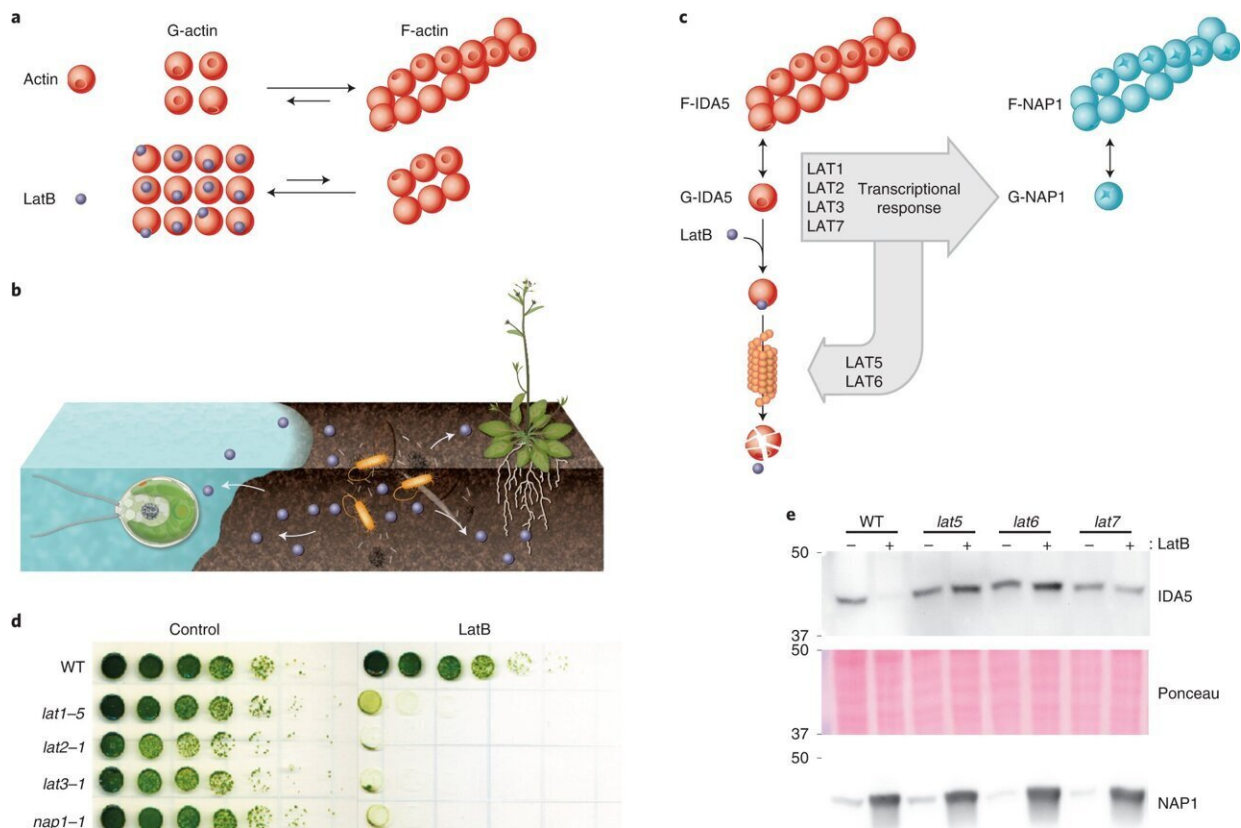


# Can algae unlock the secrets of photosynthesis?

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The approach revealed new conserved components of a defense mechanism against cytoskeleton inhibitors. a, LatB interferes with actin polymerization. b, Soil microorganisms deploy (arrows) actin inhibitors (blue circles) for a competitive advantage in their environment. c, *Chlamydomonas* responds to actin inhibition by degrading its conventional actin, IDA5, and upregulating an alternative actin, NAP1. d, Growth of new *lat* mutants identified in this study (*lat5-1*, *lat6-1* and *lat7-2*) was compared to previously isolated *lat1-5*, *lat2-1*, *lat3-1* and *nap1-1* mutants<sup>66</sup> in the absence (control) and presence (LatB) of 3

