

MAITREYA J. DUNHAM, PhD
DEPARTMENT OF GENOME SCIENCES
UNIVERSITY OF WASHINGTON

EDUCATION

Massachusetts Institute of Technology	Biology	BS	1995-1999
Stanford University	Genetics	PhD	1999-2003

APPOINTMENTS

Lewis-Sigler Fellow (independent position)	Princeton University	2003-2008
Assistant Professor	University of Washington	2008-2014
Associate Professor	University of Washington	2014-

HONORS AND AWARDS

Ned Holt Prize, one of three MIT Biology Departmental Awards, 1999
Stanford Graduate Fellow, 1999-2003
National Science Foundation Fellowship (declined), 2000
Howard Hughes Medical Institute Predoctoral Fellow, 2000-2003
Marian E. Smith Junior Faculty Award, 2009
Pew Scholar (declined), 2010
Rita Allen Foundation Scholar, 2010-2015
Rising Star Young Investigator, Genome Technology Magazine, 2010
Basil O'Connor Scholar, March of Dimes, 2011-2013
CIFAR Senior Fellow, Genetic Networks, Canadian Institute for Advanced Research, 2012-2017
Howard Hughes Medical Institute Faculty Scholar, 2016-2021

OTHER PROFESSIONAL EXPERIENCE AND MEMBERSHIPS

Member, Genetics Society of America, 2000-
Consultant, Schering-Plough Research Institute, Infectious Diseases, 2007
Member, Scientific Advisory Board, SynBERC, NSF center for synthetic biology, 2009-2016
Associate Editor, BMC Genomics, 2010-2015
Editorial Board, Genome Research, 2010-
Consultant, Cargill Bio TDC, 2011
Inaugural Editorial Board Member, Genetics & Genomics section, Scientific Reports, 2011-2014
Instructor, Cold Spring Harbor Yeast Genetics and Genomics Course, 2012-
Member, American Society for Microbiology, 2015-
Editorial Board, Yeast, 2015-
Co-Founder, Phase Genomics, 2015-
Member, Engineering Biology Research Consortium, 2016-

PUBLICATIONS

Evolution of protein phosphorylation across 18 fungal species. Studer RA, Rodriguez-Mias RA, Haas KM, Hsu JI, Viéitez C, Solé C, Swaney DL, Stanford LB, Liachko I, Böttcher R, Dunham MJ, de Nadal E, Posas F, Beltrao P, Villén J. *Science*. 2016; 354(6309):229-232.
High-Throughput Identification of Adaptive Mutations in Experimentally Evolved Yeast Populations. Payen C, Sunshine AB, Ong GT, Pogachar JL, Zhao W, Dunham MJ. *PLoS Genetics*. 2016; 12(10):e1006339.
Neocentromeres Provide Chromosome Segregation Accuracy and Centromere Clustering to Multiple Loci Along a *Candida albicans* Chromosome. Burrack LS, Hutton HF, Matter KJ,

