Scientists identify two new proteins connected to plant development

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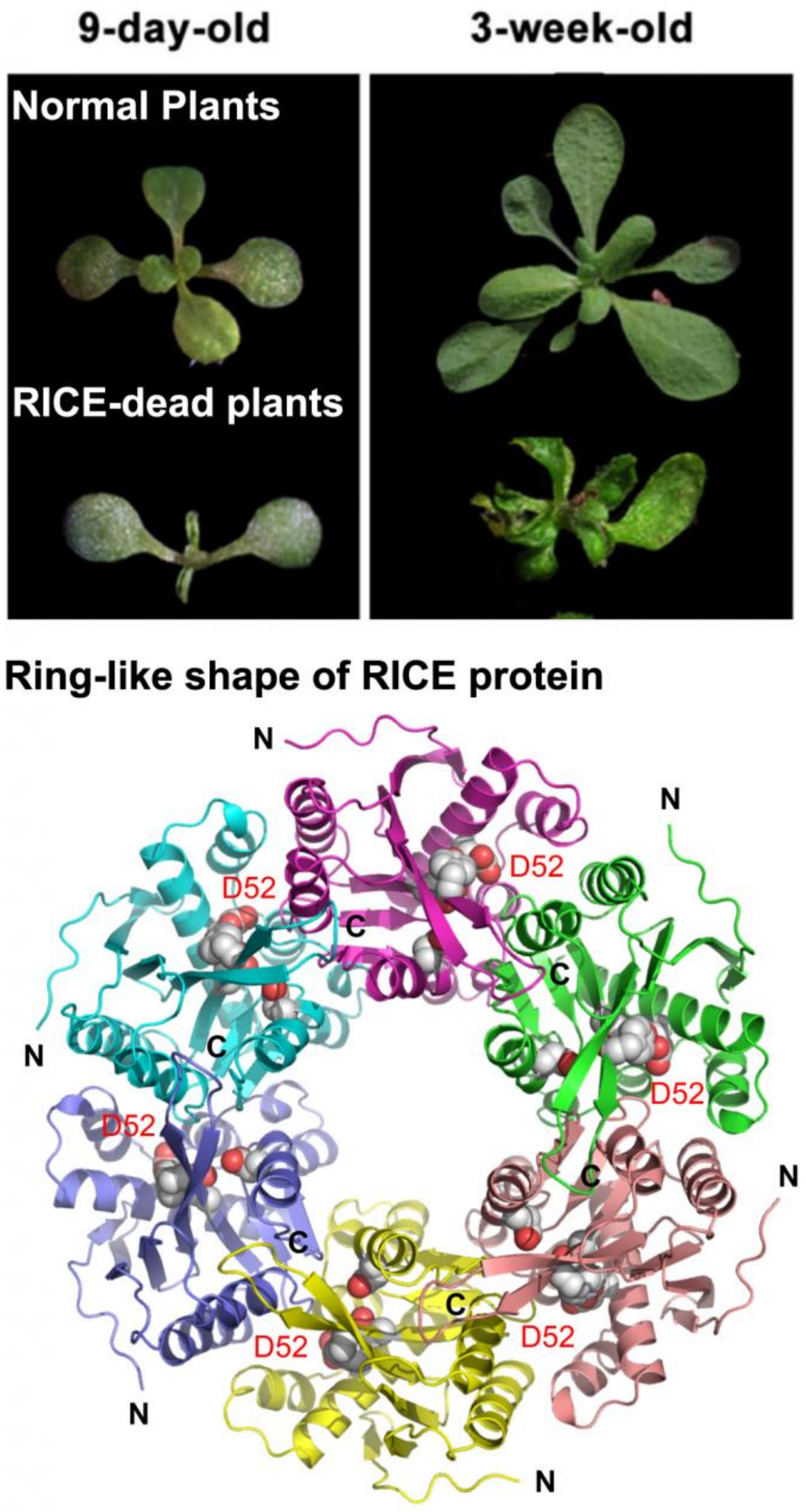
9-day-old
3-week-old
Normal Plants
RICE-dead plants
Ring-like shape of RICE protein
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The discovery in the model plant Arabidopsis of two new proteins, RICE1 and RICE2, could lead to better ways to regulate plant structure and the ability to resist crop stresses such as drought, and ultimately to improve agricultural productivity, according to researchers at Texas A&M AgriLife Research. Credit: Dr. Xiuren Zhang

The discovery of two new proteins could lead to better ways to regulate plant structure and the ability to resist crop stresses such as drought, thus improving agriculture productivity, according to researchers at Texas A&M AgriLife Research.

