



## OPEN ACCESS

EDITED AND REVIEWED BY  
Simon Gilroy,  
University of Wisconsin-Madison,  
United States

## \*CORRESPONDENCE

Jiabao Ye  
✉ yejiabao@yangtzeu.edu.cn  
Feng Xu  
✉ xufeng@yangtzeu.edu.cn

RECEIVED 06 February 2024

ACCEPTED 27 February 2024

PUBLISHED 11 March 2024

## CITATION

Wang C, Zeng S, Liu Y, Ye J and Xu F (2024)  
Editorial: Non-coding RNA regulation of  
secondary metabolism in plants.  
*Front. Plant Sci.* 15:1382709.  
doi: 10.3389/fpls.2024.1382709

## COPYRIGHT

© 2024 Wang, Zeng, Liu, Ye and Xu. This is an  
open-access article distributed under the terms  
of the [Creative Commons Attribution License  
\(CC BY\)](https://creativecommons.org/licenses/by/4.0/). The use, distribution or reproduction  
in other forums is permitted, provided the  
original author(s) and the copyright owner(s)  
are credited and that the original publication  
in this journal is cited, in accordance with  
accepted academic practice. No use,  
distribution or reproduction is permitted  
which does not comply with these terms.

# Editorial: Non-coding RNA regulation of secondary metabolism in plants

Caini Wang<sup>1</sup>, Shaohua Zeng<sup>2</sup>, Yongliang Liu<sup>3</sup>, Jiabao Ye<sup>1\*</sup>  
and Feng Xu<sup>1\*</sup>

<sup>1</sup>College of Horticulture and Gardening, Yangtze University, Jingzhou, China, <sup>2</sup>South China Botanical Garden, Chinese Academy of Sciences (CAS), Guangzhou, China, <sup>3</sup>Department of Plant and Soil Sciences and Kentucky Tobacco Research and Development Center, University of Kentucky, Lexington, KY, United States

## KEYWORDS

secondary metabolism, lncRNA, miRNA, regulatory mechanism, plant

## Editorial on the Research Topic

### Non-coding RNA regulation of secondary metabolism in plants

Secondary metabolites have been a recent Research Topic for many years in plants. What we usually see, smell and taste are the primary metabolites that give plants their color, scent and acidity. However, the synthesis and regulation of secondary metabolites, such as terpenoids, flavonoids, alkaloids, phenolic acids, and other secondary metabolites, directly affect the production of primary metabolites in plants. They are multifunctional, defending against natural enemies, resisting insects and diseases, signaling, and producing medicinal components that are beneficial to the human body, among other things. Based on this, the biosynthesis and regulation of plant secondary metabolism has been highly active Research Topic for many years. Many researchers have been studying the complex regulatory network formed by enzyme genes and transcription factors (TFs) to understand the synthesis and regulation of these secondary metabolites. In recent years, more and more studies have revealed that non-coding RNAs are involved in this regulatory network, mediating the expression of TFs indirectly affecting the biosynthesis of plant secondary metabolites.

Non-coding RNAs are a class of RNAs that do not code for proteins, including short-stranded miRNAs and long-stranded is concerns. They can attach to multiple target genes or multiple non-coding RNAs that interact with the same protein, DNA, or RNA, and thus play a role in cellular functions. In this Research Topic, we present many articles that have provided new insights into plant secondary metabolism biosynthesis. [Lin et al.](#) compared the red leaves of the bud mutation branches of *Acer pictum subsp. mono* with those of the green leaves of the wild-type branches and found a significant decrease in chlorophyll and carotenoids, and a significant increase in anthocyanins and various antioxidant enzymes in red leaves. The miR160b targeting *ApSUS*, miR6300 targeting *ApTPR*, *ApUFGT*, and *ApNRT*, and miR396g targeting *ApUGP2* were detected by transcriptome and miRNA sequencing, which suggests that miR160b, miR6300, and miR396g are the key miRNAs for the regulation of the stabilization of anthocyanin accumulation in the process of leaf color change. [Hou et al.](#) revealed that 6 mM exogenous salicylic acid (SA) induced the

accumulation of folate (5-methyltetrahydrofolate) and methionine (Met) in *Setaria italica* (L.) P. Beauv. Hou et al. found that in *S. italica*, the expression level of the *DHFR1* gene, which is associated with folate biosynthesis, was up-regulated in Nov-m0139-3p. On the other hand, *DHFR2* was down-regulated in Nov-m0731-5p and up-regulated 4.27-fold in Nov-m0461-5p and 1.32-fold in Nov-m0664-3p. Additionally, *CYSC1*, which is associated with Met synthesis, was regulated by Nov-m0319-3p, Nov-m0416-5p, and Nov-m0042-5p.

Along with this, the researchers found that non-coding RNAs can be modified by N<sup>6</sup>-methyladenosine (m<sup>6</sup>A) and these RNAs can have important functions during plant growth. Rudy et al. revealed that m<sup>6</sup>A can post-transcriptionally modify RNA and induce leaf senescence in barley. Additionally, transgene is particularly susceptible to small RNA (sRNA)-mediated silencing, and different terminators can differentially affect the production of siRNAs at the level of the transgene and its expression. de Felippes et al. identified the HSP18.2 terminator in *Arabidopsis thaliana* that improves high-level transgene expression, thus providing a new strategy for achieving robust and efficient transgene expression.

Besides miRNA gene expression, which is involved in plant growth and development and secondary metabolism, lncRNAs can also be involved in the regulation of plant growth and development through transcriptional and post-transcriptional regulation of gene expression. Jiang et al. found an increase in seed germination and a significant decrease in seed dormancy during seed maturation by treating wheat seeds at high and ambient temperatures. Whole-transcriptome sequencing analysis revealed that the high-temperature-mediated gibberellin (GA) biosynthesis gene *TaGA20ox1* (TraesCS3D02G393900) was involved in dormancy, and the *TaCDPK21* (TraesCS7A02G267000) gene of the calcium signaling pathway showed a negative regulatory role in dormancy. In addition, not only the newly identified miR27319, which is located at the key node of this regulatory network, acts positively in seed dormancy, but also *TaDOG1-3A*, *GID1-1D*, *TaMFT-3A* and *TaMFT-3D* target novel lncRNAs (MSTRG.4103020.1, MSTRG.861889.1, MSTRG.729470.1 and MSTRG.891662.2) to regulate the molecular mechanism of seed dormancy.

Here, we report that noncoding RNAs are involved in the biosynthesis and regulation of plant secondary metabolites, providing valuable insights into the study of natural plant

secondary metabolism. So far, the regulation mechanism of secondary metabolite biosynthesis has attracted extensive attention, and many of studies have focused on the key genes in the secondary metabolite biosynthesis pathway. In the future, it is crucial to invest in the functional studies of non-coding RNAs related to secondary metabolite biosynthesis, which is conducive to the in-depth unraveling of complex secondary metabolite biosynthesis mechanisms and metabolic pathways.

## Author contributions

CW: Writing – original draft. SZ: Writing – review & editing. YL: Writing – review & editing. JY: Writing – original draft, Writing – review & editing. FX: Writing – original draft, Writing – review & editing.

## Acknowledgments

We thank all the authors for contributing their scholarly work to our Research Topic, and we would like to express our deep gratitude to all reviewers for their valuable help in the evaluation of the manuscript.

## Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

## Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.