- Applen Clancey SE, Liachko I, Plemmons AE, Saha A, Turman B, Thevandavakkam MA, Ay F, Dunham M, Berman J. *PLoS Genetics*. 2016 12(9):e1006317.
- Characterization of a panARS-based episomal vector in the methylotrophic yeast *Pichia pastoris* for recombinant protein production and synthetic biology applications. *Microbial Cell Factories*. 2016 Aug 11;15(1):139.
- The hidden complexity of Mendelian traits across yeast natural populations. Hou J, Sigwalt A, Pflieger D, Peter J, de Montigny J, Dunham MJ, Schacherer J. *Cell Reports*. 2016; 16(4):1106-14.
- Comprehensive Analysis of the *SUL1* Promoter of *Saccharomyces cerevisiae*. Rich MS, Payen C, Rubin AF, Ong GT, Sanchez MR, Yachie N, Dunham MJ, Fields S. *Genetics*. 2016 May;203(1):191-202.
- High Throughput Analyses of Budding Yeast ARSs Reveal New DNA Elements Capable of Conferring Centromere-Independent Plasmid Propagation. Hoggard T*, Liachko I* (*co-first authors), Burt C, Meikle T, Jiang K, Craciun G, Dunham M#, Fox CA# (#co-senior authors). *G3*. 2016 April 1;6(4):993-1012.
- Aneuploidy shortens replicative lifespan in *Saccharomyces cerevisiae*. Sunshine AB, Ong GT, Nickerson DP, Carr D, Murakami CJ, Wasko BM, Shemorry A, Merz AJ, Kaeberlein M, Dunham MJ. *Aging Cell*. 2016; 15(2):317-24.
- Chemostat Culture for Yeast Physiology and Experimental Evolution. Dunham MJ, Kerr EO, Miller AW, Payen C. Budding Yeast: A Laboratory Manual. ed. Boone C, Andrews B, Fields S, Davis T. 2016 Cold Spring Harbor Laboratory Press.
- Experimental evolution and resequencing analysis of yeast. Payen C and Dunham MJ. 2015 *Methods in Molecular Biology*. *Yeast Functional Genomics: Methods and Protocols*. ed. Devaux F. 2016 1361:361-74.
- Origin-Dependent Inverted-Repeat Amplification: Tests of a Model for Inverted DNA Amplification. Brewer BJ, Payen C, Di Rienzi SC, Higgins MM, Ong G, Dunham MJ, Raghuraman MK. *PLoS Genet*. 2015 23;11(12):e1005699.
- Methods in Yeast Genetics and Genomics, 2015 Edition: A CSHL Course Manual. Dunham MJ, Gartenberg M, Brown GW. 2015 Cold Spring Harbor Laboratory Press.
- Evolutionary engineering of a wine yeast strain revealed a key role of inositol and mannoprotein metabolism during low-temperature fermentation. López-Malo M, García-Rios E, Melgar B, Sanchez MR, Dunham MJ, Guillamón JM. *BMC Genomics*. 2015 Jul 22;16:537.
- The fitness consequences of aneuploidy are driven by condition-dependent gene effects. Sunshine AB, Payen C, Ong GT, Liachko I, Tan KM, Dunham MJ. *PLoS Biology*. 2015 May 26;13(5):e1002155.
- Accurate identification of centromere locations in yeast genomes using Hi-C. Varoquaux N, Liachko I, Ay F, Burton JN, Shendure J, Dunham MJ, Vert JP, Noble WS. *Nucleic Acids Research*. 2015 43(11):5331-9.
- Control of plasma membrane permeability by ABC transporters. Khakhina S, Johnson SS, Manoharlal R, Russo SB, Blugeon C, Lemoine S, Sunshine AB, Dunham M, Cowart LA, Devaux F, Moye-Rowley WS. *Eukaryot Cell*. 2015 May;14(5):442-53.
- A low cost turbidostat for use in synthetic circuit characterization. Takahashi CN, Miller AW, Dunham MJ, Klavins E. *ACS Synthetic Biology*. 2015 Jan 16;4(1):32-8.
- The enduring utility of continuous culturing in experimental evolution. Gresham D, Dunham MJ. *Genomics*. 2014 Dec;104(6 Pt A):399-405.
- Ploidy-Regulated Variation in Biofilm-Related Phenotypes in Natural Isolates of *Saccharomyces cerevisiae*. Hope EA, Dunham MJ. *G3*. 2014 Jul 24;4(9):1773-86.
- Species-level deconvolution of metagenome assemblies with contact probability maps. Burton JN, Liachko I, Dunham MJ, Shendure J. *G3*. 2014 May 22;4(7):1339-46.

