

PROFESSIONAL POSITIONS

Phase Genomics Inc.

Senior Bioinformatics Engineer

Seattle, WA

2017-present

- Performed computational biology research and technical writing in an industrial setting.
- Designed algorithms, developed software in a cutting-edge genomics service company.
- Worked actively with customers to provide solutions to biological problems using Hi-C data.

University of Washington

Seattle, WA

Postdoctoral Fellow; advisor: Christine Queitsch.

2016-2017

- *Short tandem repeat genotyping reveals variation, functional effects, and signatures of selection.*

Graduate Research Assistant; advisors: Christine Queitsch and Elhanan Borenstein.

2010-2016

- *Evolutionary constraint of gene acquisition in prokaryotic evolution.*
- *Contribution of microsatellites to phenotypic and epistatic variance.*
- *Independent genetic pathways for thermoresponsive flowering and thermomorphogenesis in A. thaliana.*

Fred Hutchinson Cancer Research Center

Seattle, WA

Research Technician; supervisor: Sue Biggins.

2008-2010

EDUCATION

University of Washington

Seattle, WA

PhD, Genome Sciences

June 2016

Dissertation: "Observations about the effects of epistasis on evolution and complex traits."

Reed College.

Portland, OR

BA, Biology. Phi Beta Kappa

May 2008

Thesis: "Microevolution of *Gasterosteus aculeatus* in the Johnson Creek watershed."

FELLOWSHIPS AND AWARDS

- 2015: UW Graduate School Fund for Excellence and Innovation Travel Grant
- 2011-2013: NIH NHGRI Genomics Training Grant 2T32HG35-16
- 2008: Phi Beta Kappa (Reed College)
- 2007-8: Miller Undergraduate Research Foundation grant, Reed College
- 2004-8: 3 Commendations for Excellence in Scholarship, Reed College

PEER-REVIEWED PUBLICATIONS (see also [Pubmed](#), [bioRxiv](#), [Google scholar](#))

- Harrop T..., **Press MO et al.** (2020). "High-quality Assemblies for Three Invasive Social Wasps from the *Vespula* Genus." G3 Early Online <https://doi.org/10.1534/g3.120.401579>
- Gaytán I..., **Press MO et al.** (2020). "Degradation of Recalcitrant Polyurethane..." *Frontiers in Microbiology* 10:2986. <https://doi.org/10.3389/fmicb.2019.02986>
- Bickhart D..., **Press MO et al.** (2019). "Assignment of virus and antimicrobial resistance genes to microbial..." *Genome Biology* 20:153. <https://doi.org/10.1186/s13059-019-1760-x>
- Stalder T, **Press MO**, Sullivan S, Liachko I, Top EM (2019). "Linking the resistome and plasmidome to the microbiome." *ISME J Advance Online*, (<https://doi.org/10.1038/s41396-019-0446-4>)
- **Press MO**, Hall AN, Morton EA, Queitsch C (2019). "Substitutions are boring: some arguments about parallel mutations and repetitive DNA." *Trends in Genetics* 25(4):253-264
- **Press MO et al.** (2018). "Massive variation of short tandem repeats with functional consequences across strains of *Arabidopsis thaliana*." *Genome Research Advance Online*, doi:10.1101/gr.231753.117

- Stewart R, ... **Press M** et al. (2018). "Assembly of 913 microbial genomes from metagenomic sequencing of the cow rumen." *Nature Communications*.
- **Press MO**, Queitsch C (2017). "Variability in a Short Tandem Repeat Mediates Complex Epistatic Interactions in *Arabidopsis thaliana*." *Genetics*, 205(1): 455-464.
- **Press MO**, Lanctot A, Queitsch C (2016). "PIF4 and ELF3 act independently in *Arabidopsis thaliana* thermoresponsive flowering." *PLOS ONE* 11(8): e0161791.
- **Press MO**, Queitsch C, Borenstein E (2016). "Evolutionary assembly patterns of prokaryotic genomes." *Genome Research* 26: 826-833.
- Carlson KD, Sudmant PH, **Press MO**, et al. (2015). "MIPSTR: a method for multiplex genotyping of germ-line and somatic STR variation across many individuals." *Genome Research* 25(5):750-761.
- Rival P*, **Press MO***, Bale J*, et al. (2014). "The conserved *PFT1* tandem repeat is crucial for proper flowering in *Arabidopsis thaliana*" *Genetics* 198(2): 747-754.
- **Press MO**, Carlson KD, Queitsch C (2014). "The overdue promise of short tandem repeat variation for heritability." *Trends in Genetics* 30(11) 504-512.
- **Press MO***, Li* et al. (2013). "Genome-scale co-evolutionary analysis identifies functions and clients of bacterial Hsp90." *PLOS Genetics* 9(8): e1003631
- Undurraga S, **Press MO**, et al. (2012). "Background-dependent effects of polyglutamine variation in the *Arabidopsis thaliana* gene *ELF3*." *PNAS* 109(47):19363-7.
- Ranjitkar P, **Press MO**, et al. (2010). "An E3 ubiquitin ligase prevents ectopic localization of the centromeric histone H3 variant via the centromere targeting domain." *Molecular Cell* 40(3): 455-64.

