



Transcriptional and post-transcriptional regulation of the miR171-*LaSCL6* module during somatic embryogenesis in *Larix kaempferi*

Qiao-Lu Zang¹ · Yao Zhang² · Su-Ying Han² · Wan-Feng Li¹ · Li-Wang Qi¹

Received: 15 June 2020 / Accepted: 21 August 2020 / Published online: 4 September 2020
© The Author(s) 2020

Abstract

Key message Expression analysis of *Larix kaempferi* mature miR171s and their primary transcripts and target gene *LaSCL6* during somatic embryogenesis revealed the transcriptional and post-transcriptional regulation of the miR171-*LaSCL6* module.

Abstract Somatic embryogenesis provides a useful experimental system for studying the regulatory mechanisms of plant development. The level and activity of microRNA171 (miR171) fluctuate during somatic embryogenesis in *Larix kaempferi*, but the underlying mechanisms are still unclear. Here, in *L. kaempferi* we identified five members of the miR171 family, which cleave *LaSCL6* mRNA at different sites. In addition, we improved the method of measuring miRNA activity in a more direct way. Furthermore, we measured the expression patterns of mature miR171s and their primary transcripts during somatic embryogenesis in *L. kaempferi* and found that their patterns differed, indicating that the transcription of *MIR171* genes and the subsequent cleavage of their intermediate products are regulated. Taken together, our findings not only offer a means to study the regulation of miRNA activity, but also provide further insight into the regulation of *L. kaempferi* somatic embryogenesis by miR171-*LaSCL6*.

Keywords Gene expression · Japanese larch · *LaSCL6* · microRNA171 · microRNA activity · Embryogenic cultures

Introduction

Somatic embryogenesis is not only a valuable technique in clonal propagation and genetic improvement, but is also an ideal experimental system in which to study the mechanisms that regulate plant development (Dobrowolska et al. 2017; Godee et al. 2017; Zhang et al. 2019). The induction of embryonic cultures and the maintenance of embryonic potential are important for clonal plant production through

somatic embryogenesis. However, after certain subculture period, the conifer embryonic cultures may become non-embryogenic and this prevents the formation of somatic embryos and limits utilization of this technique (Klimaszewska et al. 2016; Zhang et al. 2010). Thus, studying the molecular events controlling various stages of somatic embryogenesis could lead to a better understanding of the whole process and potentially improve the efficiency of this technique.

Many genetic factors, including microRNAs (miRNAs), have been found to control the process of somatic embryogenesis, such as *AGAMOUS-LIKE* (Gao et al. 2020), *FUSCA* (Liu et al. 2018), *LEAFY COTYLEDON* (Wang et al. 2020), miR156 (Long et al. 2018), miR166 (Li et al. 2016), and miR171 (Li et al. 2017). MiRNAs repress gene expression through mRNA degradation and translational inhibition (Awan et al. 2018; Djuranovic et al. 2012; Yang et al. 2019). Recently, the function of miR171 in somatic embryogenesis of angiosperm and gymnosperm has attracted increasing attention (Li et al. 2017, 2014; Zang et al. 2019). The miR171 family is highly conserved, and functions via regulating its target gene

Communicated by K. Klimaszewska.

Electronic supplementary material The online version of this article (<https://doi.org/10.1007/s00468-020-02026-2>) contains supplementary material, which is available to authorized users.

✉ Wan-Feng Li
liwf@caf.ac.cn

✉ Li-Wang Qi
lwqi@caf.ac.cn

Extended author information available on the last page of the article

SCARECROW-LIKE6 (*SCL6*, also known as *HAIRY MERISTEM* or *LOST MERISTEMS*), which is a member of the *GRAS* (*GAI-RGA-SCR*) family (Jiang et al. 2018; Llave et al. 2002; Pysh et al. 1999; Wang et al. 2010). In citrus, lily and larch, the abundance of mature miR171 is higher in embryogenic cultures than that in non-embryogenic cultures (Li et al. 2017; Wu et al. 2015; Zhang et al. 2010). Furthermore, higher miR171 activity occurs in larch embryogenic cultures (Li et al. 2014). These data show that during somatic embryogenesis, the level and activity of miR171 fluctuate, as to the underlying regulatory mechanisms, little is known.

In plants, there are generally four steps in the processes from miRNA biogenesis to its binding to target mRNA: (1) the primary miRNA transcript (pri-miRNA) is generated by transcription of the *MIRNA* gene (Voinnet 2009); (2) pri-miRNA is cleaved by DICER-LIKE1 (DCL1) to release the precursor miRNAs (pre-miRNAs) with different cleavage modes (Jones-Rhoades et al. 2006; Bologna et al. 2009; Schwab and Voinnet 2009; Zhu et al. 2013); (3) pre-miRNAs are cleaved by DCL1 to generate mature miRNAs (Kurihara et al. 2006); and (4) mature miRNAs bind to their target mRNAs to control their expression (Awan et al. 2018; Djuranovic et al. 2012; Yang et al. 2019). Each step can be controlled to affect the level and activity of miRNA, but these processes during somatic embryogenesis have received little attention.

The activity of miRNA can be assessed by analyzing the levels of the initial and non-cleaved transcripts of the target mRNA using RNA blotting, quantitative reverse transcription polymerase chain reaction (qRT-PCR), and semi-quantitative RT-PCR (Li et al. 2014; Llave et al. 2002; Tsuji et al. 2006). In our previous work, we found higher activity of miR171 in embryogenic cultures of *L. kaempferi* by analyzing the levels of the initial and non-cleaved transcripts of *LaSCL6* using qRT-PCR (Li et al. 2014). In addition, three cleavage sites within the *LaSCL6* mRNA sequence have been reported (Li et al. 2014), suggesting that *LaSCL6* mRNAs are cleaved by different members of the miR171 family. Identification of miR171 members will help to determine the relationships between miR171 members and *LaSCL6* and reveal the control of miR171 levels and activity.

In this study, we identified five miR171 members and analyzed the expression patterns of the mature miR171s and their primary transcripts and *LaSCL6* during somatic embryogenesis. The results provide further insights into the regulatory roles of the miR171-*LaSCL6* module in the somatic embryogenesis of *L. kaempferi*.

