

## Comment on “Systematic Identification and Analysis of Light-responsive Circular RNA and Co-expression Networks in Lettuce (*Lactuca sativa*)”

Zhao Yang, Yongjun Wu\*

College of Life Sciences, Northwest A&F University, Yangling, Shaan Xi, China

\*Correspondence should be addressed to Yongjun Wu; wuyongjun@nwfau.edu.cn

**Received date:** August 18, 2020, **Accepted date:** October 21, 2020

**Copyright:** © 2020 Yang Z, et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Light is one of the most important environmental factors that affect plant growth and development, and it is also the main energy source for plants and other living things. Plants use light to assimilate inorganic matter into organic matter through photosynthesis and store them in the form of chemical energy. As an environmental signal, light mediates the whole process of plant growth and development, from seed germination, seedling growth to plant reproduction, senescence and dormancy [1].

### Effects of Light Intensity on Plant Growth and Development

Light intensity is a major ecological factor affecting plant growth. Plants respond to different light intensity through genetic adaptability and phenotypic adaptability [2]. As a regulatory signal in the entire life of plants, light regulates the growth and development of plants [1].

Research shows that the transition from vegetative growth to reproductive growth requires certain conditions, which indicates that the vegetative growth and reproductive growth of plants are coordinated and mutually restricted. At the same time, plants also need to adapt to the external conditions, in which light is the most important factor [1]. For example, radishes need a period of long sunshine to sprout and blossom, while chrysanthemums need a shorter sunshine for buddings. If the light intensity is insufficient, the photosynthetic rate will be reduced, and the yield of cucumber will be affected. Light not only affects plant height, leaf area, plant dry matter weight and other biomass, but also strongly affects plant flower bud differentiation, delay flowering and fruit ripening and other physiological phenomena [3]. Sufficient light intensity promotes flower budding and fruit maturity and improves the quality of fruit. Enhanced light has an effect

on phenotypic process of plants including flowering period of plants and number of flowers as well [2].

Due to the difference in genotypes, different plants have different levels of adaptability to light intensity. The long-term adaptation of plants to light intensity is often manifested in morphogenesis, such as the growth of aboveground parts, root morphology, leaf microstructure [4]. The light intensity also has a certain effect on the biomass accumulation and distribution of plants [5].

### Molecular Mechanism of Light Intensity Affecting Plant Development

Light can be recognized and accepted by light receptors. According to the wavelength of perceived light, photoreceptors can be divided into three categories: The red and far-infrared photoreceptors (phytochromes, PHY A-E), blue/ultraviolet (UV-A) cryptochromes (CRY1 and CRY2), phototropins (photot1 and photot2), and UV-B receptor uvr8 [6,7]. Complex and strictly regulated photoresponse networks sense light signals through specific photoreceptors, and then transmit them to light regulatory factors to regulate the expression of related genes [8-10].

It has been found that plants mainly respond to the light signals received by phytochrome to regulate the expression of related genes through two signal transduction pathways: Constitutively Photomorphogenic/Deetiolated/FUSCA (COP/DET/FUS) complex pathway and Phytochrome Interacting Factors (PIFs) pathway [11,12], proteins of both pathways are inhibitors of plant photomorphogenesis. In dark environment, phytochrome exists in cytoplasm as Pr type in a physiological inactive state. At this time, the COP/DET/FUS complexes and PIFs proteins in

the nucleus inhibit the expression of genes related to photomorphogenesis. However, when the settings change from dark to light, the phytochrome absorbs red light and transforms into Pfr type with physiological activity and quickly gets transferred to the nucleus, which inhibits the activity of COP/DET/FUS complexes and PIFs proteins, thus activating the expression of genes involved in photomorphogenesis. As a signal center in cells, PIFs gather multiple signal transduction pathways and participate multiple gene transcription networks, thus affecting many aspects of morphogenesis downstream.

## Response of Non-coding RNA to Light Intensity

Depending on whether RNA itself has the ability to encode proteins, RNA can be divided into coding RNAs and non-coding RNAs (ncRNAs). More and more studies showed that ncRNA plays an important role in regulating gene expression at various levels during the growth and development of eukaryotes [13]. MicroRNA(miRNA), long non-coding RNA (lncRNA) and circular RNA (circRNA) are the three most widely studied ncRNAs. Studies have shown that plant miRNA, lncRNA and circRNA play an important role in regulating plant growth and development as well as various stress responses [14,15].

Plant miRNAs are often upregulated or down regulated under stress. For example, Li et al. [16] found that miR169 was down regulated under drought stress, which increases the transcription level of nuclear factor ya5 (nfy5) in an abscisic acid (ABA) - dependent manner. Studies showed that lncRNA also respond to kinds of stress. Zhang et al. [17] reported that maize lncRNAs are responsive to drought stress.

