

## PROFESSIONAL EXPERIENCE

### Phase Genomics Inc.

Seattle, WA

Senior Bioinformatics Engineer

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 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

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

- **Press MO**, Hall AN, Morton EA, Queitsch C (in press). "Substitutions are boring: some arguments about parallel mutations and repetitive DNA." *Trends in Genetics*. OSF Preprints: <https://doi.org/10.31219/osf.io/5typz>
- **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, Auffret M, Warr A, Wiser A, **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

- Bickhart D, ..., **Press MO**, ..., Smith T (2018). "Assignment of virus and antimicrobial resistance genes to microbial hosts in a complex microbial community by combined long-read assembly and proximity ligation." bioRxiv: <https://doi.org/10.1101/491175>
- Stalder T, **Press MO**, Sullivan S, Liachko I, Top EM (2018). "Linking the resistome and plasmidome to the microbiome." bioRxiv: <https://www.biorxiv.org/node/144784.abstract>
- **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>
- English translation of Woltereck R (1909). "Weitere experimentelle Untersuchungen über Art-veränderung, speziell über das Wesen quantitativer Artunterschiede bei Daphniden". *Verhandlungen der deutschen zoologischen Gesellschaft* 19 (1909): 110–73. In progress, available at <https://github.com/maximilianpress/miscellaneous/blob/master/experimental-investigations-variation.pdf>.
  - This classic paper originates the idea of the reaction norm in heredity and organismal development, and has not been previously translated to English.

### SELECTED PRESENTATIONS

- 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: Thermomorphogenesis Meeting 2016: "PIF4 and ELF3 Act Independently in *Arabidopsis thaliana* Thermoresponsive Flowering". Halle, Germany
- Platform Talk: The Allied Genetics Conference, July 2016: "The variable ELF3 polyglutamine is an epistatic hub." Orlando, FL
- Talk: Congress of the Society for Molecular Biology and Evolution, July 2015: "Evolutionary Assembly Patterns of Prokaryotic Genomes." Vienna, Austria
- Talk: 6<sup>th</sup> International Conference on the Hsp90 chaperone machine, September 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.

## 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.*
- **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.

## REFERENCES

- **Dr. Christine Queitsch**, University of Washington Dept. Genome Sciences.  
[queitsch@uw.edu](mailto:queitsch@uw.edu)
- **Dr. Elhanan Borenstein**, University of Washington Dept. Genome Sciences.  
[elbo@uw.edu](mailto:elbo@uw.edu)
- **Dr. Joe Felsenstein**, University of Washington Dept. Genome Sciences.  
[joe@gs.washington.edu](mailto:joe@gs.washington.edu)
- **Dr. Sue Biggins**, Fred Hutchinson Cancer Research Center, Howard Hughes Medical Institute.  
[sbiggins@fhcrc.org](mailto:sbiggins@fhcrc.org)