Materials and methods

Plant materials

The induction and proliferation of cell cultures and somatic embryo maturation were performed according to the previous studies (Zhang et al. 2010, 2012, 2019). The immature seeds of *L. kaempferi* were collected in the middle of June from Dagujia seed orchard (42° 22' N, 124° 51' E), Liaoning Province, in northeast China. The embryonal-suspensor mass was induced from immature embryos on induction medium and then cultured on proliferation medium. The subculture was performed every 3 weeks. During subculture, some embryogenic cultures transformed into non-embryogenic cultures. Embryogenic and non-embryogenic cultures were isolated, cultured separately on proliferation medium, and harvested after culture for 14 days. After growth for 3 weeks on proliferation medium, the embryogenic cultures were then transferred to maturation medium and cultures were collected at 0, 7, 14, 21, 28, 35, and 42 days. All the samples were stored at -80 °C until DNA and RNA extraction.

Sequence cloning and analysis of *MIR171* genes

The genomic DNA of *L. kaempferi* was isolated from the embryonal-suspensor mass with the CTAB plant genome DNA rapid extraction kit (Aidlab, China) according to the manufacturer's protocols. *MIR171* sequences were amplified from genomic DNA with Platinum® Taq DNA polymerase (Invitrogen, USA) with specific primers (Table S1), which were designed based on the annotation of miRNA (Liu et al. 2016; Zhang et al. 2012) of *L. kaempferi*. The PCR products were purified with the Gel Extraction kit (Tiangen, China), ligated into the pEASY®-T1 simple cloning vector (Transgen, China), and sequenced. The stem-loop secondary structures of miR171 precursors were analyzed with the Mfold web server (<https://unafold.rna.albany.edu/?q=mfold>) using the default parameters.

Sequence alignment and cleavage site analysis

The mature sequences of miR171s from *Arabidopsis thaliana* (Ath-miR171a, Ath-miR171b, and Ath-miR171c) and *Picea abies* (Pab-miR171a, Pab-miR171b, and Pab-miR171c) were obtained from PmiREN (<https://www.pmiren.com/>) (Guo et al. 2019). The sequence of miR171a from *Pinus densata* (Pde-miR171a) was identified by Hai et al. (2017). Together with *L. kaempferi* miR171s (Lka-miR171s), these miR171 sequences were aligned with ClustalX (Thompson et al. 1997). The relationships between

the sequences of *Lka*-miR171s and *LaSCL6* mRNA were analyzed using the psRNATarget web server (<https://plant.grn.noble.org/psRNATarget/analysis?function=3>) (Dai and Zhao 2011).

Expression patterns of miR171s and *LaSCL6* detected by qRT-PCR

Total RNA was isolated with the RNAiso Plus reagent kit (TaKaRa, Japan) according to the manufacturer's protocols and then reverse-transcribed into cDNA with the Mir-X miRNA First Strand Synthesis Kit (Clontech, USA) and TransScript® II one-step gDNA removal and cDNA Synthesis SuperMix kit (Transgen, China). TB Green™ Advantage® qPCR Premix (Clontech, USA) was used to assess the expression levels of mature miR171s, and TB Green® Premix Ex Taq™ (Tli RNase H Plus) (Takara, Japan) was used to assess the expression levels of the initial and non-cleaved transcripts of *LaSCL6* and primary transcripts of miR171s. The primers, which are located downstream from the miR171 cleavage sites, were used for initial (both

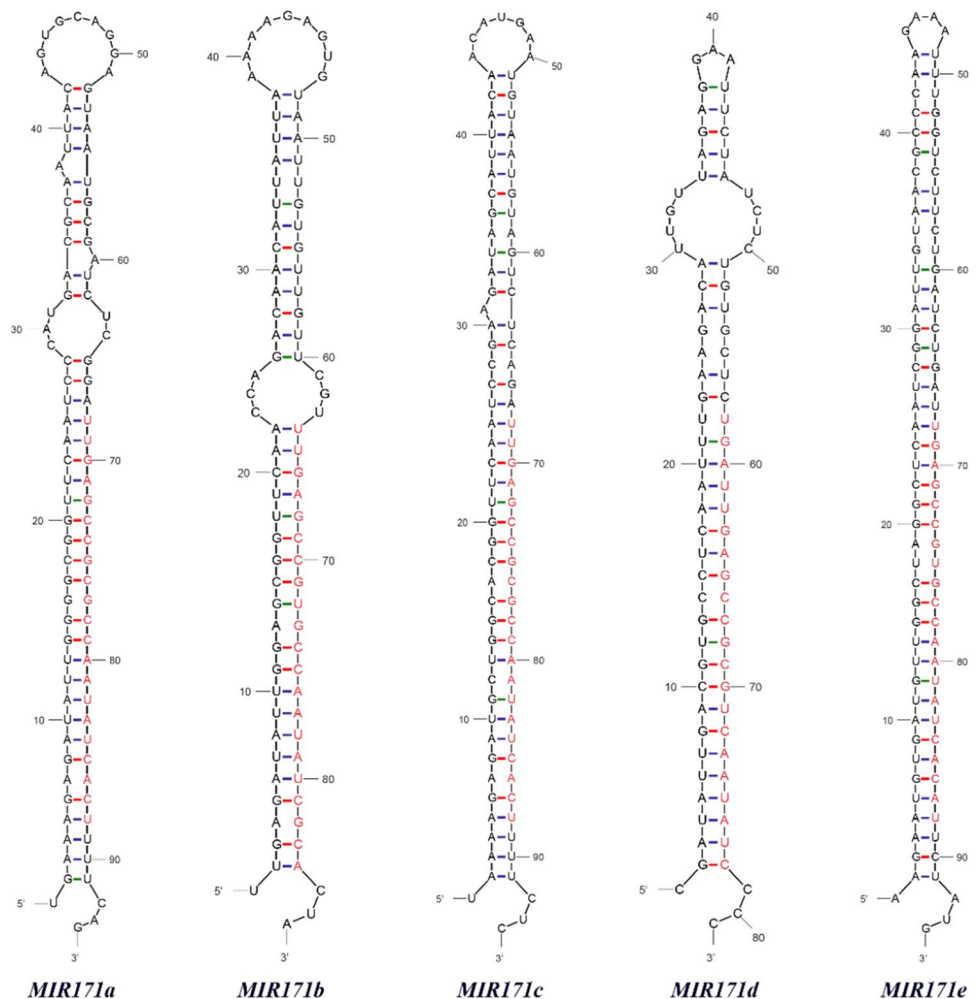
non-cleaved and cleaved) transcripts of *LaSCL6*; the primers, which span the miR171 cleavage sites, were used for non-cleaved transcripts of *LaSCL6* (Li et al. 2014). *L. kaempferi* translation elongation factor-1 alpha 1 (*LaEF1A1*) served as the internal control (Li et al. 2014). All the primer sequences are listed in Table S1. The qRT-PCR was performed with three biological replicates and data are shown as the mean \pm SD. Analysis of variance (ANOVA) was performed and the *P* value was generated between two samples.

