries, and non-profit institutions

EXPERIENCE

Gloucester Marine Genomics Institute, Gloucester, MA

Research Scientist.....Mar 2021 - Present

- Develop molecular diagnostic assays using CRISPR/Cas technology including amplification-free detection, LAMP isothermal amplification, and SHERLOCK to detect aquatic animal disease

University of Washington School of Aquatic and Fishery Sciences, Seattle, WA

Postdoctoral Research Associate.....Sept 2018 - Feb 2021

Advisor: Steven Roberts, Ph.D.

- Assess epigenetic and transcriptomic variation and identify molecular markers that differ within Atlantic salmon and Pacific geoduck clam populations exposed to different environmental conditions through analyzing and interpreting genome-wide methylation bisulfite sequencing and RNA-seq data (collaboration with the Gallardo-Escarat  lab at the Universidad de Concepci n)
- Assess effects of altered seawater pH on reproductive development through developing a qPCR assay on non-lethal, temporally-collected hemolymph samples in adult Pacific geoduck, and on larval developmental physiology (respiration rate, growth, survival, genome-wide methylation) (collaboration with Jamestown-S'klallam Tribe Pt. Whitney Hatchery)
- Identify and interpret temporal proteome variation in metamorphosing Pacific oysters exposed to different temperatures (collaboration with Taylor Shellfish Hatchery, Quilcene, WA)
- Assess physiological response of pteropods to low oxygen and pH conditions through survival, development, lipidomics, and metabolomics analysis (collaboration with NOAA NWFSC)
- Lead cooperative field, hatchery, and laboratory research in collaboration with Jamestown-S'klallam Tribe Fisheries Division, Taylor Shellfish Hatchery, and NOAA NWFSC Conservation Biology Division

NOAA Northwest Fisheries Science Center, Conservation Biology, Seattle, WA

NSF Graduate Research Internship Program Fellow.....Jun 2017 - May 2018

Advisors: Krista Nichols Ph.D. and Paul McElhany Ph.D.

- Assess physiological impacts of ocean acidification on Dungeness crabs through metabolomics analysis
- Develop and implement bioinformatics pipelines for analyzing complex metabolomics data sets from differentially conditioned Dungeness crabs
- Carried out time-course high throughput laboratory ocean acidification exposure experiments on Dungeness crab larvae
- Did field collection and laboratory rearing of Dungeness crab larvae, juveniles and adults

Salk Institute for Biological Studies, Ecker Lab, Genomic Analysis Section, La Jolla, CA

Graduate Student ResearcherAug 2013 - Sept 2018

Research Assistant IIJul 2012 - Aug 2013

Research Assistant INov 2011 - Jun 2012
Ph.D. dissertation: High-resolution molecular networks from novel ‘omics’ approaches elucidate survival strategies in organisms from land to sea
Advisor: Joseph Ecker, Ph.D.

- Developed a DNA sequencing assay (CrY2H-seq) for high throughput protein-protein interaction mapping and coded a bioinformatics analysis pipeline to identify and quantify interactions from large sequence datasets
- Performed network simulations for observed network validation
- Generated model predictions to evaluate assay performance
- Performed quality control, network analysis, data integration, and functional analysis to interpret biological significance of protein interaction networks
- Generated comprehensive protein-protein interactome map for *Arabidopsis thaliana* using CrY2H-seq to iteratively screen billions of interactions *en masse*
- Did high throughput engineering of thousands of expression clones

Dana Farber Cancer Institute, Center for Cancer Systems Biology, Vidal Lab, Boston, MA

Research Technician IAug 2010 - Oct 2011
Research TraineeJan 2010 - Aug 2010

- Generated comprehensive human protein-protein interactome map from high throughput yeast two-hybrid screening, protein complementation assay, and well-nucleic-acid-programmable-protein-array assay
- Developed a high throughput well-nucleic-acid-programmable-protein-array validation assay
- Generated protein-protein interactome map from high throughput yeast two-hybrid screening of autism genes and isoforms against a human ORFeome
- Constructed clone collections of Kaposi’s Sarcoma and Epstein-Barr viral genes by high throughput gateway cloning for yeast two-hybrid screening against a human ORFeome to further define potential cancer driver and passenger proteins

Simmons College, Department of Chemistry, Roecklein-Canfield Lab, Boston, MA

Undergraduate Researcher.....July 2009 - June 2010
B.S. Honors Thesis: The effectiveness of the GST fusion system for isolating Epstein-Barr viral thymidine kinase, a potential target for antiviral antitumor therapies.

