Maximilian Oliver Press, PhD
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PROFESSIONAL POSITIONS

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 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

- 2019-present: Fellow, Linnean Society of London
- 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)

- Gaytán I…, **Press MO** *et al.* (2020). “Degradation of Recalcitrant Polyurethane…” *Frontiers in Microbiology* 10:2986. https://doi.og/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* 13, 2437–2446
- **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* 28: 1169-1178.

- 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..." *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..." *Molecular Cell* 40(3): 455-64.

*: equal contribution to publication.

Working manuscripts

- 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
- **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: Woltereck R (1909). "Weitere experimentelle Untersuchungen…". *Verhandl. d. deutsch. zoolog Ges.* 19 (1909): 110–73. OSF doi:10.31219/osf.io/fvme6
    - This previously untranslated classic paper introduces the idea of the reaction norm.

PRESENTATIONS

- Poster (virtual): The Allied Genetics Conference 2020. "The Origin of Reaction Norms."
- 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, PCI 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. queitsch@uw.edu**
- **Dr. Elhanan Borenstein, University of Tel Aviv. elbo@uw.edu**