Results

Relationships between miR171 and *LaSCL6*

Five *MIR171* genes were identified in *L. kaempferi*. After analysis of the stem-loop secondary structures of the precursors of miR171s, we found that all the mature sequences of the miR171 family were located on the 3' arm of the stem-loop structure and the miR171a and miR171c sequences were the same (Fig. 1). *L. kaempferi* miR171s

Fig. 1 Stem-loop secondary structures of *MIR171* genes of *L. kaempferi*. Segments corresponding to the mature miR171s are shown in red



shared high sequence identity with those from the other three species (Fig. 2). The sequence of Lka-miR171b was the same as Pab-miR171c, and one nucleotide change was found in Lka-miR171d and Ath-miR171a (Fig. 2).

The predicted target sequences of the miR171s were present in the *LaSCL6* mRNA sequence (Fig. 3). When counting G:U pairs as 0.5 mismatches, *LaSCL6* had 1.5 mismatches to miR171a/c, 0.5 mismatches to miR171b/d, and 2.5 mismatches to miR171e (Fig. 3). Further analysis showed that the cleavage sites 1, 2, and 3 (S1, S2, and S3) were located between the nucleotides paired to positions 10 and 11 of miR171d, miR171a/b/c, and miR171e, respectively (Fig. 3).

Expression patterns of *LaSCL6* during somatic embryogenesis

The expression patterns of initial and non-cleaved transcripts of *LaSCL6* during somatic embryogenesis were analyzed by qRT-PCR with *LaEF1A1* as the internal control. The level of *LaSCL6* initial transcripts in embryogenic cultures was about 16.2 times higher than that in non-embryogenic cultures ($P < 0.05$) (Fig. 4a), while the level of non-cleaved transcripts of *LaSCL6* was about 7.6 times higher than that in non-embryogenic cultures ($P < 0.05$) (Fig. 4a). During the maturation of somatic embryos, the levels of initial and non-cleaved transcripts of *LaSCL6* were higher at days 21, 28, and 42 with different fold-changes ($P < 0.05$) (Fig. 4c).

We further calculated the ratio between the expression levels of non-cleaved and initial *LaSCL6* transcripts in each sample using the relative quantitative analysis method. The ratios were lower in embryogenic cultures than in non-embryogenic cultures ($P < 0.05$) (Fig. 4b) and were lower at day 0 than at other days in the maturation of somatic embryos ($P < 0.05$) (Fig. 4d).

Fig. 2 Multiple sequence alignment of mature miR171s with ClustalX. Identical residues are indicated by asterisks. Pde, *Pinus densata*; Ath, *Arabidopsis thaliana*; Pab, *Picea abies*; Lka, *Larix kaempferi*

		***** * *****	
Pde-miR171a	5'	UGAUUGAGCCGUGCCAAUAUC-----	3'
Ath-miR171a	5'	UGAUUGAGCCGCGCCAAUAUC-----	3'
Ath-miR171b/c	5'	---UUGAGCCGUGCCAAUAUCACG--	3'
Pab-miR171a/b	5'	---UUGAGCCGCGUCAUAUACCCC--	3'
Pab-miR171c	5'	---UUGAGCCGUGCCAAUAUCGCA--	3'
Lka-miR171a/c	5'	---UUGAGCCGCGCCAAUAUCACU--	3'
Lka-miR171b	5'	---UUGAGCCGUGCCAAUAUCGCA--	3'
Lka-miR171e	5'	----UGAGCCGUGCCAAUAUCACAU	3'
Lka-miR171d	5'	UGAUUGAGCCGCGUCAUAUAC-----	3'

