Stanford



Martin Jonikas

Assistant Professor, Biology

Bio

ACADEMIC APPOINTMENTS

- Assistant Professor, Biology

HONORS AND AWARDS

- NIH Director's New Innovator Award, National Institutes of Health (2015)
- Young Investigator Award, Air Force Office of Scientific Research (2010)
- Graduate Course Teaching Award, University of California, San Francisco (2006)
- NSF Graduate Research Fellowship, National Science Foundation (2005)

PROFESSIONAL EDUCATION

- Ph.D., Univ. California, San Francisco , Molecular Biology and Genetics (2009)
- B.S., Mass. Institute of Technology , Aerospace Engineering (2004)

LINKS

- Jonikas Lab Website: https://sites.google.com/site/jonikaslab/

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Photosynthesis provides energy for nearly all life on Earth. As humans increasingly change this planet, it is essential that we understand this process and the organisms that perform it. Our lab aims to dramatically accelerate our understanding of photosynthetic organisms by developing and applying novel functional genomics strategies in the green alga Chlamydomonas reinhardtii. In the long run, we dream of engineering photosynthetic organisms to address the challenges that our civilization faces in agriculture, health and energy.

Our lab is focused around three synergistic areas:

I. Systems biology of photosynthetic organisms

Many fundamental systems-level questions about photosynthetic organisms remain unanswered. What is the full set of genes required for photosynthesis? Which parts work together? What do all the uncharacterized parts do?

The green alga Chlamydomonas reinhardtii is a powerful model photosynthetic organism. The green plant photosynthetic apparatus is highly conserved and thus can be studied in Chlamydomonas. Chlamydomonas can grow as a haploid and in the absence of a functional photosynthetic apparatus, allowing rapid isolation of mutants of interest. Its unicellular nature and short doubling time enable higher throughput experiments than alternative systems.

We are developing transformative tools to enable high-throughput studies of gene function in Chlamydomonas. We have developed a new tool, which increases the pace at which mutated genes in Chlamydomonas can be identified by >1,000-fold. We are presently using this tool to develop a genome-wide collection of Chlamydomonas insertion mutants as a powerful resource for the research community.

II. Molecular mechanisms of efficient photosynthesis

Photosynthetic organisms growing in nearly all environments must cope with rapid fluctuations in light intensity. The sunlight intensity in most environments can change dramatically in a fraction of a second due to e.g. clouds or leaves moving in the wind. Yet, almost nothing is known about the molecular mechanisms that enable efficient photosynthesis under fluctuating light. We recently discovered that plants have evolved a mechanism that enhances photosynthetic efficiency in changing light environments. We found that this mechanism works by accelerating fluxes of ions across the photosynthetic (thylakoid) membrane.

The Chlamydomonas Carbon Concentrating Mechanism (CCM) allows it to use CO2 much more efficiently than C3 crop plants. If we understood how this CCM works, we could engineer it into crop plants to increase their growth rates and reduce their need for water and fertilizer. We are working with our collaborators in the NSF project Combining Algal and Plant Photosynthesis to identify and transfer CCM components into the model C3 plant Arabidopsis, as a first step towards ultimately enhancing CO2 uptake in wheat and rice.

III. Lipid metabolism in photosynthetic eukaryotes

We are discovering and characterizing new genes with roles in algal lipid metabolism and its regulation. Photosynthetic organisms have the potential to play an important role in the production of renewable fuels and high-value lipids. Yet, many key aspects of lipid metabolism remain poorly characterized. For example, fatty acids are made in the chloroplast, but we don't understand how they get out of the chloroplast and to the rest of the cell. We have developed a new method that is allowing us to identify large numbers of new genes with roles in algal lipid metabolism. We are now using this method to systematically identify novel genes with roles in algal lipid metabolism.

Teaching

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biology (School of Humanities and Sciences) (PhD Program)

Publications

PUBLICATIONS

- **A repeat protein links Rubisco to form the eukaryotic carbon-concentrating organelle** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*

Mackinder, L. C., Meyer, M. T., Mettler-Altmann, T., Chen, V. K., Mitchell, M. C., Caspari, O., Rosenzweig, E. S., Pallesen, L., Reeves, G., Itakura, A., Roth, R., Sommer, F., Geimer, et al
2016; 113 (21): 5958-5963

- **An Indexed, Mapped Mutant Library Enables Reverse Genetics Studies of Biological Processes in Chlamydomonas reinhardtii.** *Plant cell*
  Li, X., Zhang, R., Patena, W., Gang, S. S., Blum, S. R., Ivanova, N., Yue, R., Robertson, J. M., Lefebvre, P. A., Fitz-Gibbon, S. T., Grossman, A. R., Jonikas, M. C.
  2016; 28 (2): 367-387

