

Hot temperatures can trigger an RNA response in plants

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A new study used rice seedlings to demonstrate that the stress of hotter temperatures may trigger a response in a plant's RNA to manage the change in its environment. Credit: Peter Nguyen

The stress of hotter temperatures may trigger a response in a plant's RNA, or ribonucleic acid—part of a cell's genetic messaging system—to help manage this change in its environment, according to a team of Penn State researchers.

In a study on rice plants, the researchers found that a sudden increase in heat led to changes in the structure of the plant's RNA, which was linked to a loss in the number of its messenger RNAs—or mRNAs. The mRNA molecule is a particular type of RNA, which transfers DNA instructions to the ribosome in a cell during the protein-making process.

Because plants are not able to regulate their own temperatures, as humans do, or move from the heat source, this process may be one of the ways plants cope under hot temperatures and drought conditions, said Sarah M. Assmann, Waller Professor of Biology, Eberly College of Science.

While more studies would be needed, this study may serve as an important first step to help farmers produce more heat and drought-resistant crops, according to the researchers, who announced their findings today (Nov. 5) in the *Proceedings of the National Academy of Sciences*.

"Rice is a staple food for half the world's population and is particularly important for subsistence agriculture in some parts of the world, so it's a vital food crop," said Assmann. "With climate change—and with the goal that we need to increase food production to feed the world's

growing population—we are always trying to understand how plants are responding to climate stress, so, potentially, in the future, we could improve crop varieties, either through breeding or other mechanisms, to get better stress tolerance and better yields."

The researchers examined more than 14,000 different RNAs to look for changes in the molecules' intricately folded structures that could signal acute heat stress, said Philip Bevilacqua, Distinguished Professor of Chemistry and of Biochemistry and Molecular Biology. Unlike the intertwined double strand—or double helix—of the DNA molecule, RNA is single-stranded.

"Because DNA has two strands, it's really locked into very few different folds, but RNA, because it is not tied up with another strand, is able to fold back on itself, so there are much more complex folds in the RNA," said Bevilacqua.

To create heat stress, the researchers subjected one group of two-week old rice seedlings to above normal temperatures—108 degrees Fahrenheit—for just ten minutes and compared those plants to a control group of plants growing at 72 degrees Fahrenheit.

"We chose such a short time because the re-folding of the RNA is a fast process, whereas the downstream processes, such as protein production, are slower and we were particularly interested in how the RNA refolded," said Bevilacqua.

The researchers found that the folds in the RNA of the [plants](#) suffering from [heat stress](#) were looser than those in the [control group](#). The unfolding of the mRNA, then, correlated with a loss in the abundance of mRNA, suggesting that mRNA unfolding promotes its degradation, a method that cells use to regulate which genes express and when.

"One of the main things we discovered is that there's a correlation between the RNAs that tend to unfold at their ends and a reduction in the abundance of those RNAs and since the RNAs code for proteins you can loosely infer that would then result in a reduction of the encoded proteins, including enzymes and all the myriad functions that proteins perform," said Assmann.

According to Bevilacqua, this process offers hints on next steps in future research into more heat and drought resistant crops.

"So, if loss of structure results in loss of abundance and if that loss of abundance is not optimal, then you could imagine that we could change the sequences of the ends of the RNA, making them more stable, and, therefore, stabilize the production of those proteins."

Zhao Su, lead author on the paper, said the study also uncovered new insights into [gene regulation](#).

"This exciting study reveals a new layer of gene regulation that was previously not appreciated," Su said. "In particular, we showed that mRNAs encoding one specific type of regulatory proteins, transcription factors, are especially targeted for degradation by unfolding under high temperatures."

According to both Bevilacqua and Assmann, studies, such as this RNA analysis, which is one of the first to analyze the RNA process in the plant itself, or in vivo, could not happen without the interdisciplinary teamwork of their labs. Bevilacqua's and Assmann's labs have been collaborating for about ten years, according to Assmann.

"What I really think is interesting about this study in particular is that it incorporates all of the different skill sets and all the different talents of our labs," said Assmann. "This is what makes science exciting."

More information: Zhao Su et al., "Genome-wide RNA structurome reprogramming by acute heat shock globally regulates mRNA abundance," *PNAS* (2018).

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