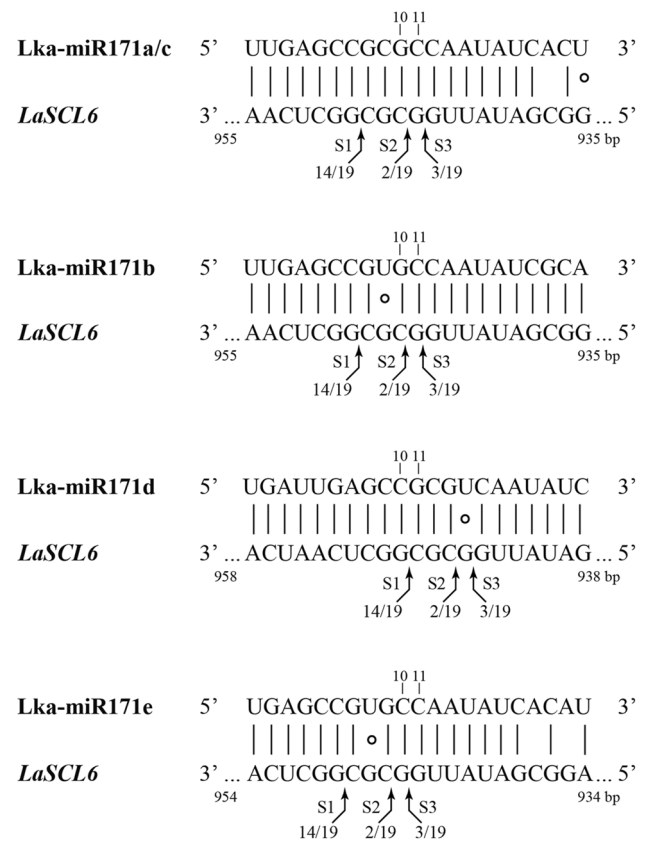
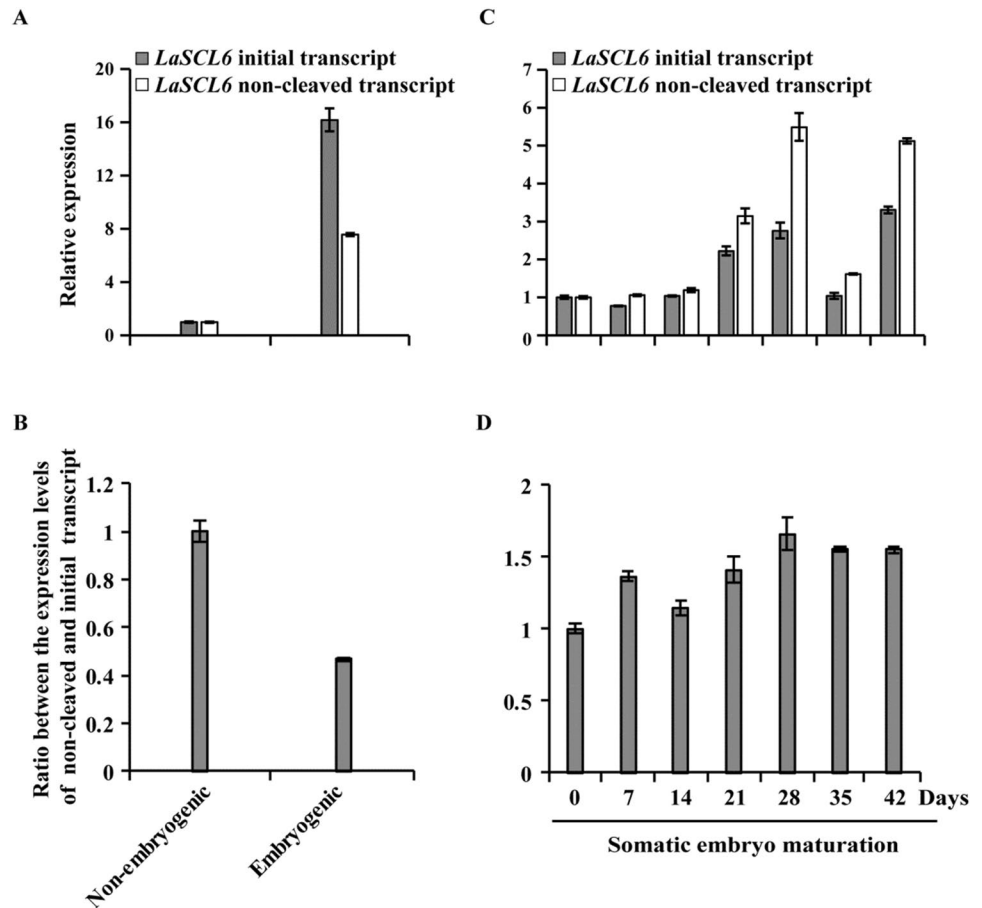


Fig. 3 Relationships between miR171s and *LaSCL6*. Relationships between the sequences of miR171s and *LaSCL6* mRNA. The matches are indicated by straight lines and G:U wobbles are represented by circles. The numbers above indicate the nucleotides paired to the positions of miRNA. Arrows above S1, S2, and S3 indicate the positions of the cleaved mRNA fragments identified by RNA ligase-mediated amplification of cDNA ends (RLM-5' RACE), and the numbers below refer to the frequency of RLM-5' RACE clones corresponding to the cleavage sites (Li et al. 2014)

Fig. 4 Analysis of miR171 activity. **a** Expression patterns of initial and non-cleaved transcripts of *LaSCL6* in embryogenic and non-embryogenic cultures with *LaEF1A1* as the internal control. **b** Ratios of the expression levels of non-cleaved and initial *LaSCL6* transcripts in embryogenic and non-embryogenic cultures calculated using the relative quantitative analysis method. **c** Expression patterns of initial and non-cleaved transcripts of *LaSCL6* during the maturation of somatic embryos with *LaEF1A1* as the internal control. **d** Ratios between the expression levels of non-cleaved and initial *LaSCL6* transcripts during the maturation of somatic embryos calculated using the relative quantitative analysis method



Expression patterns of mature miR171s and their primary transcripts during somatic embryogenesis

The expression patterns of mature miR171s and their primary transcripts during somatic embryogenesis were measured by qRT-PCR with *LaEF1A1* as the internal control. The levels of primary transcripts of miR171a/b/c/e were higher in embryogenic cultures ($P < 0.05$) (Fig. 5a, b, c, e), while that of miR171d showed almost no difference in embryogenic and non-embryogenic cultures ($P > 0.05$) (Fig. 5d). The levels of mature miR171b/d/e were higher in embryogenic cultures ($P < 0.05$), but their fold-changes (64.4, 5.1, and 17.0) (Fig. 5g, h, i) differed from those for their primary transcripts (6.2, 1.1, and 6.1) (Fig. 5b, d, e). During the maturation of somatic embryos, higher levels of mature miR171s were detected at day 0 ($P < 0.05$) (Fig. 5o–r), but the expression of their primary transcripts showed different patterns (Fig. 5j–n).