- GC-rich DNA elements enable replication origin activity in the methylotrophic yeast *Pichia pastoris*. Liachko I, Youngblood RA, Tsui K, Nislow C, Brewer BJ, Dunham MJ. *PLoS Genetics*. 2014 Mar 6;10(3):e1004169.
- The dynamics of diverse segmental amplifications in populations of *Saccharomyces cerevisiae* adapting to strong selection. Payen C, Di Rienzi SC, Ong GT, Pogacher JL, Sanchez JC, Sunshine AB, Raghuraman MK, Brewer BJ, and Dunham MJ. *G3*. 2014 Mar 20;4(3):399-409.
- An autonomously replicating sequence for use in a wide range of budding yeasts. Liachko I and Dunham MJ. *FEMS Yeast Research*. 2014 Mar;14(2):364-7.
- Genome-wide consequences of deleting any single gene. Teng X, Dayhoff-Brannigan M, Cheng W, Gilbert CE, Sing CN, Diny NL, Wheelan SJ, Dunham MJ, Boeke JD, Pineda FJ, Hardwick JM. *Molecular Cell*. 2013 Nov 21;52(4):485-94.
- Identification of new functional domains in the budding yeast Ndc80 kinetochore protein by linker-scanning mutagenesis and high-throughput sequencing. Tien JF, Fong KK, Umbreit NT, Payen C, Zelter A, Asbury CL, Dunham MJ, Davis TN. *Genetics*. 2013 195(1):159-70.
- A new system for comparative functional genomics of *Saccharomyces* yeasts. Caudy A, Guan Y, Jia Y, Hansen C, DeSevo C, Hayes AP, Agee J, Alvarez J, Arellano H, Barrett D, Bauerle C, Bradley PH, Breunig JS, Bush E, Cappel D, Capra E, Chen W, Clore J, Combs P, Doucette C, Demuren O, Fellowes P, Freeman S, Frenkel E, Gadala-Maria D, Gawande R, Glass D, Grossberg S, Gupta A, Hammonds-Odie L, Hoisos A, Hsi J, Inukai S, Karczewski KJ, Ke X, Kojima M, Leachman S, Lieber D, Liebowitz A, Liu J, Liu Y, Martin T, Mena J, Mendoza R, Mhyrvold C, Millian C, Pfau S, Raj S, Rich M, Rokicki J, Rounds W, Salazar M, Salesi M, Sharma R, Silverman S, Singer C, Sinha S, Staller M, Stern P, Tang H, Weeks S, Weidmann M, Wolf A, Young C, Yuan J, Crutchfield C, McClean M, Murphy CT, Llinás M, Botstein D, Troyanskaya OG, Dunham MJ. *Genetics*. 2013 195(1):275-87.
- Integrative phenomics reveals insight into the structure of phenotypic diversity in budding yeast. Skelly DA, Merrihew GE, Riffle M, Connelly CF, Kerr EO, Johansson M, Jaschob D, Graczyk B, Shulman NJ, Wakefield J, Cooper SJ, Fields S, Noble WS, Muller EGD, Davis TN, Dunham MJ, MacCoss MJ, and Akey JM. *Genome Res*. 2013 23(9):1496-504.
- Contemporary, yeast-based approaches to understanding human genetic variation. Dunham MJ and Fowler DM. *Current Opinion in Genetics & Development*. 2013 Dec;23(6):658-64.
- The yeast Alix homolog, Bro1, functions as an ubiquitin receptor for protein sorting into multi vesicular endosomes. Pashkova N, Gakhar L, Winistorfer S, Sunshine AB, Rich M, Dunham MJ, Yu L, Piper R. *Developmental Cell*. 2013 25(5):520-33.
- Population genomics and transcriptional consequences of regulatory motif variation in globally diverse *Saccharomyces cerevisiae* strains. Connelly CF, Skelly DA, Dunham MJ, Akey JM. *Mol Biol Evol*. 2013 30(7):1605-13.
- High-Resolution Mapping and Mutational Scanning of Autonomously Replicating Sequences. Liachko I, Youngblood R, Keich U, Dunham MJ. *Genome Res*. 2013 23(4):698-704.
- Design and use of multiplexed chemostat arrays. Miller AW, Befort C, Kerr EO, Dunham MJ. *J Vis Exp*. 2013 (72).
- Comparative gene expression between two yeast species. Guan Y, Dunham MJ, Troyanskaya OG, Caudy AA. *BMC Genomics*. 2013 14:33.
- Coupling unbiased mutagenesis to high-throughput DNA sequencing uncovers functional domains in the Ndc80 kinetochore protein of *Saccharomyces cerevisiae*. Tien JF, Fong KK, Umbreit NT, Payen C, Zelter A, Asbury CL, Dunham MJ, Davis TN. *Genetics*. 2013 Sep;195(1):159-70.

