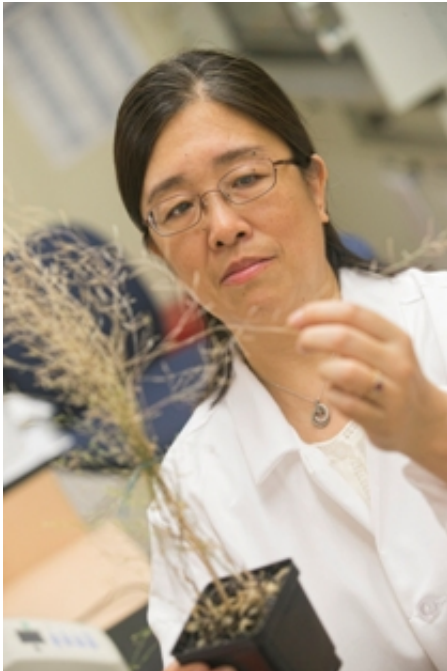


Planting a new perspective on climate research

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Stony Brook's Alison Liu examines mature seed production in an Arabidopsis plant.

(Phys.org) —A study on the mechanisms of how plants respond and adapt to elevated levels of carbon dioxide (CO₂) and higher temperatures has opened a new perspective in climate research. Lead researcher Qiong A. Liu (Alison) of the Department of Biochemistry and Cell Biology at Stony Brook University found that elevated CO₂ and higher temperatures affect the aspect of gene expression in plants that

control flowering time and cell proliferation.

The results of the study, "The Effects of Carbon Dioxide and Temperature on microRNA Expression in Arabidopsis Development," are published July 31 in the online journal *Nature Communications*.

Elevated CO₂ levels in the atmosphere have enhanced the [greenhouse effect](#) and resulted in [climate change](#)—and continued climate change within this century is inevitable. But how do these changes impact plants on a [cellular level](#)? To discover the answer, Liu focused on examining the impact that increased levels of CO₂ and increased temperature, each separately had on small RNAs in *Arabidopsis thaliana*, small [flowering plants](#) that only need about six weeks to go from germination to seed maturation.

Small RNAs are important regulators of gene expression in nearly all eukaryotes —organisms whose cells contain a nucleus and other structures within membranes. Their expressions can be altered in response to environmental stress. MicroRNAs (or miRNAs) belong to one of two types of small RNAs that function to silence the expression of their regulated [target genes](#). Therefore, increased levels of miRNAs can reduce their target gene expression, and vice versa. Since miRNA target genes are often important regulators in specific biological pathways, the identification of miRNAs that are changed in expression by [environmental stresses](#), such as elevated CO₂ concentration and temperature, can enable scientists to identify the biological pathways that are involved in regulating plant [phenotypes](#) in response to a changing environment.

"This is the first small RNA paper in the area of climate change," Liu says. "CO₂ has never been shown previously to regulate small RNA expression, and temperature-related small RNAs studies have been done previously, but only at freezing or low temperatures (the optimum

temperature for Arabidopsis is at 23°C). We found that a 3-6°C increase in temperature from optimum temperature regulates a different set of miRNAs from other temperature-regulated miRNAs, but nearly all miRNAs affected by doubling the atmospheric CO₂ concentration in an opposite direction."

Using the next generation of sequencing in combination with statistical and computational analyses, Liu and her research team provided the first genome-wide profiling that demonstrated that increasing atmospheric CO₂ concentration and temperatures within the ranges that will occur within this century can alter the expression of four functional groups of miRNAs: controlling [flowering time](#), cell division and proliferation, stress responses, and potentially cell wall carbohydrate synthesis.

"These results indicate that under global warming conditions, plant grain and biomass production can be changed through altering the expression of these miRNAs," Liu explains. "Given that nearly all of these miRNAs are conserved across multiple species, identification of these miRNAs provide us a starting ground to improve plant yields, particularly those that are economically important, to meet the upcoming challenges of global warming."

Liu adds that one pathway, a miRNA (miR156)-regulated pathway, was identified to most likely mediate elevated CO₂ concentration-induced early flowering. This result was obtained independently from other three relevant studies published at the same time in the journal *Science* and *Elife*, which demonstrated that sugar, the primary product of photosynthesis, can also regulate this pathway.

The study findings also raise other questions. Liu hopes to answer these questions by advancing the research.

"So far, we have only tested one concentration of CO₂, and 3 to 6°C

changes of temperature. We hope to get the data in a gradient of CO₂ and temperature conditions. In addition, we also will be interested in understanding how these conditions affect miRNA expression in several other tissues—root, shoot, and flower tissues, for example, at different developmental stages," she says. "In addition, further genetic investigation on identified miRNAs individually will shed new light on how their regulated pathways function in adaption to climate change."

The researcher is now testing how combined conditions of elevated CO₂ concentration and elevated temperature affect miRNAs expression. These are important experiments, she says, given that these two conditions are known to affect several miRNAs expression in the opposite directions. It is also practically more meaningful as climate change really has both CO₂ concentration and temperature increases at the same time.

Liu is also preparing a manuscript that is related to how elevated CO₂ concentration affects the genomic DNA methylation, which is another regulatory mechanism to regulate gene expression and genome stability.

Provided by Stony Brook University

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