Discussion

Regulation of *LaSCL6* by miR171 during *L. kaempferi* somatic embryogenesis

Identification of precursor is the prerequisite of identifying mature miRNA (Jones-Rhoades et al. 2006; Voinnet 2009). In the previous studies, the mature miR171s' sequences were obtained by sequencing without identifying their precursors (Li et al. 2014; Zhang et al. 2012). Here, five members of the miR171 family were identified in *L. kaempferi* after analyzing their precursors, which contributes to study the relationships between miR171 members and *LaSCL6* and the function of miR171-*LaSCL6* module during somatic embryogenesis. There were few mismatches (≤ 2.5) between five miR171 sequences and the *LaSCL6* mRNA sequence (Fig. 3). This near-perfect complementarity facilitated the

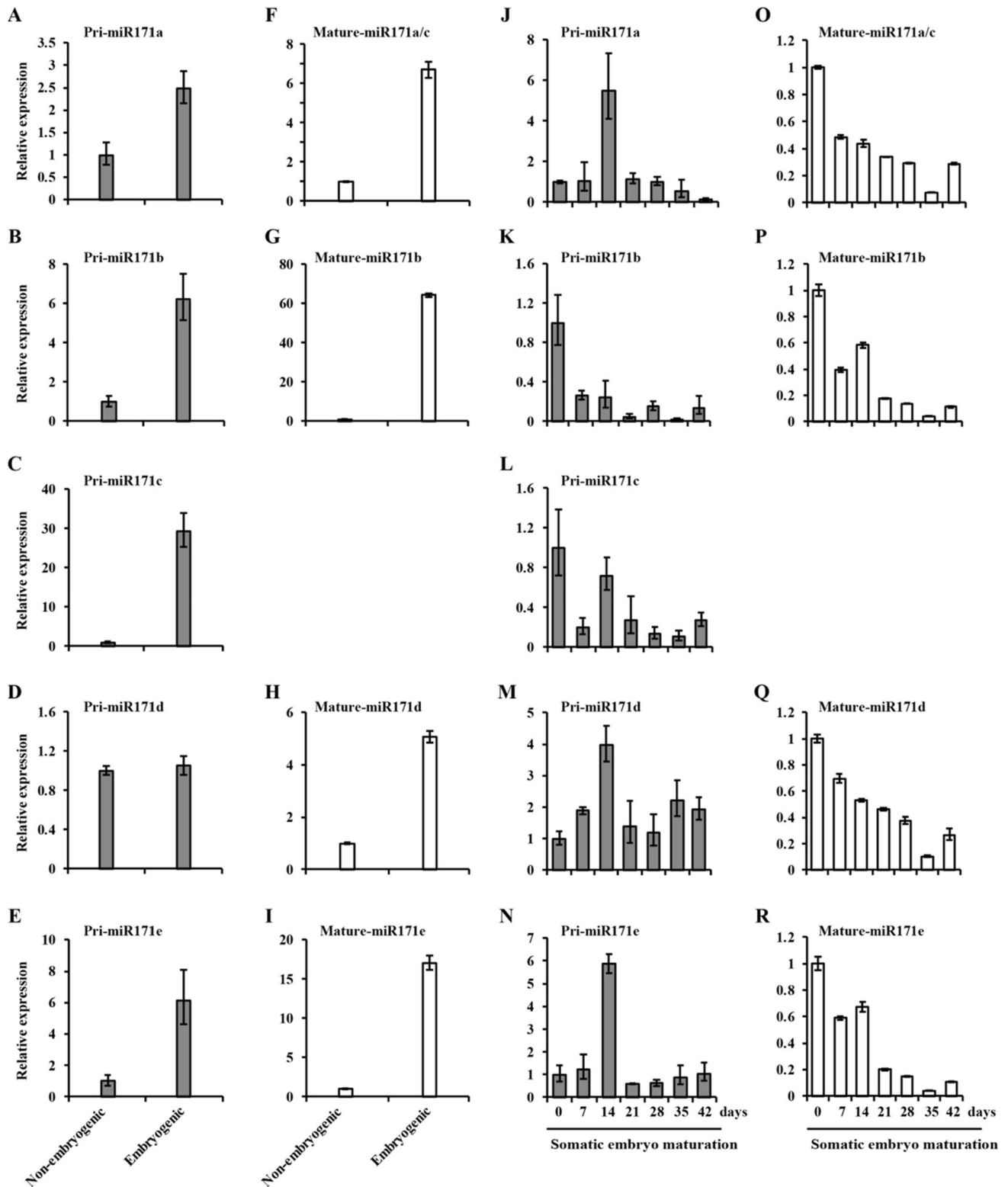


Fig. 5 Expression patterns of mature miR171s and their primary transcripts during somatic embryogenesis with *LaEF1A1* as the internal control

binding of miR171s to *LaSCL6* mRNA to cleave it. The miRNA-directed cleavage of its target mRNA generally occurs between the nucleotides paired to positions 10 and 11 of the miRNA (Mallory and Bouche 2008). Considering the occurrence of three cleavage sites in *LaSCL6* mRNA and the results of sequence alignment analysis of the miR171s and *LaSCL6* mRNA (Fig. 3), miR171a/b/c, miR171d, and miR171e might cleave *LaSCL6* mRNA at the S2, S1, and S3 sites, respectively. Notably, the frequencies of these three cleavage sites (Li et al. 2014) were different, suggesting that the roles played by the miR171s also differed. The frequency of the S1 site was higher (Fig. 3), indicating that miR171d might be more active in cleaving *LaSCL6* mRNA.

The post-transcriptional regulation of *LaSCL6* by miR171 participates in the maintenance of embryogenic potential

The levels of initial and non-cleaved transcripts of *LaSCL6* were higher in embryogenic cultures ($P < 0.05$), but the fold-changes of the levels of the initial transcripts were greater than those of the non-cleaved transcripts (Fig. 4a), indicating that more transcripts of *LaSCL6* were cleaved and higher miR171 activity occurred in embryogenic cultures (Li et al. 2014). Notably, in embryogenic and non-embryogenic cultures, the expression patterns of initial transcripts of *LaSCL6* differed from those reported in our previous study (Li et al. 2014), indicating that there is no tight relationship between *LaSCL6* transcription and the maintenance of embryogenic potential, while the same pattern of miR171 activity was detected in both studies, further indicating that it is the post-transcriptional regulation of *LaSCL6* by miR171 that participates in the maintenance of embryogenic potential (Li et al. 2014).

Dynamic change in miR171 activity during somatic embryogenesis

We assumed here that if the transcripts of a gene were not cleaved by miRNA, the levels of its initial and non-cleaved transcripts in one sample would be the same, whereas if the transcripts of a gene were cleaved by miRNA, the level of initial transcripts would be higher than that of its non-cleaved transcripts in one sample. Therefore, the activity of miRNA could be indicated intuitively by the ratio between the expression levels of the non-cleaved and initial transcripts of target gene in one sample. When the ratio in one sample is lower, it means that more transcripts are cleaved and higher miRNA activity occurs in this sample.