- Mutability and mutational spectrum of chromosome transmission fidelity genes. Stirling PC, Crisp MJ, Basrai MA, Tucker CM, Dunham MJ, Spencer FA, Hieter P. *Chromosoma*. 2012 121(3):263-75.
- Transcriptional consequences of aneuploidy. Sheltzer JM, Torres E, Dunham MJ, Amon A. *Proc Natl Acad Sci U S A*. 2012 109(31):12644-9.
- In-class Incentives that Encourage Students to Take Concepts Assessments Seriously. Smith M, Thomas K, Dunham MJ. *Journal of College Science Teaching*. 2012 42(2): 57-61.
- Multiple pathways regulate minisatellite stability during stationary phase in yeast. Kelly MK, Brosnan L, Jauert PA, Dunham MJ, Kirkpatrick DT. *G3*. 2012 2(10):1185-95.
- Two Flavors of Bulk Segregant Analysis in Yeast. Dunham MJ. *Methods in Molecular Biology. Quantitative Trait Loci (QTL): Methods and Protocols*. Ed. Rifkin SA. 2012 871:41-54.
- Genetic Analysis of Desiccation Tolerance in *Saccharomyces cerevisiae*. Calahan D, Dunham M, Desevo C, Koshland DE. *Genetics*. 2011 189(2):507-19.
- Nucleosome-coupled expression differences in closely-related species. Guan Y, Yao V, Caudy A, Tsui K, Gebbia M, Dunham MJ, Nislow C, Troyanskaya OG. *BMC Genomics*. 2011 26;12:466.
- The awesome power of yeast evolutionary genetics: New genome sequences and strain resources for the *Saccharomyces sensu stricto* genus. Scannell DR, Zill OA, Rokas A, Payen C, Dunham MJ, Eisen MB, Rine J, Johnston M, Hittinger CT. *Genes, Genomes, and Genetics*. 2011 1(1):11-25.
- Origin-dependent inverted-repeat amplification: a replication-based model for generating palindromic amplicons. Brewer BJ, Payen C, Raghuraman MK, Dunham MJ. *PLoS Genet*. 2011 7(3):e1002016.
- Whole-genome sequencing of a laboratory-evolved yeast strain. Araya CL, Payen C, Dunham MJ, Fields S. *BMC Genomics*. 2010 11:88.
- Systematic planning of genome-scale experiments in poorly-studied species. Guan Y, Dunham MJ, Caudy AC, Troyanskaya OG. *PLoS Comput Biol*. 2010 6(3):e1000698.
- Identification of Aneuploidy-tolerating Mutations. Torres EM, Dephore N, Panneerselvam A, Tucker CM, Whittaker C, Gygi SP, Dunham MJ, Amon A. *Cell*. 2010 143(1):71-83.
- Competitive repair by naturally dispersed repetitive DNA during non-allelic homologous recombination. Hoang ML, Tan FJ, Lai DC, Celniker SE, Hoskins RA, Dunham MJ, Zheng Y, Koshland D. *PLoS Genet*. 2010 6(12):e1001228.
- Experimental Evolution in Yeast: A Practical Guide. Dunham MJ. *Methods in Enzymology. Volume 470. Guide to Yeast Genetics: Functional Genomics, Proteomics and Other Systems Analysis*. Ed. Weissman J, Guthrie C, Fink G. 2010 470:487-507.
- Translocation and Assembly of Mitochondrially Coded *Saccharomyces cerevisiae* Cytochrome c Oxidase Subunit Cox2 by Oxa1 and Yme1, in the Absence of Cox18. Fiumera HL, Dunham MJ, Saracco SA, Butler CA, Kelly JA, Fox TD. *Genetics*. 2009 182(2):519-28.
- Predicting cellular growth from gene expression signatures. Airoidi EM, Huttenhower C, Gresham D, Lu C, Caudy AA, Dunham MJ, Broach JR, Botstein D, Troyanskaya OG. *PLoS Computational Biol*. 2009 5(1):e1000257.
- The Ras/cAMP pathway and the CDK-like kinase Ime2 regulate the MAPK Smk1 and spore morphogenesis in *Saccharomyces cerevisiae*. McDonald CM, Wagner M, Dunham MJ, Shin ME, Ahmed NT, Winter E. *Genetics*. 2009 181(2):511-23.
- Telomere behavior in a hybrid yeast. Martin OC, DeSevo CG, Guo BZ, Koshland DE, Dunham MJ, and Zheng Y. *Cell Research. Cell Res*. 2009 19(7):910-2.
- The Repertoire and Dynamics of Evolutionary Adaptations to Controlled Nutrient-Limited Environments in Yeast. Gresham D, Desai MM, Tucker CM, Jenq HT, Pai DA, Ward A, DeSevo CG, Botstein D, and Dunham MJ. *PLoS Genet*. 2008 4(12):e1000303.

