

Scientists work with RNA silencing and plant stem cells

May 16 2011

Research on controlling the stem cells of plants could eventually lead to learning how to make them produce more fruit, seed and leaves, according to Dr. Xiuren Zhang, Texas AgriLife Research scientist and professor with the Texas A&M University department of biochemistry and biophysics. Results of a nearly three-year project led by an AgriLife Research team headed by Zhang was published in *Cell*, one of the most cited scientific peer-review journals in the world.

"Working with the shoot meristem area, we may (eventually) control fruit and seed yield or plant mass by manipulating the development and maintenance of plant <u>stem cells</u>. We can also engineer plant shapes by doing this," Zhang said.

In plants, the shoot meristem area is composed of undifferentiated cells, which means they can be programmed by the plant to become various structures — leaf, stem, branches flower, etc. — much as mammalian stem cells can be programmed to produce different organs, he said.

The team worked with *Arabidopsis*, a plant also known as rock cress, which is related to cabbage and mustard. *Arabidopsis* is often used for studying plant biology because it is the first plant to have its entire genome sequenced.

Previous studies had shown that the an *Arabidopsis* gene known as argonaute 10, or simply AGO10, plays a critical role in regulating meristem cell development. *Arabidopsis* has 10 AGO genes, and it was



known that AGO10 is involved in various biological processes such as meristem development and proper leaf formation, but by exactly what mechanism it performed these roles was not clear, Zhang said.

"However, although the genetic functions of AGO10 have been described, the molecular mechanism by which it regulates SAM (shoot apical meristem) development remained unknown," Zhang wrote in the Cell article. "Here we demonstrate that AGO10 specifically interacts with miR166/165."

The abbreviation miR166/165 refers to microRNA, a type of small RNA molecule that regulates gene expression, Zhang explained. MicroRNAs are deceptively simple in structure, often only about 20 bases in length, whereas regular RNA may be composed of hundreds or thousands of bases.

Though composed of only a few bases, microRNAs often perform a critical function by switching the expression of certain genes off. Turning off gene expression is just as important a regulatory mechanism in plant development as switching genes on, Zhang noted.

Interfering with microRNA being loaded into a 'decoy' protein can cause various mutant phenotypes such as stunted growth in *Arabidopsis* <u>plants</u>.

This switching-off function of microRNA has been known for more than a decade. Further work had shown that it is microRNAs that actually guide the argonaute to actually do the switching off, sort of how a software application controls a smart phone or computer, according to Zhang.

Work by Zhang's team had demonstrated that if miR166/165 did not load into AGO10, or the AGO10 gene was missing, then the meristem part of the plant would be deformed, but why this was so remained a



mystery.

Zhang and his team proposed that AGO10 functions as "a decoy for miR166/165" to prevent it being loaded into other AGO proteins, particularly AGO1, which "plays a potent but inhibitory role in correct development of the meristem area cells," he said.

"In other words, if miR166/165 is loaded into AGO1, they would shut their <u>target genes</u> off," Zhang said. "But if miR166/165 is loaded into AGO10 protein, they won't switch-off target genes. Thus, AGO10 works in an opposite way compared to AGO1: It protects target genes and secures their expression."

Provided by Texas A&M AgriLife Communications

Citation: Scientists work with RNA silencing and plant stem cells (2011, May 16) retrieved 26 April 2024 from <u>https://phys.org/news/2011-05-scientists-rna-silencing-stem-cells.html</u>

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