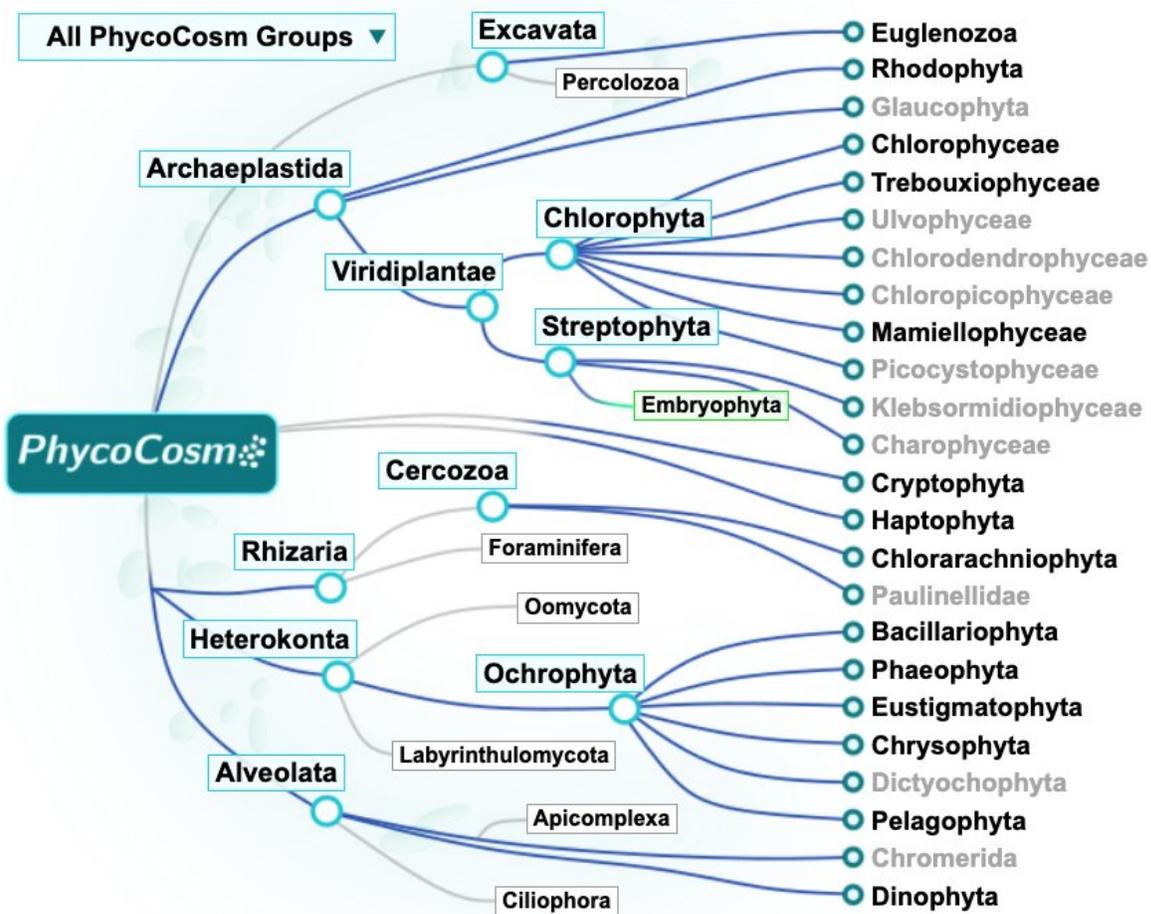


A one-stop shop for analyzing algal genomes

December 22 2020, by Alison F. Takemura



Credit: DOE/Joint Genome Institute

Interested in the genomes of algae? You now have one place where you can browse the genetic blueprints of these photosynthetic organisms. [PhycoCosm](#) is one of the largest data repositories of its kind, with an

interactive browser that allows algal scientists and enthusiasts to look deep into more than 100 algal genomes, compare them, and visualize supporting experimental data.

Algae are important organisms. They play key roles in global carbon cycling, are sources of natural products, and have potential as biofuel feedstocks. Understanding the genetic underpinnings responsible for these traits takes us closer to harnessing [algae](#) for bioenergy and the greater bioeconomy. By bringing together publicly available genomic data on algae into one place, PhycoCosm allows users to easily compile data that answers what genes are present in which organisms, when are they expressed, and what they do.

The name PhycoCosm stems from the Greek phykos, meaning seaweed. Seaweeds are algae, but many kinds of algae exist. During the course of evolution, algal organisms sprung up in almost all branches of eukaryotes ([organisms](#) with a nucleus). In part because of this evolutionary diversity, algal genomes can be incredibly complex and difficult to sequence and understand.

A team of researchers led by Algal Genomics Program lead Igor Grigoriev and data scientist Alan Kuo at the U.S. Department of Energy (DOE) Joint Genome Institute (JGI), a DOE Office of Science User Facility located at Lawrence Berkeley National Laboratory (Berkeley Lab), have unveiled PhycoCosm in the *Nucleic Acids Research* journal. The [genome](#) portal reinforces the JGI's new strategic focus on exploring algal biology, diversity, and ecology.

PhycoCosm has many components that make it useful for [scientific inquiry](#): it shows a full phylogenetic tree of more than 100 sequenced algal genomes—many sequenced by the JGI—so researchers can easily explore the evolutionary and functional relationships among the different algae. Scientists can use PhycoCosm's genome browser to see their

favorite alga's predicted genes and their organization, and analyze genes in the nucleus and organelles such as the chloroplast. In the cases where data are available, a user can also analyze [gene expression](#) from published experiments; study DNA methylation, which gives clues to how an organism may tune gene expression; and investigate corresponding proteins. PhycoCosm's built-in connection to the DOE Systems Biology Knowledgebase (KBase) also allows researchers to study how metabolites flow through and transform in algae.

PhycoCosm joins other online data portals and tools created by JGI researchers, including the Integrated Microbial Genomes and Microbiomes (IMG/M) system for microbial and metagenome datasets, [MycoCosm](#) for comparative analysis of fungal genomes, and [Phytozome](#) for comparing plant genomes.

Kuo and Grigoriev encourage scientists to both use PhycoCosm's data repository and contribute to it. And for those still needing their algae sequenced, Grigoriev and Kuo recommend they apply through the JGI's Community Science Program.

More information: Igor V Grigoriev et al. PhycoCosm, a comparative algal genomics resource, *Nucleic Acids Research* (2020). [DOI: 10.1093/nar/gkaa898](#)

Provided by DOE/Joint Genome Institute

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