- Fis1 deficiency selects for compensatory mutations responsible for cell death and growth control defects. Cheng WC, Teng X, Park HK, Tucker CM, Dunham MJ, and Hardwick JM. *Cell Death Differ.* 2008 15(12):1838-46.
- Comparing whole genomes using DNA microarrays. Gresham D, Dunham MJ, Botstein D. *Nat Rev Genet.* 2008 9(4):291-302.
- Effects of aneuploidy on cellular physiology and cell division in haploid yeast. Torres EM, Sokolsky T, Tucker CM, Chan LY, Boselli M, Dunham MJ and Amon A. *Science.* 2007 317(5840):916-24.
- Viewing the Larger Context of Genomic Horizontal Integration. Hibbs M, Wallace G, Dunham M, Li K, and Troyanskaya O. *Proceedings of the 11th Int. Conf. on Information Visualization (IV07)*, 2007.
- Functional analysis of gene duplications in *Saccharomyces cerevisiae*. Guan Y, Dunham MJ, and Troyanskaya OG. *Genetics.* 2007 175(2):933-43.
- Global Mapping of Transposon Location. Gabriel A, Dapprich J, Kunkel M, Gresham D, Pratt S, and Dunham MJ. *PLoS Genetics.* 2006 2(12):e212.
- Mapping Novel Traits by Array-assisted Bulk Segregant Analysis in *Saccharomyces cerevisiae*. Brauer MJ, Christianson CM, Pai DA, and Dunham MJ. *Genetics.* 2006 173(3):1813-6.
- Genome-wide detection of polymorphisms at nucleotide resolution with a single DNA microarray. Gresham D, Ruderfer DM, Pratt SC, Schacherer J, Dunham MJ, Botstein D, and Kruglyak L. *Science.* 2006 311(5769):1932-6.
- Accurate detection of aneuploidies in array CGH and gene expression microarray data. Myers CL, Dunham MJ, Kung SY, and Troyanskaya OG. *Bioinformatics.* 2004 20(18):3533-43.
- Characteristic Genome Rearrangements in Experimental Evolution of *S. cerevisiae*. Dunham MJ, Badrane H, Ferea T, Adams J, Brown PO, Rosenzweig RF, and Botstein D. *Proc Natl Acad Sci USA.* 2002 99(25):16144-9.
- Protein microarrays for highly parallel detection and quantitation of specific proteins and antibodies in complex solutions. Haab BB, Dunham MJ, and Brown PO. *Genome Biology.* 2001 2(2):RESEARCH0004.
- Asymmetric leaves1* mediates leaf patterning and stem cell function in *Arabidopsis*. Byrne ME, Barley R, Curtis M, Arroyo JM, Dunham M, Hudson A, and Martienssen RA. *Nature.* 2000 408(6815):967-71.
- ika1* and *rag1* as Markers for the Development of the Zebrafish Immune System. Dunham MJ and Steiner L. *MIT Biology Undergraduate Journal.* 1999 2:49-53.

