



Michelle Hays

Postdoctoral Scholar, Genetics

 Curriculum Vitae available Online

Bio

HONORS AND AWARDS

- Life Science Alliance Exchange Grant Recipient, Life Science Alliance/EMBL (2023)
- Hanna Gray Fellow, Howard Hughes Medical Institute (2022-ongoing)
- Postdoctoral NRSA Fellowship awardee, F32 NIAID Ruth L. Kirschstein Postdoctoral Individual National Research Service Award (2021-2024)
- Postdoctoral Fellowship awardee, School of Medicine Dean's Postdoctoral Fellowship (2021)
- Postdoctoral Fellow, Stanford Center for Computational, Evolutionary and Human Genomics (CEHG) (2020-2021)
- Postdoctoral Training Grant awardee, Stanford Genomics Training Program NHGRI training grant (2020-2021)
- Graduate Research Fellowship Program (GRFP) awardee, National Science Foundation (2015-2019)
- Predoctoral Training Grant awardee, University of Washington NHGRI Genome Training Grant (2014-2015)

STANFORD ADVISORS

- Gavin Sherlock, Postdoctoral Faculty Sponsor

Research & Scholarship

LAB AFFILIATIONS

- Gavin Sherlock, Sherlock (2/10/2020)

Publications

PUBLICATIONS

- **The Viral K1 Killer Yeast System: Toxicity, Immunity, and Resistance.** *Yeast (Chichester, England)*
Chan, A., Hays, M., Sherlock, G.
2025
- **Genetic conflicts in budding yeast: The 2mu plasmid as a model selfish element.** *Seminars in cell & developmental biology*
Hays, M.
2024; 161-162: 31-41
- **Paths to adaptation under fluctuating nitrogen starvation: The spectrum of adaptive mutations in *Saccharomyces cerevisiae* is shaped by retrotransposons and microhomology-mediated recombination.** *PLoS genetics*
Hays, M., Schwartz, K., Schmidtke, D. T., Aggeli, D., Sherlock, G.
2023; 19 (5): e1010747
- **A natural variant of the essential host gene MMS21 restricts the parasitic 2-micron plasmid in *Saccharomyces cerevisiae*.** *eLife*
Hays, M. n., Young, J. M., Levan, P. F., Malik, H. S.

2020; 9

- **Independent Origins of Yeast Associated with Coffee and Cacao Fermentation.** *Current biology : CB*
Ludlow, C. L., Cromie, G. A., Garmendia-Torres, C., Sirr, A., Hays, M., Field, C., Jeffery, E. W., Fay, J. C., Dudley, A. M.
2016; 26 (7): 965-71
- **Aneuploidy underlies a multicellular phenotypic switch.** *Proceedings of the National Academy of Sciences of the United States of America*
Tan, Z., Hays, M., Cromie, G. A., Jeffery, E. W., Scott, A. C., Ah Yong, V., Sirr, A., Skupin, A., Dudley, A. M.
2013; 110 (30): 12367-72
- **Use of pleiotropy to model genetic interactions in a population.** *PLoS genetics*
Carter, G. W., Hays, M., Sherman, A., Galitski, T.
2012; 8 (10): e1003010
- **Spatiotemporal patterns of gene expression during development of a complex colony morphology.** *PloS one*
Cromie, G. A., Tan, Z., Hays, M., Sirr, A., Dudley, A. M.
2024; 19 (12): e0311061
- **Data-driven multiscale modeling reveals the role of metabolic coupling for the spatio-temporal growth dynamics of yeast colonies.** *BMC molecular and cell biology*
Intosalmi, J., Scott, A. C., Hays, M., Flann, N., Yli-Harja, O., Lähdesmäki, H., Dudley, A. M., Skupin, A.
2019; 20 (1): 59
- **Transcriptional Profiling of Biofilm Regulators Identified by an Overexpression Screen in *Saccharomyces cerevisiae*** *G3-GENES GENOMES GENETICS*
Cromie, G. A., Tan, Z., Hays, M., Sirr, A., Jeffery, E. W., Dudley, A. M.
2017; 7 (8): 2845–54
- **Dissecting Gene Expression Changes Accompanying a Ploidy-Based Phenotypic Switch.** *G3 (Bethesda, Md.)*
Cromie, G. A., Tan, Z., Hays, M., Jeffery, E. W., Dudley, A. M.
2017; 7 (1): 233-246
- **Identification and characterization of a drug-sensitive strain enables puromycin-based translational assays in *Saccharomyces cerevisiae*.** *Yeast (Chichester, England)*
Cary, G. A., Yoon, S. H., Torres, C. G., Wang, K., Hays, M., Ludlow, C., Goodlett, D. R., Dudley, A. M.
2014; 31 (5): 167-78
- **High-throughput tetrad analysis.** *Nature methods*
Ludlow, C. L., Scott, A. C., Cromie, G. A., Jeffery, E. W., Sirr, A., May, P., Lin, J., Gilbert, T. L., Hays, M., Dudley, A. M.
2013; 10 (7): 671-5
- **Predicting the effects of copy-number variation in double and triple mutant combinations.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
Carter, G. W., Hays, M., Li, S., Galitski, T.
2012: 19-30