$\mu\text{M}$  LatB. e, Immunoblot of conventional (IDA5) and alternative (NAP1) actins shows that lat5-1, lat6-1 and lat7-2 are deficient in actin degradation. Immunoblot representative of  $n = 3$  independent experiments. f, The F-actin homeostasis pathway is conserved between green algae and plants. Mutants in Arabidopsis genes homologous to Chlamydomonas lat3, lat5 and lat6 are sensitive to LatB, as evidenced by decreased root length. g, Quantification of root length in Arabidopsis mutants. Asterisks mark significant changes relative to wild type under the same condition based on two-way analysis of variance. The exact value of  $P = 2.4 \times 10^{-47}$  (Ler versus lat3),  $P = 1.4 \times 10^{-62}$  (Col-0 versus lat5),  $P = 6.8 \times 10^{-23}$  (Col-0 versus lat6).  $n = 26$  roots examined over three independent experiments. Credit: *Nature Genetics* (2022). DOI: 10.1038/s41588-022-01052-9

A team led by current and former Carnegie plant biologists has undertaken the largest ever functional genomic study of a photosynthetic organism. Their work, published in *Nature Genetics*, could inform strategies for improving agricultural yields and mitigating climate change.

Photosynthesis is the biochemical process by which plants, algae, and certain bacteria are able to convert the Sun's energy into [chemical energy](#) in the form of carbohydrates.

"It is the foundation upon which life as we know it is able to exist," said Carnegie's Arthur Grossman, a co-author on the paper. "It makes our atmosphere oxygen rich while capturing a percentage of the [climate-change](#)-causing [greenhouse gases](#), mostly  $\text{CO}_2$ , that are spewed into the atmosphere by human activity, and it is the mainstay of our food supply."

Yet despite its fundamental importance, many of the [genes](#) associated with photosynthesis remain uncharacterized. Luckily, algae present an

accessible vehicle for elucidating the [genetic information](#) that underpins this vital process.

A catalog of mutants of the single-celled photosynthetic green alga *Chlamydomonas reinhardtii* that was initiated by Princeton University's Martin Jonikas during his tenure as a Carnegie staff associate enabled a collaborative team of plant scientists to begin to understand the functions of thousands of genes that are present in [photosynthetic organisms](#).

*Chlamydomonas* represents a group of photosynthetic [algae](#) that are found around the globe in fresh and saltwater, moist soils, and even at the surface of snow. They readily grow in the lab, even in darkness if given the right nutrients. This makes *Chlamydomonas* an excellent research tool for plant biologists, especially for those interested in the genetics of the photosynthetic apparatus, as well as many other aspects of plant biochemistry, such as responses to light and stress.

"We started with a collection of 58,000 *Chlamydomonas* mutants and exposed them to a large variety of conditions and chemical stressors," Jonikas explained. "Quantifying an individual mutant's growth enabled us to see which genes contribute to success in each environment and to start linking many of these genes to adaptive traits."

This study represented 78% of *Chlamydomonas* genes—nearly 14,000—providing a framework for prioritizing which genes are good candidates for further research and enabling scientists to begin to hypothesize about the possible functions of poorly understood genes in photosynthetic organisms.

"We anticipate that our work will guide the functional characterization of genes across the tree of life," Grossman said.

"We are very happy to see how resources generated by Carnegie

scientists are enabling the [research community](#) and advancing the field at such a broad scale," added Zhiyong Wang, the acting director of Carnegie's Department of Plant Biology.

The knowledge gleaned from this research could underpin strategies for improving the yields of important food and biofuel crops in a warming world, as well as programs to capture and store carbon pollution from the atmosphere.

**More information:** Friedrich Fauser et al, Systematic characterization of gene function in the photosynthetic alga *Chlamydomonas reinhardtii*, *Nature Genetics* (2022). [DOI: 10.1038/s41588-022-01052-9](https://doi.org/10.1038/s41588-022-01052-9)

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