

Plant Improvement Using Microrna-Based Biotechnology

Amal A. Alyamani¹, Salman Aloufi²

¹Department of Biotechnology, College of Science, Taif University, P.O. Box 11099, Taif 21944, Saudi Arabia
a.yamani@tu.edu.sa ORCID: <https://orcid.org/0000-0001-6086-5071>

²Taif Department of Biotechnology, Faculty of Science, Taif University, Taif 21974, Saudi Arabia s.aloufi@tu.edu.sa

Abstract:

Micro-RNAs are becoming a novel target for plant improvement. miRNAoverexpressing transgenic plants exhibited higher tolerance or sensitivity to different environmental abiotic stresses as compared to their wild type, according to researchers at Aberystwyth University in the UK. Seed germination and seedling establishment will be critical for the survival, health, and overall yield of the crop. The majority of transgenic technology studies have focused on the effects of stress conditions on seed germination (i.e., adverse environmental conditions. Identifying miRNA targets will help us understand the miRNAMEDIATED mechanisms that regulate plant growth and development. Further study of miRNAs could provide new tools for increasing crop yield and/or improving crop quality.

Keywords: MicroRNA-based biotechnology, Plant Improvement, MicroRNAs in plants.

Introduction

Transgenic crops provide enormous benefits to both humans and the environment. The initial stage in genetically engineering crops is to identify and clone interested genes. MicroRNAs (miRNAs) have emerged as a unique target for developing new crop cultivars. MiRNAs are a type of gene regulator that works at the post-transcriptional level.

Scientists have shown that manipulating a single miRNA gene can significantly increase crop yield and biomass. They have also shown it can improve crop tolerance to environmental stresses and improve crop adaptation to climate change. iR172 can efficiently guide the cleavage of its target transcripts. MiRNAs control gene expression at the post-transcriptional stage by repressing mRNA translation as well

as cleaving mRNAs directly. This shows that miRNAs may play a more complex role in controlling gene expression in plants than they do in animals. (Schwab et al., 2005).

miRNA biogenesis and evolution

Many miRNA families are evolutionarily conserved across all major lineages of plants. This suggests that miRNA-mediated gene regulation appears to have existed at the earliest stages of plant evolution. Several processes for miRNA origin have been postulated, including duplication of preexisting miRNA genes or protein-coding genes. (Nozawa et al., 2010).

MiRNA genes are transcribed by RNA polymerase II (Pol II). Pol II recruits a gene promoter to make the transcription happen (Kim et al, 2011). MiRNA guide and passenger (miRNA* strands with 2-nt 3' overhangs are usually fully compatible with one other. (Yu et al., 2005)

The principles of miRNA identification, expression, and functional analysis in plants

Identification of miRNAs is the first step to elucidate miRNA function. MiRNAs are conserved from worms to our human beings in animals and from flowering eudicots to flowering plants. Homologue-based comparative genomics approach has been widely used to identify plant miRNA since 2005. (Llave & Llave, 2002a; Park, 2002; Reinhart & Co., 2002b).

Computational tools and resources can be used to identify plant miRNAs and their targets. .

MiRNEST (integrative database resources for animal, plant, and virus miRNA data) contains miRNA information from 522 plant and animal species. There are currently 30,424 mature miRNAs from 206 species in the miRbase database. Some of them also combine expression and functional analyses. (Addo-Quaye et al., 2009).

Biotechnology and genetic analysis of phyto-miRNA

Gene silencing is one of the reverse genetic methods. Gene silencing can be accomplished in a variety of ways, including RNA interference (RNAi). Short interfering RNAs (siRNAs) can cause RNAi and microRNAs can cause gene silencing. (Eamens et al., 2017; Zhou & Luo, 2013; Ivashuta et al., 2011).

Phyto-miRNAs In biotechnology experiments, biogenesis and the foundation of particular silencing for plant genes

Next generation sequencing (NGS)-based roaches were used to identify miRNAs in various plants. MIR genes are usually transcribed by RNA polymerase II as primary long transcripts (pri-miRNAs). Next, miRNA: *miRNA is processed into a form that shows a high degree of complementary with its target..(Chi et al., 2009).

MiRNA-based biotechnology can help with plant development, fruit and seed development, as well as plant biomass yield. .

miRNAs regulate root development

Root tissues are developed from the root apical meristem (RAM). Plant roots play an important role in growth and development as well response to different abiotic and biotic stresses. Auxin, cytokine, and gibberellins are among the plant hormones that interact to govern RAM cell proliferation and elongation.. (Khan, 2011; Meng et al., 2010).(Wang et al., 2005).

MicroRNAs and innovative biotechnological approaches for increasing plant stress tolerance by altering their expression

In plants, miRNA targets form a broad group of genes involved in numerous biological processes, including development and defense responses to pathogens, insects, and environmental stresses. Understanding how plants respond to environmental stresses is important for the development of biotechnological tools to improve desirable agronomic traits..(Dong and Pei, 2014; Hajyzadeh et al., 2015; Ni et al., 2012; Trumbo et al., 2015; Zhang,2015).

CRISPR/Cas9, CRISPR-mediated gene editing, and other techniques have been shown to be useful for modulating miRNA accumulation in a variety of ways, according to a study published in the Journal of Biological Engineering (JBE) by researchers at the University of Bristol.