MicroRNAs could also play an important role in radiation-induced changes in gene expression, hence it is critical for the manifestation of light-induced cellular phenotypes and physiological responses [18]. Recently, Dong et al. [19] found microRNAs in tomato leaves showing differential expression patterns under different light qualities. While, a novel mechanism, miRNA-biogenetic inconsistency triggered by light was accounted for the intricacy of miRNA biogenesis during de-etiolation [20]. Until now, there are few reports about lncRNAs related to light treatment. *HIDDEN TREASURE 1* was described as a positive regulator of photomorphogenesis under red light treatment [21]. Recently, Sun et al. [22] identified a blue light-induced lncRNA that plays a role in blue light-directed plant photomorphogenesis.

## CircRNA May Play an Important Role in Response to Light Treatment

CircRNA is a special class of endogenous closed-loop

ncRNAs, which is a new research hotspot of ncRNA family after miRNA and lncRNA [23]. CircRNA is a class of RNA molecules with extremely high stability because its 3' and 5' ends are connected by a covalent bond [24]. Studies have shown that circRNA is widely distributed and ubiquitous in eukaryotes [25]. Although circRNAs have been shown to play an important role in the regulation of gene expression, most of their functions remain unknown.

In recent years, studies have shown that plant circRNA can respond to a variety of environmental stresses. He et al. [26] found that circRNAs in grass carp in response to GCRV infection. While some studies discovered that circRNAs in maize, Arabidopsis and wheat could respond to drought stress [27,28]. Zhu et al. [29] identified a large number of cucumbers circRNAs and revealed their possible biological roles in response to salt stress.

In “Systematic identification and analysis of light-responsive circular RNA and co-expression networks in lettuce (*Lactuca sativa*)”, Yang et al. [30] studied light response circRNA. This is the first report of circRNA in plant light response. In this study, Hong Kong Glass lettuce were treated under  $60 \pm 2 \mu\text{mol}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$ ,  $175 \pm 2 \mu\text{mol}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$  and  $340 \pm 2 \mu\text{mol}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$  light intensity. Using RNA deep sequence technology, 9 circRNAs libraries were constructed, 1650 circRNAs were identified. The results showed that 119 circRNAs were shared among the three treatment groups, and 484, 537, and 334 circRNAs were specific to the treatment groups. In order to verify the authenticity of the identified circRNA, specific primers were used in amplifying 10 circRNAs. The results of GO/KEGG analysis suggested that chloroplast related genes played an important role in the light response of lettuce leaves, especially sensitive to circRNA related regulation. Finally, a Light-responsive circRNA-miRNA-mRNA co-expression network was concluded.

## Conclusion

The work of Yang et al. [30] revealed the light response circRNA for the first time and found some candidate circRNAs. However, how these circRNAs respond to light intensity and what are their targets and many other unknowns require further study.

Altogether, the discovery of photoresponse circRNAs will provide a new direction for further understanding the mechanism of plant light regulation.

## References

1. Kami C, Lorrain S, Hornitschek P, Fankhauser C. Light-regulated plant growth and development. *Current Topics in Developmental Biology* 2010 Jan 1;91:29-66.