- Developed and optimized a GST immunoprecipitation assay for isolation of Epstein-Barr viral proteins

EDUCATION

Ph.D. in Biological Sciences.....Sept 2018
University of California San Diego, La Jolla, CA

B.S. in Biochemistry.....May 2010
Magna Cum Laude and honors thesis, Simmons College, Boston, MA

TECHNICAL SKILLS AND TRAINING

Molecular and Cellular Biology: Illumina and Oxford Nanopore DNA sequencing, whole genome, RNAseq and Bisulfite sequencing library preparation, PCR, qPCR, oligo design, ELISA, immuno-blotting and precipitation, recombinant DNA techniques, nucleic acid and protein purification, cell culture and transfection, histological techniques

Marine Biology: respirometry measurement with PreSens equipment, animal rearing systems design, construction and implementation, seawater chemistry analysis

Laboratory Automation: Tecan liquid handling robots, plate readers, titrators

Computation: Genomics, epigenomics, proteomics, and metabolomics data analysis, regression analysis, multivariate statistical methods, statistical computing and simulation, data reduction and integration, molecular network analysis (Cytoscape, Qiagen IPA), Linux environment familiarity, Bash and Python/Jupyter scripting, R, data management, supercomputing, GitHub (<https://github.com/shellytrigg>), Slack, Google Suite applications, Microsoft Office applications

Training: LC-MS Data processing and statistics course, UC Davis (Jan 2018); Visiting Scientist Network Analysis Training Program, Broad Institute (Jan-Feb 2016); NSF Graduate Data Science Workshop, University of Washington (Aug 2015); Biostatistics Refresher Course, UC San Diego (Aug 2015); Software Carpentry, Salk Institute (Jun 2013, Jan 2014); Tecan EVO Training Course (Aug 2012)

LEADERSHIP ACTIVITIES

Management:

- Trained, supervised, and managed 4 research assistants, 2 technicians, and 8 students from various backgrounds
- Mentored 2 graduate students at UC San Diego, 2 undergraduate and 3 graduate students at University of Washington, and 1 undergraduate student at NOAA NW Fishery Science Center

Committees:

- Postdoctoral representative of UW SAFS Communications Committee, 2018 - present
- Chair of UC San Diego Biology Department Peer Mentoring Committee, 2015-2016
- Chair of UC San Diego Quantitative Biology graduate seminar series, 2015-2016
- Member of the Salk Institute Partnerships in Science committee 2014-2016
- Member of UC San Diego STEM Education and Diversity group 2014-2016
- Member of Association of Women in Science San Diego Outreach Committee, 2012-2016

PUBLICATIONS

Shelly A. Trigg^{*}, YR Venkataraman^{*}, MR Gavery, SB Roberts, D Bhattacharya, A Downey-Wall, JM Eirin-Lopez, KM Johnson, KE Lotterhos, JR Puritz, and HM Putnam. (2021) Invertebrate methylomes provide insight into mechanisms of environmental tolerance and reveal methodological biases. ***Molecular Ecology Resources*** (in press). <https://doi.org/10.1101/2021.03.29.437539>.

BC Willige, M Zander, CY Yoo, A Phan, RM Garza, Shelly A. Trigg, Y He, JR Nery, H Chen, M Chen, JR Ecker, and J Chory. (2021) Phytochrome-interacting factors trigger environmentally responsive chromatin dynamics in plants. ***Nature Genetics***. 53:955-961. <https://doi.org/10.1038/s41588-021-00882-3>

Shelly A. Trigg, KM Mitchell, R Elliot, B Eudeline, B Vadopalas, EB Timmins-Schiffman, SB Roberts. (2020) Temporal proteomic profiling reveals insight into critical developmental processes and temperature-influenced physiological response differences in a bivalve mollusc. ***BMC Genomics***. <https://doi.org/10.1186/s12864-020-07127-3>.

Shelly A. Trigg, P McElhany, M Maher, D Perez, DS Busch, and KM Nichols. (2019) Uncovering mechanisms of global ocean change effects on Dungeness crab (*Cancer magister*) through metabolomics analysis. ***Scientific Reports***. <https://doi.org/10.1101/574798>.

Shelly A. Trigg, RM Garza, A MacWilliams, JR Nery, A Bartlett, R Castanon, A Goubil, J Feeney, R O'Malley, SC Huang, ZZ Zhang, M Galli, and JR Ecker (2017) CrY2H-seq: a massively multiplexed assay for deep coverage interactome mapping. ***Nature Methods***. 14(8):819-825. <https://doi.org/10.1038/nmeth.4343>

Shelly A. Trigg, RM Garza, A MacWilliams, JR Nery, A Bartlett, R Castanon, A Goubil, J Feeney, R O'Malley, SC Huang, ZZ Zhang, M Galli, and JR Ecker (2017) CrY2H-seq interactome screening. ***Protocol Exchange***. doi:10.1038/protex.2017.058.

