

VANESSA I. GUERRA, PhD

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COMPUTATIONAL BIOLOGIST

Evolutionary & computational biologist with progressive experience in molecular biology, genomics, reproductive research—passionate about analyzing multi-omic data to drive scientific discovery, advancements in startup environment. *PhD, Biology*, Simon Fraser University; *MS, Biology*, SFSU.

HIGHLIGHTS:

- **Strong Scientific Background:** Expert in Sanger sequencing, cloning, primer design, molecular protocol adaptations—including NGS (next-generation sequencing) library construction & analysis, in both genomics, transcriptomics.
- **Bioinformatics Experience:** Solid generalist; helped teach bioinformatics workshops at Wake Forest University, Simon Fraser University [SFU], UC Davis; write programs with Perl, R, Unix / AWK; leverage bioinformatics tools to assess evolution of reproductive genes, including those of humans.
- **Novel Scientific Research:** Recently published paper on *Acanthaster* (see **Addendum**), developing bioinformatics pipeline to process RNA-seq data / transcriptomic data. Discovered previously-undescribed polymorphic reproductive genes by detecting novel mode of reproduction (hermaphrodite)—illustrating need for using RNA-seq data.
- **Extensive Wet-Lab Experience:** Served as lab manager, performing both wet lab and dry lab work; attended course at Duke University to learn how to prepare NGS libraries. Experienced in cloning, PCR, cycle sequencing, nucleotide isolation (DNA / RNA extractions), NGS library preparation (RNA, DNA); willing to learn qPCR or CRISP on own time.
- **Natural Leader:** Co-founded omics club at SFU (google.com/sfuomics) to bring together many Omics researchers & students—that were hard-to-locate, operating in myriad disparate departments, including Computing Science, Biomedical Physiology & Kinesiology, Math.
- **Highly-Regarded Researcher:** Spent several years as guest at Smithsonian Institution performing PhD work; have authored (6) manuscripts for peer-reviewed journals, including (2) first-author papers.
- **Persuasive Communicator:** Recognized for seamlessly communicating scientific & technical processes to nontechnical stakeholders while solving complex problems at intersection of bioinformatics, biology. Bilingual: fluent English, Spanish.
- **Data Science:** Design and employ *ad hoc* tools in Perl, Unix, R for analyzing / displaying complex datasets.

SIGNATURE STRENGTHS:

Biology • Genomics • Customer Service • Balancing Competing Priorities • Matrixed Environments • Multi-omic Data (NGS, RNA seq, GWAS) • Coding • Data Science / Management • Developing Computational Pipelines • Leading Multiple Concurrent Projects • Collaborating with / Working as Wet & Dry Lab Scientists • RNA seq / GWAS Data • Research Scientist

PROFESSIONAL EXPERIENCE

Visiting Research Fellow, Smithsonian's National Museum of Natural History. Washington, DC; 2018 – present
Studied reproductive adaptive genes in sea stars.

Postdoctoral Scholar, Life & Environmental Sciences, University of California Merced; CA; January 2021 – June 2021
Leading multi-species genomic analyses to better understand susceptibility to environmental change. Led multi-institutional marine networks (MariNet) consortium. Organize, lead multispecies collection initiative on California coast.

Intern, Smithsonian Conservation Biology Institute's Center for Species Survival; Washington, DC; 2019 – 2020
Characterized evolution of gamete recognition genes of carnivores.

Research Asst., Simon Fraser Univ. & Smithsonian; Burnaby, BC / Wash, DC; 2015-20
Analyzed reproductive adaptive genes in sea stars and chordates using genome and transcriptome analysis (assemblies, SNP calling, annotation, differential expression, selection analysis, etc.). Worked with Cluster team, bioinformaticians.

- Developed computational pipeline for numerous NGS analysis (genomic, transcriptomic).
- Created Perl, Unix shell, R scripts to read protein data from multiple files—and assign, enter into database.

Laboratory Manager, Wake Forest University; Winston-Salem, NC; 2014 – 2015
Developed NGS protocols for marine science, led workshops. Trained undergraduate / graduate students in molecular biology, wet-lab work, Equipment maintenance. Identified parasitic copepods from rockfish using DNA barcoding.

- Enabled transparent, reproducible data analysis by devising best practice documentation for NGS analysis.
- Co-designed and launched NGS solutions, analyzed omics data in partnership with research scientists.
- Processed nucleic acid isolation and quantification, PCR amplification, prepared DNA / RNA library.

VANESSA I. GUERRA, PHD – PG. 2

Graduate Student, San Francisco State University; CA; 2010 – 2014

Described genetic variation in reproductive gene influencing population genetic diversity in marine invasive species, *Ciona robusta*. (via cloning, Sanger sequencing, primer optimization, genome analysis). Performed field collection and taxonomical identification of marine invertebrates; led wet-lab research in cell culture, molecular biology.

- Developed Unix shell, Perl, AWK program to process NGS data.

Intern, Smithsonian Environmental Research Center; San Francisco, CA; 2009 – 2010

Managed new marine invasion: led initiative to identify, remove species. Collected, analyzed data.

Junior Specialist, University of California Davis; 2010

Led volunteer initiative to identify and remove invasive species, *Undaria pinnatifida*; performed data analysis.

Marine Laboratory Technician, Humboldt State University Marine Laboratory; Arcata, CA; 2008 – 2009

TEACHING EXPERIENCE

Instructor, Marine Genomics, University of California Davis; 2021

Evolutionary Genomics Laboratory Consultant, Simon Fraser University; 2018

Led laboratory exercises for genome transcriptome analysis (Unix, cluster use, assemblies, SNP calling, trees, differential expression, general statistical tests).

Invertebrate Biology Teaching Assistant (TA), Simon Fraser University; 2016 – 2018

Taught characteristics and functions of marine invertebrates.

Software Carpentries Instructor, Simon Fraser University Library; 2018

Led and assisted Unix, GitHub, R classes.

Population Genetics TA, Simon Fraser University; CA; 2015

Prepared and led tutorials and lectures. Prepared and led tutorials, guest lecturer.

Microbiology Open Lab Supervisor, San Francisco State University; CA; 2011 – 2013

Supervised wet lab practices, trained students in laboratory benchwork, performed equipment maintenance.

Marine Invertebrates TA, San Francisco State University; CA; 2010

Helped identify marine invertebrates.

EDUCATION

PhD, Biology, Simon Fraser University; Burnaby, British Columbia, 2020

Thesis: Evolution of mating systems and reproductive genes in sea stars

MA, Biology, Concentration: Ecology, Evolution & Conservation Biology, San Francisco State University; CA; 2014

Thesis: Population variation at a self-incompatibility locus in a marine invasive species

BS, Biology, Humboldt State University; Arcata, CA; 2010

SPECIALIZED COURSES

Workshop, “Best practices for using NGS-based datasets to determine statistically robust evidence of positive selection & convergent evolution of polar organisms,” The Society for Integrative & Comparative Biology; 2018-2019

Data Carpentry Instructor, The Carpentries; 2018

Comparative Invertebrate Embryology, University of Washington, Friday Harbor Laboratories; 2017

Comparative Genomics, Simon Fraser University; 2015

Benchwork Training: NGS Techniques, Duke University Marine Laboratory; 2014

Genome Evolution, Genome Annotation, San Francisco State University; 2013

Genetics for Conservation, Red de Genética de la Conservación; 2012

Advanced Ascidian Taxonomy, Smithsonian Tropical Research Institute; 2011

NAUI SCUBA Instructor course, University of California, Santa Cruz; 2010