The two proteins, named RICE1 and RICE2, are described in the May issue of the journal *eLife*, based on the work of Dr. Xiuren Zhang, AgriLife Research biochemist in College Station.

Zhang explained that DNA contains all the information needed to build a body, and molecules of RNA take that how-to information to the sites in the cell where they can be used.

But cells make their own RNA, and they only need so much in order to develop properly and respond well to their environment. So plants make an even smaller molecule, called microRNA or miRNA, that removes the extra RNA and stop it from making proteins. That process is called RNA silencing.

Understanding silencing is important because researchers can use the technique to help a plant overcome barriers to growth or ability to deal with unfavorable environments by tweaking the amount of RNA.

"One key player in RNA silencing is the multi-component complex called RISC (RNA-induced Silencing Complex), which contains microRNA and enzymes called AGOs," Zhang said. "MicroRNA starts as twins, so to speak, but one of the twins leaves and disappears when AGO protein moves in."

Once the microRNA has identified its RNA target for silencing, the AGOs cut the RNA into two pieces, known as the 5-prime and 3-prime cleavage fragments.

"These fragments are basically the starting and ending sections of RNA molecules. But, the two resulting fragments must be cleared away rapidly, so the RISC can move on to the next target," he said.

"It's like eating in a restaurant during rush hour," Zhang explained. "You eat quickly and leave. Then the waitstaff clears the table and resets it to serve the next guests."

Researchers have known how the 3-prime cleavage fragment was removed but were less clear how the 5-prime cleavage fragment was dealt with, he said.

"What was known was that the 5-prime cleavage fragment is marked with a chemical called uridine," Zhang said. "Somehow, uridine tells the RISC, which holds the miRNA, that this fragment needs to be destroyed."

Using proteomic analysis, a powerful biochemical approach, Zhang and colleagues deciphered the constituents of one kind of RISC in arabidopsis, a model plant often used in research. They found RICE, or RISC-Interacting Clearing Exoribonuclease, proteins there.

Further study of the biochemical features of RICE proteins showed them to be enzymes that degrade RNA. Using crystallography, Dr. Pingwei Li, AgriLife Research biochemist in College Station, found that RICE1 has a ring-like shape with six identical molecules.

"This ring-shape structure is very important because the protein can not survive if the ring-shape is disrupted," Li said. That would lead to problems during the development of the plant.

Zhang and colleagues then analyzed the shape of RICE1 and identified its 'active' region, which is responsible for degrading the RNA fragments, hidden on the adjacent site of two RICE molecules.

"When these active regions were blocked, the microRNA levels were low, but the 5-prime cleavage fragments that are marked with uridine were high," he said. "Also, the RISC complex could not work properly, which led to problems during the plant growth and development."

These results suggest that RICE proteins degrade 5-prime cleavage fragments modified with uridine to keep RISC alive.

RICE proteins are similar in plants and animals, Zhang said, so it is likely their counterparts in humans will have a similar role to the plant proteins and thus be important for development in the human body.

Zhang said the next challenge will be to explore how RICE proteins work in more detail, which may lead to new ways to manipulate the efficacy of RISC and the levels of microRNAs to alter organism architecture and to improve stress tolerance in biotechnological applications.

More information: Zhonghui Zhang et al. RISC-Interacting Clearing 3'- 5' Exoribonucleases (RICEs) degrade uridylated cleavage fragments to maintain functional RISC in Arabidopsis, *eLife* (2017). DOI:

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