

# Research characterizes evolution of pathway for reproductive fitness in flowering plants

February 11 2019

---



Credit: CC0 Public Domain

Small RNAs (sRNAs) are key regulators involved in plant growth and development. Two groups of sRNAs are abundant during development of pollen in the anthers—a critical process for reproductive success. One of these pathways for sRNA production, previously believed present in grasses and related monocots, has now been demonstrated to be present widely in the flowering plants, evolved over 200 million years ago, and is arguably one of the evolutionary innovations that made them so successful.

The research, led by Blake Meyers, Ph.D., member, Donald Danforth Plant Science Center and professor, Division of Plant Sciences, University of Missouri and his collaborators at South China Agriculture University, the University of Delaware, and the University of Maryland, published their findings, "24-nt reproductive phasiRNAs are broadly present in angiosperms," in the journal *Nature Communications*.

"We've been studying this [pathway](#) extensively in maize as part of a project supported by the National Science Foundation. Quite unexpectedly, we found the pathway in the tropical tree that produces lychee fruit, which, as a eudicot, is distant from the grasses. When we analyzed other eudicot plant genomes, we found that this pathway was present in many of them—a complete surprise to us, since we thought it was only in the monocots," said Meyers. "There are some key differences between the pathway in eudicots and in grasses, and characterizing these in our study has given us insights into how sRNA and reproductive biology has diverged in these groups of [plants](#)."

Meyers explained that the long-standing view was that this pathway was specific to the grasses. In a companion piece of work, Meyers and his colleagues have demonstrated that maize, a monocot and member of the [grass](#) family, requires this pathway for full male fertility. But their paper in *Nature Communications* upends this view, demonstrating that the pathway emerged prior to the split between eudicots and monocots. One of the big mysteries they are trying to address is the precise molecular function of these sRNAs in pollen development. To address this question in eudicots, Meyers and his team are using *Fragaria vesca*, a diploid, also known as woodland strawberries as a model for their experiments. The genome of *Fragaria vesca* was sequenced in 2010 and is often used as a model due to its small genome size, short reproductive cycle and ease of propagation.

"The explosion of [flowering plants](#) was a remarkable thing in evolution,

and they represent most species used for food and fuel," said Meyers. "Understanding the genetic mechanisms by which flowers develop will be important for improving [crop yields](#) and breeding better varieties, particularly for making the high-yielding hybrid crops that support modern agriculture."

**More information:** Rui Xia et al, 24-nt reproductive phasiRNAs are broadly present in angiosperms, *Nature Communications* (2019). [DOI: 10.1038/s41467-019-08543-0](#)

Provided by Donald Danforth Plant Science Center

Citation: Research characterizes evolution of pathway for reproductive fitness in flowering plants (2019, February 11) retrieved 26 April 2024 from <https://phys.org/news/2019-02-characterizes-evolution-pathway-reproductive.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.