X Yang, [15 others], Shelly A. Trigg, [20 others], and M Vidal. (2016) Widespread expansion of protein interaction capabilities by alternative splicing. ***Cell***. 164(4):805-817. <https://doi.org/10.1016/j.cell.2016.01.029>

T Rolland, [53 others], Shelly A. Trigg, [14 others], and M Vidal. (2014) A proteome-scale map of the human interactome network. ***Cell***. 159(5):1212-1226. <https://doi.org/10.1016/j.cell.2014.10.050>

R Corominas, [8 others], Shelly A. Trigg, [18 others], M Vidal, and LM Iakoucheva. (2014) Protein interaction network of alternatively spliced isoforms from brain links genetic risk factors for autism. ***Nature communications***. 5:3650. <https://doi.org/10.1038/ncomms4650>

Rozenblatt-Rosen, [36 others], [Shelly Wanamaker](#), [13 others], and M Vidal. (2012) Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. *Nature*. 487(7408):491-495. <https://doi.org/10.1038/nature11288>

MANUSCRIPTS IN PREPARATION/REVIEW

[Shelly A. Trigg](#), G Nunez-Acuna, V Valenzuela-Munoz, D Valenzuela-Miranda, C Gallardo-Escárate, and SB Roberts. (2020) Epigenomic and transcriptomic relationships in Atlantic salmon infested with sea lice under a changing environment. (*In preparation*)

[Shelly A. Trigg](#), DS Busch, P McElhany, M Maher, D Perez, C O'Brien, and KM Nichols. (2020) Searching for signs of resilience in over-wintering juvenile pteropods to ocean acidification and deoxygenation. (*In preparation*)

HM Putnam, [Shelly A. Trigg](#), SJ White, LH Spencer, B Vadopalas, A Natarajan, J Hetzel, E Jaeger, J Soohoo, C Gallardo-Escárate, FW Goetz, and SB Roberts. (2020) Environmental memory through dynamic DNA methylation provides acclimatization of geoduck clams to ocean acidification. (*In preparation*)

SELECT PRESENTATIONS (5 of 22)

[Shelly A. Trigg](#) (May 2021) Diversity in animal response to environmental change. Academic Data Science Alliance Data Science 2021 Coast to Coast seminar series. <https://github.com/shellytrigg/talk-Coast2Coast2021>

[Shelly A. Trigg](#) (Jan 2021) Exploring the tolerance of Pacific geoduck to low pH through comparative physiology, genomics, and DNA methylation. Society for Integrated and Comparative Biology 2021 Virtual Annual Meeting. <https://github.com/shellytrigg/talk-SICB2021>

[Shelly A. Trigg](#). (Jan 2020) Influence of ocean acidification on DNA methylation patterns in geoduck clams. Plant and Animal Genome Conference XXVIII, San Diego, CA, talk. <https://github.com/shellytrigg/talk-pag2020>.

Recipient of PAG XXVIII USDA NRSP8 Aquaculture Travel Grant.

[Shelly A. Trigg](#). (Nov 2019) Environmental influence on the Atlantic salmon epigenome during sea lice infestation. International Conference on Integrative Salmonid Biology, Edinburgh, UK, talk. <https://doi.org/10.6084/m9.figshare.10882775.v1>. **Recipient of University of Washington College of the Environment Travel Award.**

[Shelly A. Trigg](#), P McElhany, M Maher, D Perez, DS Busch, and KM Nichols. (May 2019) What happens to Dungeness crab in high CO₂: experiments and questions. 2019 WOAC Ocean Acidification Science Symposium, Seattle, WA, talk and poster. **Invited speaker.**

GRANTS AND FELLOWSHIPS

USDA NRSP8 Small Funding Award (\$10K), 2020

USDA NRSP8 PAGXXVIII Aquaculture Travel Award (\$1K), 2020

UW Data Science Postdoctoral Fellowship (\$7K), 2019 - present

UW College of the Environment Travel Award (\$1K), 2019

NSF GRIP Fellowship with NOAA Northwest Fisheries Science Center (\$5K), 2017- 2018

NSF PAMP EAGER: Using novel, clone-free sequencing methods to discover host-microbe protein-protein interactions (Co-authors: Shelly Trigg, Paulo Teixeira, Jeff Dangl (CO-PI), and Joseph Ecker (CO-PI); \$300K), 2016

NSF Graduate Research Fellowship (\$138K), 2014-2018