2. Walters RG. Towards an understanding of photosynthetic acclimation. *Journal of Experimental Botany.* 2005 Jan 1;56(411):435-47.
3. Bayat L, Arab M, Aliniaefard S, Seif M, Lastochkina O, Li T. Effects of growth under different light spectra on the subsequent high light tolerance in rose plants. *AoB Plants.* 2018 Oct;10(5):ply052.
4. Kaiserli E, Perrella G, Davidson ML. Light and temperature shape nuclear architecture and gene expression. *Current Opinion in Plant Biology.* 2018 Oct 1;45:103-11.
5. Perin G, Jones PR. Economic feasibility and long-term sustainability criteria on the path to enable a transition from fossil fuels to biofuels. *Current Opinion in Biotechnology.* 2019 Jun 1;57:175-82.
6. Deng XW, Quail PH. Signalling in light-controlled development. *Seminars in Cell & Developmental Biology.* 1999 Apr 1;10(2):121-129.
7. Demarsy E, Fankhauser C. Higher plants use LOV to perceive blue light. *Current Opinion in Plant Biology.* 2009 Feb 1;12(1):69-74.
8. Gyula P, Schäfer E, Nagy F. Light perception and signalling in higher plants. *Current Opinion in Plant Biology.* 2003 Oct 1;6(5):446-52.
9. Ma L, Li J, Qu L, Hager J, Chen Z, Zhao H, et al. Light control of Arabidopsis development entails coordinated regulation of genome expression and cellular pathways. *The Plant Cell.* 2001 Dec 1;13(12):2589-607.
10. Quail PH. Phytochrome photosensory signalling networks. *Nature Reviews Molecular Cell Biology.* 2002 Feb;3(2):85-93.
11. Leivar P, Quail PH. PIFs: pivotal components in a cellular signaling hub. *Trends in Plant Science.* 2011 Jan 1;16(1):19-28.
12. Lau OS, Deng XW. The photomorphogenic repressors COP1 and DET1: 20 years later. *Trends in Plant Science.* 2012 Oct 1;17(10):584-93.
13. Morris KV, Mattick JS. The rise of regulatory RNA. *Nature Reviews Genetics.* 2014 Jun;15(6):423-37.
14. Ye CY, Chen L, Liu C, Zhu QH, Fan L. Widespread noncoding circular RNAs in plants. *New Phytologist.* 2015 Oct;208(1):88-95.
15. Li LJ, Leng RX, Fan YG, Pan HF, Ye DQ. Translation of noncoding RNAs: focus on lncRNAs, pri-miRNAs, and circRNAs. *Experimental Cell Research.* 2017 Dec 1;361(1):1-8.
16. Li WX, Oono Y, Zhu J, He XJ, Wu JM, Iida K, et al. The Arabidopsis NFYA5 transcription factor is regulated transcriptionally and posttranscriptionally to promote drought resistance. *The Plant Cell.* 2008 Aug 1;20(8):2238-51.
17. Zhang W, Han Z, Guo Q, Liu Y, Zheng Y, Wu F, et al. Identification of maize long non-coding RNAs responsive to drought stress. *PloS One.* 2014 Jun 3;9(6):e98958.
18. Jayanthi A, Setaluri V. Light-Regulated Micro RNA s. *Photochemistry and photobiology.* 2015 Jan;91(1):163-72.
19. Dong F, Wang C, Dong Y, Hao S, Wang L, Sun X, et al. Differential expression of microRNAs in tomato leaves treated with different light qualities. *BMC Genomics.* 2020 Dec;21(1):1-1.
20. Choi SW, Ryu MY, Viczián A, Jung HJ, Kim GM, Arce AL, et al. Light triggers the miRNA-biogenetic inconsistency for de-etiolated seedling survivability in Arabidopsis thaliana. *Molecular Plant.* 2020 Mar 2;13(3):431-45.
21. Wang Y, Fan X, Lin F, He G, Terzaghi W, Zhu D, Deng XW. Arabidopsis noncoding RNA mediates control of photomorphogenesis by red light. *Proceedings of the National Academy of Sciences of the United States of America.* 2014 Jul 15;111(28):10359-64.
22. Sun Z, Huang K, Han Z, Wang P, Fang Y. Genome-wide identification of Arabidopsis long noncoding RNAs in response to the blue light. *Scientific Reports.* 2020 Apr 10;10(1):1-10.
23. Greene J, Baird AM, Brady L, Lim M, Gray SG, McDermott R, et al. Circular RNAs: biogenesis, function and role in human diseases. *Frontiers in Molecular Biosciences.* 2017 Jun 6;4:38.
24. Chen LL. The biogenesis and emerging roles of circular RNAs. *Nature reviews Molecular Cell Biology.* 2016 Apr;17(4):205-11.
25. Wang PL, Bao Y, Yee MC, Barrett SP, Hogan GJ, Olsen MN, et al. Circular RNA is expressed across the eukaryotic tree of life. *PloS One.* 2014 Mar 7;9(3):e90859.
26. He L, Zhang A, Xiong L, Li Y, Huang R, Liao L, et al. Deep circular RNA sequencing provides insights into the mechanism underlying grass carp reovirus infection. *International Journal of Molecular Sciences.* 2017 Sep;18(9):1977.

27. Zhang P, Fan Y, Sun X, Chen L, Terzaghi W, Bucher E, et al. A large-scale circular RNA profiling reveals universal molecular mechanisms responsive to drought stress in maize and Arabidopsis. *The Plant Journal*. 2019 May;98(4):697-713.

28. Wang Y, Yang M, Wei S, Qin F, Zhao H, Suo B. Identification of circular RNAs and their targets in leaves of *Triticum aestivum* L. under dehydration stress. *Frontiers in Plant Science*. 2017 Jan 5;7:2024.

29. Zhu YX, Jia JH, Yang L, Xia YC, Zhang HL, Jia JB, et al. Identification of cucumber circular RNAs responsive to salt stress. *BMC Plant Biology*. 2019 Dec 1;19(1):164.

30. Yang Z, Yang Z, Xie Y, Liu Q, Mei Y, Wu Y. Systematic Identification and Analysis of Light-Responsive Circular RNA and Co-expression Networks in Lettuce (*Lactuca sativa*). *G3: Genes, Genomes, Genetics*. 2020 Jul 1;10(7):2397-410.