PREPRINTS

- Experimental evolution reveals favored adaptive routes to cell aggregation in yeast. Hope EA, Amorosi CJ, Miller AW, Dang K, Heil CS, Dunham MJ. *bioRxiv.* Posted December 6, 2016. doi: <http://dx.doi.org/10.1101/091876>
- The dynamic three-dimensional organization of the diploid yeast genome. Kim S, Liachko I, Brickner DG, Cook K, Noble WS, Brickner JH, Shendure J, Dunham MJ. *bioRxiv.* Posted December 5, 2016. doi: <http://dx.doi.org/10.1101/091827>
- Selection on heterozygosity drives adaptation in intra- and interspecific hybrids. Heil CSS, DeSevo CG, Pai DA, Tucker CM, Hoang ML, Dunham MJ. *bioRxiv.* Posted September 1, 2016. doi: <http://dx.doi.org/10.1101/073007>
- Single-molecule sequencing and conformational capture enable de novo mammalian reference genomes. Bickhart DM, Rosen BD, Koren S, Sayre BL, Hastie AR, Chan S, Lee J, Lam ET, Liachko I, Sullivan ST, Burton JN, Huson HJ, Kelley CM, Hutchison JL, Zhou Y, Sun J, Crisa A, Ponce de Leon FA, Schwartz JC, Hammond JA, Waldbieser GC, Schroeder SG, Liu GE, Dunham MJ, Shendure J, Sonstegard TS, Phillippy AM, Van Tassell CP, Smith

TPL. bioRxiv. Posted July 18, 2016. doi: <http://dx.doi.org/10.1101/064352>
Differential paralog divergence modulates evolutionary outcomes in yeast. Sanchez MR, Miller AW, Liachko I, Sunshine AB, Lynch B, Huang M, DeSevo CG, Pai DA, Tucker CM, Hoang MJ, Dunham MJ. bioRxiv. Posted July 12, 2016. doi: <http://dx.doi.org/10.1101/063248>

PATENT APPLICATIONS

Liachko I, Dunham M. Pan-Yeast Autonomously Replicating Sequence, application filed, 2014.
Burton J, Shendure J, Liachko I, Dunham M. Chromosome Conformation Capture Tools for Deconvolution of Metagenomes, application filed, 2014.

RESEARCH SUPPORT

PI NSF MCB-1516330: Determinants of hybrid fitness and genome plasticity, 2015-2019.
PI NIH/NIGMS R01 GM094306: Causes and consequences of gene copy number change in adapting yeast populations, 2011-2017 (NCE).
PI Canadian Institute for Advanced Research: CIFAR Senior Fellow, Genetic Networks program, 2012-2017.
PI Howard Hughes Medical Institute Faculty Scholar, 2016-2021.
Co-PI NIH/NIGMS R01 GM101091: Genetic basis of stress tolerance in natural populations of yeast, 2012-2017 (NCE, awaiting NOA for renewal). Co-PIs: David Hess and Joseph Schacherer.
Co-PI NSF 1243710: Comparative genomics of chromosome replication among budding yeasts, 2013-2017 (NCE). Co-PIs: Bonny Brewer and M.K. Raghuraman.
Co-PI NSF BEACON Center: Reducing Yeast Evolvability, 2016-2017. Co-PI: Jeff Barrick.
Co-PI NSF BEACON Center: Identifying the reservoirs of antibiotic resistance, 2016-2017. Co-PI: Eva Top.
Co-I NIH/NIGMS P41 RR011823: Comprehensive biology: Exploiting the yeast genome, 2009-2016 (NCE). PI: Michael MacCoss.
Co-I JGI Community Sequencing Program: Pioneering fungal mutagenesis using Tn-seq, 2014- (ongoing sequencing support). PIs: Adam Arkin and Rachel Brem.
Co-I NIH R24GM115277: F-CAP: Functionalization of Variants in Clinically Actionable Pharmacogenes, 2015-2018. Co-PIs: Allan Rettie and Doug Fowler.

COMPLETED RESEARCH SUPPORT

PI Marian E. Smith Junior Faculty Award, 2009.
PI Royalty Research Fund: Fitness determinants associated with copy number changes in yeast, 2010-2011.
PI March of Dimes: Basil O'Connor Starter Scholar Research Award, 2011-2013.
PI Rita Allen Foundation: Rita Allen Foundation Scholar, 2010-2015.
PI NSF 1120425: Genomic architecture of adaptation in yeast experimental evolution, 2011-2016.
Co-PI NSF BEACON Center: The evolutionary origins of phenotypic plasticity, 2013-2014. Co-PI: Ben Kerr.
Co-PI NSF BEACON Center: Examining stability and lability of an interspecific mutualism using experimental co-evolution, 2014-2015. Co-PI: Ian Dworkin.
Co-PI UW Commercialization Gap Fund: Chromosome Conformation Capture for Genome and Metagenome Assembly, 2015-2016. Co-PI: Jay Shendure.