Using this method, we re-analyzed the changes in miR171 activity during somatic embryogenesis. Higher activity of miR171 occurred in embryogenic cultures during subculture

($P < 0.05$) (Fig. 4b) and in the cultures at day 0 during the maturation of somatic embryos ($P < 0.05$) (Fig. 4d).

In the previous studies, the activity of miRNA was assessed by analyzing the levels of the target mRNA with another gene as internal control (Li et al. 2014; Tsuji et al. 2006). In this paper, we adjusted the method and used the initial transcript of the target gene as the internal control without using another gene, so that the miRNA activity was shown more simply and intuitively. This method not only offers a powerful tool to assess miRNA activity, but also helps in investigations of the mechanisms of miRNA-directed gene regulation in plant development.

Regulation of miR171 is involved in *L. kaempferi* somatic embryogenesis

The processes of miRNA biogenesis can affect its activity (Viswanathan et al. 2008; Yue et al. 2011), but little attention has been paid to the control of miR171 biogenesis during somatic embryogenesis (Li et al. 2017, 2014; Zang et al. 2019; Zhang et al. 2012). Here we measured the expression of mature miR171s and their primary transcripts during somatic embryogenesis and analyzed their relationships to clarify the regulation of miR171s.

Higher levels of miR171a/b/c/e primary transcripts were found in embryogenic cultures ($P < 0.05$) (Fig. 5a, b, c, e), indicating that the transcription of miR171a/b/c/e was stronger and involved in the maintenance of embryogenic potential. Higher levels of mature miR171b/d/e occurred in embryogenic cultures ($P < 0.05$) (Fig. 5g–i), but their fold-changes were higher than those for their pri-miRNAs (Fig. 5b, d, e), indicating that more pri-miR171b/d/e was cleaved into mature miR171b/d/e and that their cleavage was regulated. Notably, the level of pri-miR171d in embryogenic and non-embryogenic cultures showed almost no difference ($P > 0.05$) (Fig. 5d), but that of mature miR171d was higher in embryogenic cultures ($P < 0.05$) (Fig. 5h), indicating that the regulation of miR171d occurred in steps (2) and (3) of its biogenesis but not in step (1).

During the maturation of somatic embryos, the levels of all mature miR171s were higher at day 0 ($P < 0.05$) (Fig. 5o–r), indicating that miR171s are more active in pro-embryogenic development (Fig. 4d). Meanwhile, the levels of their primary transcripts were not always higher at day 0 (Fig. 5j–n), indicating that the regulation of their transcription and cleavage were different and complex.

The cleavage of *MIR171* transcripts was regulated during their biogenesis, and this might result from the differential expression of the activity of DCL1 and its partners (Kurihara et al. 2006). Of course, other factors involved in miRNA biogenesis such as transcription factors (*Mediator 17/18* and *Cell Division Cycle 5*) (Zhang et al. 2015), RNA-binding proteins (Ren and Yu 2012), and decapping proteins

(Motomura et al. 2012), might also participate in the regulation of miR171 biogenesis.

Embryogenic culture differs from non-embryogenic culture in the mode of cell division, cell structure and morphology, histological structure, and cell fate (Quiroz-Figueroa et al. 2002). The abundance and activity of miR171 were different between the embryogenic and non-embryogenic cultures, suggesting that miR171-*LaSCL6* functions in the maintenance of embryogenic potential. Notably, *SCL6* interacts with WUSCHEL and SQUAMOSA PROMOTER BINDING PROTEIN LIKE to regulate meristem activity (Zhou et al. 2018) and flowering (Xue et al. 2014), respectively, adding more information about the function of miR171-*SCL6* module and helping to reveal the molecular mechanism of somatic embryogenesis.

Author contribution statement Q-LZ carried out the study, analyzed the data, and wrote the manuscript. YZ and S-YH helped to culture the plant materials. W-FL designed the study, helped to analyze the data, and revised the manuscript. L-WQ provided suggestions on the experimental design and analyses. All authors read and approved the manuscript.

Acknowledgements The authors thank Dr. Chao Sun (Research Institute of Forestry, Chinese Academy of Forestry) for help in sequence cloning and Dr. IC Bruce (Peking University) for critical reading of the manuscript.

Funding This work was supported by the National Natural Science Foundation of China (31770714), the Fundamental Research Funds for the Central Non-profit Research Institution of CAF (CAFYB-B2017QA001), the Basic Research Fund of the Research Institute of Forestry (RIF2014-07), the National Transgenic Major Program (2018ZX08020-003), and the National Key R&D Program of China (2017YFD0601204-2).

Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

Data archiving statement The sequences of *MIR171alb/clde* in *L. kaempferi* have been submitted to GenBank with the accession numbers MN790738, MN790739, MN790740, MN790741, and MN790742, respectively.

Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will

need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>.

