New study released on plant metabolism

An international team of scientists has released a study on the relationship between plant genomes and cell metabolism

A recent study sheds new light on metabolic networks in plants. A metabolic network is the overall set of biochemical reactions in a cell. As more organisms have their genomes sequenced, it has become possible to investigate their metabolic networks in detail and understand more about the relationship between individual genes and metabolic processes.

The scientists used *Arabidopsis thaliana*, or Thale Cress, a small flowering plant related to cabbage and mustard, which was the first plant to have its genome fully sequenced. The team included several scientists from RIKEN's Plant Science Center in Yokohama, as well as researchers from Sweden, Germany and elsewhere in Japan.

They studied the differences between the metabolic networks of wild-type *A. thaliana* and two genetically engineered mutant varieties. One of these mutants lacked a gene that enables the plant to produce chemicals known as flavonoids, which protect the plant against environmental stresses such as ultraviolet light. The other was engineered to accumulate up to 40 times more of an amino acid called methionine than occurs in a wild-type plant.

Recent advances have made it possible to analyse the levels of individual metabolites, the products of the cell's metabolism, with great precision. The team used a technique known as gas chromatography time-of-flight mass spectrometry, or GC-TOF-MS. In this method, the cell molecules are ionized, meaning they are given an electrical charge, and then accelerated by an electrical field of a known strength. Different types of molecules take different amounts of time to fly to the detector, and by measuring this time of flight it is possible to identify the individual chemicals present in a cell. In future, scientists hope to build GC-TOF-MS databases of plant metabolisms and make them available to the public, as has been done with many genomes as they have been sequenced.

The team found that the levels of some metabolites remained the same regardless of
the genetically engineered mutation. They also invented a method for identifying metabolites that were unique in each of the mutants. The focus of their research was on understanding the basic regulation mechanisms of plant metabolisms, and they believe that those metabolites whose levels were unchanged give clues about those mechanisms.

One particular experiment focused on the adaptive mechanism of plants to UV light. They did this by shining UV light on wild-type A. thaliana and a mutant plant engineered so it could not produce the flavanoids that normally protect against UV light. They then compared the level of metabolites in the two plants. Surprisingly, they found that the mutant was still able to adapt to defend itself. The metabolic network was adapted in a way that still protected the plant, suggesting that the plant has a backup mechanism for defence against harmful UV rays.

This research also lays the groundwork for future studies of plant metabolisms. In particular, the team believes they have identified the group of genes responsible for regulating the metabolic networks of cells. In future, it is likely that the precise function of each gene involved in regulation will be better understood.

Original work:

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