Gene library constructed for cassava plant

A team of scientists from RIKEN and a research institute in Colombia have assembled a large library of genetic data on the cassava plant, an important food plant in developing countries, especially in Africa. The researchers aim for the gene library to be a resource in understanding the functions of each gene of the plant, to aid in improving it through genetic modification.

Cassava is used in many foods for human consumption, as well as for animal fodder and as a raw material for industrial goods such as plywood. It is one of the highest-yielding starch-producing crops in the world, with a yield greater than rice or corn and second only to sugar cane. Because of this, and because producing starch from cassava is relatively cheap, it is now being eyed as a biomass source for fuel production. Given the current high oil prices, with many countries moving to increase biofuel use, this is significant. Understanding the cassava genome will help to develop the plant to this end.

The scientists participating in the project were from RIKEN's Genomic Sciences Center and Plant Science Center in Yokohama, and from the International Center for Tropical Agriculture in Cali, Colombia. Cassava is native to South America, and the continent is a major global producer.

The primary method used by the team was to compare the DNA of cassava with that of other plants where the genome and its functioning are already somewhat understood. These included poplar and Arabidopsis, a small plant related to mustard that is widely used in genetic research, and was the first plant to have its genome sequenced. When the same gene is found in cassava as in another plant where its function is already known, it is an indicator of its likely function in cassava as well.

The team built a full-length complementary DNA (cDNA) library for cassava under normal conditions, as well as under stressful conditions such as excessive heat, drought, high aluminum content in the soil and post-harvest physiological deterioration. They then sequence-characterized them using expressed sequence tags (ESTs), short
sequences of nucleotides often used to identify gene transcripts, and which are commonly used in gene discovery and gene sequence determination. Because these sequences consist of cDNA, complementary to messenger RNA, which has already been transcribed from a DNA template, the ESTs represent portions of genes that have already been expressed. The researchers compared these to ESTs in other plants, such as Arabidopsis, and were able to assign a functional classification to many of them.

One characteristic of cassava is its ability to grow in harsh conditions. It can thrive in marginal, low fertility, acidic soils, where it is particularly efficient in its use of nutrients. Due to its extreme drought resistance, it is also an important food source for areas prone to or suffering from drought-related famine. It is most productive however, in hot, humid climates with plenty of sunshine.

Traditional breeding methods have had some success in developing new cassava varieties, but progress has been slow. But using genetic modification, cassava may be made resistant to bacterial and viral diseases and pests. To this end, the scientists concentrated on finding genes that help the plant adapt to environmental stress. The library is particularly rich in such genes, the team said in its report. It will therefore be an important resource for gene discovery, characterization and cloning. The researchers said they hope that in the near future it will aid in further understanding of the cassava genome.

Original work:
Sakurai, T., Plata, G., Rodríguez-Zapata, F., Seki, M., Salcedo, A., Toyoda, A., Ishiwata, A., Tohme, J., Sakaki, Y., Shinozaki, K. and Ishitani, M.
Sequencing analysis of 20,000 full-length cDNA clones from cassava reveals lineage specific expansions in gene families related to stress response. BMC Plant Biology, published online on Dec. 20, 2007

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