References

- Awan HM, Shah A, Rashid F, Wei S, Chen L, Shan G (2018) Comparing two approaches of miR-34a target identification, biotinylated-miRNA pulldown vs miRNA overexpression. *RNA Biol* 15:55–61. <https://doi.org/10.1080/15476286.2017.1391441>
- Bologna NG, Mateos JL, Bresso EG, Palatnik JF (2009) A loop-to-base processing mechanism underlies the biogenesis of plant microRNAs miR319 and miR159. *EMBO J* 28:3646–3656. <https://doi.org/10.1038/emboj.2009.292>
- Dai X, Zhao PX (2011) psRNATarget: a plant small RNA target analysis server. *Nucleic Acids Res* 39:W155–159. <https://doi.org/10.1093/nar/gkr319>
- Djuranovic S, Nahvi A, Green R (2012) miRNA-mediated gene silencing by translational repression followed by mRNA deadenylation and decay. *Science* 336:237–240. <https://doi.org/10.1126/science.1215691>
- Dobrowolska I, Businge E, Abreu IN, Moritz T, Egertsdotter U (2017) Metabolome and transcriptome profiling reveal new insights into somatic embryo germination in Norway spruce (*Picea abies*). *Tree Physiol* 37:1752–1766. <https://doi.org/10.1093/treephys/tpx078>
- Gao YR, Sun JC, Sun ZL, Xing Y, Zhang Q, Fang KF, Cao QQ, Qin L (2020) The MADS-box transcription factor *CmAGL11* modulates somatic embryogenesis in Chinese chestnut (*Castanea mollissima* Blume). *J Integr Agr* 19:1033–1043. [https://doi.org/10.1016/S2095-3119\(20\)63157-4](https://doi.org/10.1016/S2095-3119(20)63157-4)
- Godee C, Mira MM, Wally O, Hill RD, Stasolla C (2017) Cellular localization of the *Arabidopsis* class 2 phytohemoglobin influences somatic embryogenesis. *J Exp Bot* 68:1013–1023. <https://doi.org/10.1093/jxb/erx003>
- Guo Z, Kuang Z, Wang Y, Zhao Y, Tao Y, Cheng C, Yang J, Lu X, Hao C, Wang T, Cao X, Wei J, Li L, Yang X (2019) PmiREN: a comprehensive encyclopedia of plant miRNAs. *Nucleic Acids Res* 48:D1114–D1121. <https://doi.org/10.1093/nar/gkz894/5585553>
- Hai BZ, Qiu ZB, He YY, Yuan MM, Li YF (2017) Characterization and primary functional analysis of *Pinus densata* miR171. *Biol Plant* 62:318–324. <https://doi.org/10.1007/s10535-018-0774-7>
- Jiang S, Chen Q, Zhang Q, Zhang Y, Hao N, Ou C, Wang F, Li T (2018) Pyr-miR171f-targeted *PyrSCL6* and *PyrSCL22* genes regulate shoot growth by responding to IAA signaling in pear. *Tree Genet Genomes* 14:20. <https://doi.org/10.1007/s11295-018-1233-5>
- Jones-Rhoades MW, Bartel DP, Bartel B (2006) MicroRNAs and their regulatory roles in plants. *Annu Rev Plant Biol* 57:19–53. <https://doi.org/10.1146/annurev.arplant.57.032905.105218>
- Klimaszewska K, Hargreaves C, Lelu-Walter MA, Trontin JF (2016) Advances in conifer somatic embryogenesis since year 2000. In: Germana M, Lambardi M (eds) *In vitro embryogenesis in higher plants. Methods in molecular biology*, vol 1359. Humana Press, New York. https://doi.org/10.1007/978-1-4939-3061-6_7
- Kurihara Y, Takashi Y, Watanabe Y (2006) The interaction between DCL1 and HYL1 is important for efficient and precise processing of pri-miRNA in plant microRNA biogenesis. *RNA* 12:206–212. <https://doi.org/10.1261/rna.2146906>
- Li WF, Zhang SG, Han SY, Wu T, Zhang JH, Qi LW (2014) The post-transcriptional regulation of *LaSCL6* by miR171 during maintenance of embryogenic potential in *Larix kaempferi* (Lamb.) Carr. *Tree Genet Genomes* 10:223–229. <https://doi.org/10.1007/s11295-013-0668-y>