- **Ion antiport accelerates photosynthetic acclimation in fluctuating light environments** *NATURE COMMUNICATIONS*
  Armbruster, U., Carrillo, L. R., Venema, K., Pavlovic, L., Schmidtmann, E., Kornfeld, A., Jahns, P., Berry, J. A., Kramer, D. M., Jonikas, M. C.
  2014; 5

- **High-Throughput Genotyping of Green Algal Mutants Reveals Random Distribution of Mutagenic Insertion Sites and Endonucleolytic Cleavage of Transforming DNA** *PLANT CELL*
  Zhang, R., Patena, W., Armbruster, U., Gang, S. S., Blum, S. R., Jonikas, M. C.
  2014; 26 (4): 1398-1409

- **Comprehensive Characterization of Genes Required for Protein Folding in the Endoplasmic Reticulum** *SCIENCE*
  Jonikas, M. C., Collins, S. R., Denic, V., Oh, E., Quan, E. M., Schmid, V., Weibezahn, J., Schwappach, B., Walter, P., Weissman, J. S., Schuldiner, M.
  2009; 323 (5922): 1693-1697

- **Introducing an algal carbon-concentrating mechanism into higher plants: location and incorporation of key components.** *Plant biotechnology journal*
  Atkinson, N., Feike, D., Mackinder, L. C., Meyer, M. T., Griffiths, H., Jonikas, M. C., Smith, A. M., McCormick, A. J.
  2016; 14 (5): 1302-1315

- **High-Throughput Genetics Strategies for Identifying New Components of Lipid Metabolism in the Green Alga Chlamydomonas reinhardtii.** *Sub-cellular biochemistry*
  Li, X., Jonikas, M. C.
  2016; 86: 223-247

- **Critical role of Chlamydomonas reinhardtii ferredoxin-5 in maintaining membrane structure and dark metabolism.** *Proceedings of the National Academy of Sciences of the United States of America*
  Yang, W., Wittkopp, T. M., Li, X., Warakanont, J., Dubini, A., Catalanotti, C., Kim, R. G., Nowack, E. C., Mackinder, L. C., Aksoy, M., Page, M. D., D'Adamo, S., Saroussi, et al
  2015; 112 (48): 14978-14983

- **Molecular techniques to interrogate and edit the Chlamydomonas nuclear genome** *PLANT JOURNAL*
  Jinkerson, R. E., Jonikas, M. C.
  2015; 82 (3): 393-412

- **A fluorescence-activated cell sorting-based strategy for rapid isolation of high-lipid Chlamydomonas mutants.** *Plant journal*
  Terashima, M., Freeman, E. S., Jinkerson, R. E., Jonikas, M. C.
  2015; 81 (1): 147-159

- **Waking sleeping algal cells.** *Proceedings of the National Academy of Sciences of the United States of America*
  Li, X., Umen, J. G., Jonikas, M. C.
  2014; 111 (44): 15610-15611

- **Alternative Acetate Production Pathways in Chlamydomonas reinhardtii during Dark Anoxia and the Dominant Role of Chloroplasts in Fermentative Acetate Production.** *Plant cell*
  Yang, W., Catalanotti, C., D'Adamo, S., Wittkopp, T. M., Ingram-Smith, C. J., Mackinder, L., Miller, T. E., Heuberger, A. L., Peers, G., Smith, K. S., Jonikas, M. C., Grossman, A. R., Posewitz, et al
  2014; 26 (11): 4499-4518

- **Actin is required for IFT regulation in Chlamydomonas reinhardtii.** *Current biology*
  Avasthi, P., Onishi, M., Karpiak, J., Yamamoto, R., Mackinder, L., Jonikas, M. C., Sale, W. S., Shoichet, B., Pringle, J. R., Marshall, W. F.
  2014; 24 (17): 2025-2032

- **J Domain Co-chaperone Specificity Defines the Role of BiP during Protein Translocation** *JOURNAL OF BIOLOGICAL CHEMISTRY*

Vembar, S. S., Jonikas, M. C., Hendershot, L. M., Weissman, J. S., Brodsky, J. L.
2010; 285 (29): 22484-22494

- **Automated identification of pathways from quantitative genetic interaction data** *MOLECULAR SYSTEMS BIOLOGY*
  Battle, A., Jonikas, M. C., Walter, P., Weissman, J. S., Koller, D.
  2010; 6

- **Identification of yeast proteins necessary for cell-surface function of a potassium channel** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Haass, F. A., Jonikas, M., Walter, P., Weissman, J. S., Jan, Y., Jan, L. Y., Schuldiner, M.
  2007; 104 (46): 18079-18084