*: equal contribution to publication.

Manuscripts in review

- Mason GA, Carlson KD, **Press MO**, Bubb KL, Queitsch C (2018). "HSP90 buffers newly induced mutations in massively mutated plant lines". bioRxiv: <https://doi.org/10.1101/355735>

Working manuscripts

- **Press MO** et al. (2017). "Hi-C deconvolution of a human gut microbiome yields high-quality draft genomes and reveals plasmid-genome interactions." bioRxiv: <https://doi.org/10.1101/198713>
- Various translations from German to English of classic genetics papers, available here: <https://osf.io/63xmr/wiki/home/>.

PRESENTATIONS

- Talk: Plasmid Biology Meeting 2018. "Hi-C deconvolution of a human gut microbiome."
- Platform Talk: Genetics Society of America Population, Evolutionary, and Quantitative Genetics Meeting 2018. "Massive variation of short tandem repeats with functional consequences across strains of *Arabidopsis thaliana*." Madison, WI
- Talk: University of Washington Department of Environmental and Occupational Health Sciences Microbiome Bootcamp 2017. "Hi-C deconvolution of a human gut microbiome."
- Talk: Thermomorphogenesis Meeting 2016: "PIF4 and ELF3 Act Independently in *Arabidopsis thaliana* Thermoresponsive Flowering". Halle, Germany
- Platform Talk: Genetics Society of America Allied Genetics Conference 2016: "The variable ELF3 polyglutamine is an epistatic hub." Orlando, FL
- Talk: Congress of the Society for Molecular Biology and Evolution 2015: "Evolutionary Assembly Patterns of Prokaryotic Genomes." Vienna, Austria
- Talk: 6th International Conference on the Hsp90 chaperone machine 2012: "Evolutionary

Inference of bacterial Hsp90 functions.” Les Diablerets, Switzerland

TEACHING AND MENTORING

University of Washington

- **Teaching assistant** (GENOME 351: Human Genetics for non-majors). Spring 2014
- **Teaching assistant** (GENOME 371: Introductory Genetics). Fall 2012

Reed College

- **Tutor** (Biology 101/102: Introductory Biology) 2005-2008

SCHOLARLY SOCIETY MEMBERSHIPS

Genetics Society of America.

Society for Molecular Biology and Evolution.

Peer Community in Evolutionary Biology.

Linnean Society of London

SERVICE AND OUTREACH ACTIVITIES

- **Reviewer and sub-reviewer:** *Nature Communications, Nature Methods, Plasmid, PLoS Evolutionary Biology, Matters, PNAS, PLOS Genetics, Human Genetics, American Journal of Primatology, RECOMB 2012, Scientific Reports, Communications Biology.*
- **Co-instructor**, GRE preparation course. July 2014, July 2015, (short class for underrepresented minority undergraduates).
- **Organizer**, 2012 NHGRI UW Genome Training Grant Symposium.
- **Instructor**, Basic ideas of bioinformatics, June 2012, (short class for HS teachers).
- **Departmental coordinator**, 2012 Science Education Partnership, Genome Sciences.
- **Restoration volunteer**, Adopt-a-Stream Foundation, (Summer-Winter 2005). Wetlands restoration field work.
- **Volunteer**, Students for Empowering, Educating, Diversity and Service (SEEDS), Reed College chapter (2004-2008). Taught middle school students about wetland restoration.

SKILLS

Workplace

Scrum, sprints, Kanban, Zoom meetings, one-on-one reporting, teamwork and project collaboration, code review, DevOps rotations, project prioritizations, documentation and operating procedures.

Writing/presentation

Writing: Manuscripts for peer review, grants, white papers, documentation.

Presentation: International meetings, high-stakes clients, etc.

Computing

Coding: Python, R, bash/shell, Rust (learning!).

Tools: Pandas, bioinformatics tools (Samtools, Pysam, BWA, BEDTools, minimap2, BLAST, HMMER, etc.), paradigm-specific tools (e.g. PacBio ecosystem), LaTeX, Google Docs, MS Office.

Workflows/Paradigms: statistical analysis, data visualization, Linux OS, AWS, GitHub/GitLab/Bitbucket, continuous integration, sequence analysis and assembly, pipelining, test-driven development, software deployment and testing, conda, Docker (learning!).

REFERENCES

- **Dr. Christine Queitsch**, University of Washington. queitsch@uw.edu
- **Dr. Elhanan Borenstein**, University of Tel Aviv. elbo@uw.edu