- Li ZX, Li SG, Zhang LF, Han SY, Li WF, Xu HY, Yang WH, Liu YL, Fan YR, Qi LW (2016) Over-expression of miR166a inhibits cotyledon formation in somatic embryos and promotes lateral root development in seedlings of *Larix leptolepis*. *Plant Cell Tiss Organ Cult* 127:461–473. <https://doi.org/10.1007/s11240-016-1071-9>
- Li HY, Zhang J, Yang Y, Jia NN, Wang CX, Sun HM (2017) miR171 and its target gene *SCL6* contribute to embryogenic callus induction and torpedo-shaped embryo formation during somatic embryogenesis in two lily species. *Plant Cell Tiss Organ Cult* 130:591–600. <https://doi.org/10.1007/s11240-017-1249-9>
- Liu Y, Han S, Ding X, Li X, Zhang L, Li W, Xu H, Li Z, Qi L (2016) Transcriptome analysis of mRNA and miRNA in somatic embryos of *Larix leptolepis* subjected to hydrogen treatment. *Int J Mol Sci* 17:1951. <https://doi.org/10.3390/ijms17111951>
- Liu Z, Ge XX, Qiu WM, Long GM, Jia HH, Yang W, Dutt M, Wu XM, Guo WW (2018) Overexpression of the *CsFUS3* gene encoding a B3 transcription factor promotes somatic embryogenesis in *Citrus*. *Plant Sci* 277:121–131. <https://doi.org/10.1016/j.plantsci.2018.10.015>
- Llave C, Xie Z, Kasschau KD, Carrington JC (2002) Cleavage of scarecrow-like mRNA targets directed by a class of *Arabidopsis* miRNA. *Science* 297:2053–2056. <https://doi.org/10.1126/science.1076311>
- Long JM, Liu CY, Feng MQ, Liu Y, Wu XM, Guo WW (2018) miR156-*SPL* modules regulate induction of somatic embryogenesis in citrus callus. *J Exp Bot* 69:2979–2993. <https://doi.org/10.1093/jxb/ery132>
- Mallory AC, Bouche N (2008) MicroRNA-directed regulation: to cleave or not to cleave. *Trends Plant Sci* 13:359–367. <https://doi.org/10.1016/j.tplants.2008.03.007>
- Motomura K, Le QT, Kumakura N, Fukaya T, Takeda A, Watanabe Y (2012) The role of decapping proteins in the miRNA accumulation in *Arabidopsis thaliana*. *RNA Biol* 9:644–652. <https://doi.org/10.4161/rna.19877>
- Pysh LD, Wysocka-Diller JW, Camilleri C, Bouchez D, Benfey PN (1999) The GRAS gene family in *Arabidopsis* sequence characterization and basic expression analysis of the *SCARECROW-LIKE* genes. *Plant J* 18:111–119. <https://doi.org/10.1046/j.1365-313X.1999.00431.x>
- Quiroz-Figueroa F, Méndez-Zeel M, Sánchez-Teyer F, Rojas-Herrera R, Loyola-Vargas VM (2002) Differential gene expression in embryo-genic and non-embryogenic clusters from cell suspension cultures of *Coffea arabica*. *J Plant Physiol* 159:1267–1270. <https://doi.org/10.1078/0176-1617-00878>
- Ren G, Yu B (2012) Critical roles of RNA-binding proteins in miRNA biogenesis in *Arabidopsis*. *RNA Biol* 9:1424–1428. <https://doi.org/10.4161/rna.22740>
- Schwab R, Voinnet O (2009) miRNA processing turned upside down. *EMBO J* 28:3633–3634. <https://doi.org/10.1038/emboj.2009.334>
- Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG (1997) The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Res* 25:4876–4882. <https://doi.org/10.1093/nar/25.24.4876>
- Tsuji H, Aya K, Ueguchi-Tanaka M, Shimada Y, Nakazono M, Watanabe R, Nishizawa NK, Gomi K, Shimada A, Kitano H, Ashikari M, Matsuoka M (2006) GAMYB controls different sets of genes and is differentially regulated by microRNA in aleurone cells and anthers. *Plant J* 47:427–444. <https://doi.org/10.1111/j.1365-313X.2006.02795.x>
- Viswanathan SR, Daley G, Gregory RI (2008) Selective blockade of microRNA processing by Lin28. *Science* 320:97–100. <https://doi.org/10.1126/science.1154040>
- Voinnet O (2009) Origin, biogenesis, and activity of plant microRNAs. *Cell* 136:669–687. <https://doi.org/10.1016/j.Cell.2009.01.046>
- Wang L, Mai YX, Zhang YC, Luo Q, Yang HQ (2010) MicroRNA171c-targeted *SCL6-II*, *SCL6-III*, and *SCL6-IV* genes regulate shoot branching in *Arabidopsis*. *Mol Plant* 3:794–806. <https://doi.org/10.1093/mp/ssq042>
- Wang FX, Shang GD, Wu LY, Xu ZG, Zhao XY, Wang JW (2020) Chromatin accessibility dynamics and a hierarchical transcriptional regulatory network structure for plant somatic embryogenesis. *Dev Cell* 54:1–16. <https://doi.org/10.1016/j.devcel.1.2020.07.003>
- Wu XM, Kou SJ, Liu YL, Fang YN, Xu Q, Guo WW (2015) Genome-wide analysis of small RNAs in non-embryogenic and embryogenic tissues of citrus: microRNA and siRNA mediated transcript cleavage involved in somatic embryogenesis. *Plant Biotechnol J* 13:383–394. <https://doi.org/10.1111/pbi.12317>
- Xue XY, Zhao B, Chao LM, Chen DY, Cui WR, Mao YB, Wang LG, Chen XY (2014) Interaction between two timing microRNAs controls trichome distribution in *Arabidopsis*. *PLoS Genet* 10:e1004266. <https://doi.org/10.1371/journal.pgen.1004266>
- Yang R, Li P, Mei H, Wang D, Sun J, Yang C, Hao L, Cao S, Chu C, Hu S, Song X, Cao X (2019) Fine-tuning of miR528 accumulation modulates flowering time in rice. *Mol plant* 12:1103–1113. <https://doi.org/10.1016/j.molp.2019.04.009>
- Yue SB, Trujillo RD, Tang Y, O’Gorman WE, Chen CZ (2011) Loop nucleotides control primary and mature miRNA function in target recognition and repression. *RNA Biol* 8:1115–1123. <https://doi.org/10.4161/rna.8.6.17626>
- Zang QL, Li WF, Qi LW (2019) Regulation of *LaSCL6* expression by genomic structure, alternative splicing, and microRNA in *Larix kaempferi*. *Tree Genet Genomes* 15:57. <https://doi.org/10.1007/s11295-019-1362-5>
- Zhang S, Zhou J, Han S, Yang W, Li W, Wei H, Li X, Qi L (2010) Four abiotic stress-induced miRNA families differentially regulated in the embryogenic and non-embryogenic callus tissues of *Larix leptolepis*. *Biochem Biophys Res Commun* 398:355–360. <https://doi.org/10.1016/j.bbrc.2010.06.056>
- Zhang J, Zhang S, Han S, Wu T, Li X, Li W, Qi L (2012) Genome-wide identification of microRNAs in larch and stage-specific modulation of 11 conserved microRNAs and their targets during somatic embryogenesis. *Planta* 236:647–657. <https://doi.org/10.1007/s00425-012-1643-9>
- Zhang S, Liu Y, Yu B (2015) New insights into pri-miRNA processing and accumulation in plants. *Wiley Interdiscip Rev RNA* 6:533–545. <https://doi.org/10.1002/wrna.1292>
- Zhang LF, Lan Q, Han SY, Qi LW (2019) A *Gh3*-like gene, *LaGH3*, isolated from hybrid larch (*Larix leptolepis* × *Larix olgensis*) is regulated by auxin and abscisic acid during somatic embryogenesis. *Trees* 33:1723–1732. <https://doi.org/10.1007/s00468-019-01904-8>
- Zhou Y, Yan A, Han H, Li T, Geng Y, Liu X, Meyerowitz EM (2018) HAIRY MERISTEM with WUSCHEL confines CLAVATA3 expression to the outer apical meristem layers. *Science* 361:502–506. <https://doi.org/10.1126/science.aar8638>
- Zhu H, Zhou Y, Castillo-Gonzalez C, Lu A, Ge C, Zhao YT, Duan L, Li Z, Axtell MJ, Wang XJ, Zhang X (2013) Bidirectional processing of pri-miRNAs with branched terminal loops by *Arabidopsis* Dicer-like1. *Nat Struct Mol Biol* 20:1106–1115. <https://doi.org/10.1038/nsmb.2646>

Affiliations

Qiao-Lu Zang¹  · Yao Zhang²  · Su-Ying Han² · Wan-Feng Li¹  · Li-Wang Qi¹

Qiao-Lu Zang
zangql@caf.ac.cn

Yao Zhang
zyao@caf.ac.cn

Su-Ying Han
syhan@caf.ac.cn

Forestry and Grassland Administration, Research Institute of Forestry, Chinese Academy of Forestry, Beijing 100091, People's Republic of China

² Environment and Protection, Research Institute of Forest Ecology, Chinese Academy of Forestry, Beijing 100091, People's Republic of China

¹ State Key Laboratory of Tree Genetics and Breeding, Key Laboratory of Tree Breeding and Cultivation, National