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New databases harvest a rich bounty of information on crop plant metabolism

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The Plant Metabolic Network, which is based at Carnegie's Department of Plant Biology, has launched four new online databases that offer an unprecedented view of the biochemical pathways controlling the metabolism of corn, soybeans, wine grapes, and cassava—four important species of crop plant. The new databases will serve as a critical resource for scientists working with these species to increase crop production, enhance biofuel development, or explore novel medicines.

Meeting the ever-expanding demand for food, biofuel and phyto-pharmaceutical production will require a comprehensive understanding of the enzymes, biochemical pathways and regulatory networks that control metabolism in plants. The goal of the Plant Metabolic Network is to facilitate such understanding by providing a detailed, genome-scale view of the chemical reactions taking place in plant cells. These metabolic reactions include those that convert carbon dioxide and sunlight into chemical energy, import essential mineral nutrients from the soil into plant roots, aid plants in defending against environmental stress, and otherwise allow plants to maintain life. By providing rich information on these processes, the Plant Metabolic Network enables efforts to elucidate steps in poorly understood plant biochemical processes, as well as discover unique, previously uncharacterized enzymes important to plant life.

The Plant Metabolic Network research team consists of plant scientists, scientific curators, post-doctoral scholars, and student interns. It is led by Carnegie staff scientist Sue Rhee. The group employs a number of approaches to generate the information housed in each database, integrating techniques and concepts from a wide range of fields including molecular sequence analysis, artificial intelligence, statistics, plant molecular biology, and plant biochemistry.

The team created a computational pipeline called E2P2 to perform metabolism-related discovery on sequenced plant genomes in order to place the rapidly expanding pool of plant genomic and transcriptomic sequence data into a metabolic framework. Importantly, the pipeline allows for a consistent, systematic, and high throughput approach for metabolism-related analysis of plant genome data. The data generated by the pipeline is rigorously reviewed using the scientific literature to ensure the quality of each released database. Up to ten more databases will be forthcoming later this year. Corn, soybeans, wine grapes, and cassava were selected for early release because of their economic and agricultural importance to various regions.

"Wine grapes are an important crop for the state of California; corn and soybeans are the number one and two crops of the United States, both as a source of food and biofuel; cassava—also called manioc and yuca—is one of the most-common sources of food worldwide and a tremendously important crop for combating hunger," said Dr. Rhee.

"That's why we decided to release the databases for these plants right away, even before we started preparing a manuscript describing this work, to help researchers get started in improving production and yield of these crucial crops."

More information: http://www.plantcyc.org/

Provided by Carnegie Institution

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