

# Have you had your cereal today?

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Cereals are grasses that produce grains, the bulk of our food supply. Carnegie's Plant Biology Department is releasing genome-wide metabolic complements of several cereals including rice, barley, sorghum, and millet. Along with corn, whose metabolic complement was released previously, these species are responsible for producing over 1.5 billion tons of grains annually world-wide. Understanding how these important species harness sunlight to grow and produce seeds will help researchers improve crop yields, combat world hunger, and produce biofuel that could lower fuel costs and perhaps fight climate change.

The databases are designed to help researchers gain a detailed, genome-scale view of the chemical reactions that define a plant's metabolic life. This includes activities such as converting carbon dioxide and sunlight into chemical energy, transporting nutrients from the soil, and responding to the environment. All of the databases and data can be searched, browsed, or downloaded from the [Plant Metabolic Network](#) project website.

"We are trying to understand how the metabolic systems of plants are organized, function and evolve so that we and others can ultimately engineer a variety of different plants," says program leader Seung Yon Rhee. "This degree of across-the-board knowledge about the enzymes, [biochemical pathways](#), and [regulatory networks](#) that control a plant's metabolism is necessary for meeting the ever-expanding demand for production of food, biofuel and phyto-pharmaceuticals."

Rhee's group consists of plant biologists, scientific curators, post-

doctoral scholars, and student interns. The group employs a number of approaches to generate information, integrating techniques and concepts from a wide range of fields including genomics, computer science, statistics, evolution, [molecular biology](#), and biochemistry.

In addition to the world's most important [grain crops](#)—rice, sorghum, barley, and millet—Rhee's group is also releasing the metabolic complements of switchgrass, which is an important potential [biofuel](#) source, and Brachypodium, which serves as an experimental model used by scientists to better understand all grasses. Additionally, Rhee's group is releasing substantially expanded metabolic databases for 10 species that were already part of the site. These include corn, soybean, Arabidopsis, wine grape, cassava, poplar, moss, Selaginella, papaya, and Chlamydomonas.

Together with an all-plant metabolic pathway database called PlantCyc, the Plant Metabolic Network site contains the world's largest collection of publically available metabolic information for plants.

Provided by Carnegie Institution for Science

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