Research design and methods

Research type : A systematic review of the literature was carried out in order to find all studies that mentioned Plant Improvement Using MicroRNA-Based Biotechnology

Population and Research methods

A search strategy was designed with keywords combining MicroRNA-based biotechnology for plant improvement, MicroRNAs and their diverse functions in plants, The potential roles of microRNAs in molecular breeding, microRNA and Molecular breeding and MicroRNA and biotechnology in plant development, including articles published from October 10, 2016, to October 13, 2021. After the selection of potential eligible papers using the title and the abstract, reviewers (....) independently retrieved the full-text articles to assess the final eligibility.

Any disagreement over the eligibility of a specific study was resolved through the discussion with a fourth author Table 1.

Table 1

Search strategy criteria

Inclusion criteria
1. Study population: MicroRNA-based biotechnology for plant improvement, MicroRNAs and their diverse functions in plants, The potential roles of microRNAs in molecular breeding, microRNA and Molecular breeding and MRNA and biotechnology
Exclusion criteria
1. Studies with incomplete or lacking necessary data
2. Duplicate studies
3. Studies without accessible full-text versions
4. Studies not in English language
5. Studies on humans.

Implications and contribution to knowledge

The potential implications of the research for practice, and emphasize again Plant Improvement Using MicroRNA-Based Biotechnology:

Plant improvement is increasingly focusing on micro-RNAs. According to researchers, miRNA-overexpressing transgenic plants showed stronger tolerance or vulnerability to several environmental abiotic stresses than their wild type counterparts. The survival, health, and overall yield of the crop will be determined by seed germination and seedling establishment.

The majority of transgenic bio-technology research has focused on the impact of stress (i.e., poor environmental circumstances) on seed germination. Identifying miRNA targets will aid our understanding of miRNA-mediated plant growth and development mechanisms. MiRNAs will be studied in greater depth in the future.

Reference

1. Ara, A. ., Al Faria, L. ., Rani , R. ., & Mahbubur Rahman, A. . (2021). Diversity of Angiosperm Taxa in Chaar Khidirpur Area of Rajshahi, Bangladesh. *Journal of Scientific Research in Medical and Biological Sciences*, 2(3), 51-66. <https://doi.org/10.47631/jsrmb.v2i3.266>
2. B Z, Q W. MicroRNA, a new target for engineering new crop cultivars. *Bioengineered* [Internet]. 2016 Jan 2 [cited 2021 Oct 18];7(1):7–10. Available from: <https://pubmed.ncbi.nlm.nih.gov/26901236/>
3. Zhang B, Wang Q. MicroRNA-Based Biotechnology for Plant Improvement. *J Cell Physiol* [Internet]. 2015 Jan 1 [cited 2021 Oct 18];230(1):1–15. Available from: <https://onlinelibrary.wiley.com/doi/full/10.1002/jcp.24685>
4. Kim YJ, Zheng B, Yu Y, Won SY, Mo B, Chen X. The role of Mediator in small and long noncoding RNA production in *Arabidopsis thaliana*. *EMBO J*. 2011 Mar 2;30(5):814–22.
5. Luo Y, Guo Z, biology LL-D, 2013 undefined. Evolutionary conservation of microRNA regulatory programs in plant flower development. *Elsevier* [Internet]. [cited 2021 Oct 18]; Available from: <https://www.sciencedirect.com/science/article/pii/S0012160613002534>
6. Regulatory MA-B et BA (BBA)-G, 2008 undefined. Evolution of microRNAs and their targets: are all microRNAs biologically relevant? *Elsevier* [Internet]. [cited 2021 Oct 18]; Available from: https://www.sciencedirect.com/science/article/pii/S1874939908000473?casa_token=gEMbxncG6qQAAAAA:LbAYmnGTjI915QyqvTVY1XEg4sL8HkUzBDjzzYdqhJz4qXGDFq1J2VqBnbREIkWUPxNeh7HUcJ7

7. Addo-Quaye C, Miller W, Bioinformatics MA-, 2009 undefined. CleaveLand: a pipeline for using degradome data to find cleaved small RNA targets. *academic.oup.com* [Internet]. [cited 2021 Oct 18]; Available from: <https://academic.oup.com/bioinformatics/article-abstract/25/1/130/304557>
8. Sabzehzari M, Naghavi MR. Phyto-miRNA: A molecule with beneficial abilities for plant biotechnology. *Gene*. 2019 Jan 30;683:28–34.
9. Chi SW, Zang JB, Mele A, Darnell RB. Argonaute HITS-CLIP decodes microRNA–mRNA interaction maps. *Nat* 2009 4607254 [Internet]. 2009 Jun 17 [cited 2021 Oct 18];460(7254):479–86. Available from: <https://www.nature.com/articles/nature08170>
10. Yi F, Chen J, Yu J. Global analysis of uncapped mRNA changes under drought stress and microRNA-dependent endonucleolytic cleavages in foxtail millet. *BMC Plant Biol* [Internet]. 2015 Oct 6 [cited 2021 Oct 18];15(1). Available from: [/pmc/articles/PMC4594888/](https://pmc/articles/PMC4594888/)
11. Chakraborty, B., Labh, S. ., Rani, R. ., & Bhattacharjee, S. . (2021). Biodiversity and Management Status of Charia beel in Northern Bangladesh. *Journal of Scientific Research in Medical and Biological Sciences*, 2(2), 63-80. <https://doi.org/10.47631/jsrmb.v2i2.232>
12. Hackenberg M, ... PG-P biotechnology, 2015 undefined. Differential expression of micro RNA s and other small RNA s in barley between water and drought conditions. *Wiley Online Libr* [Internet]. 2014 Jan 1 [cited 2021 Oct 18];13(1):2–13. Available from: <https://onlinelibrary.wiley.com/doi/abs/10.1111/pbi.12220>
13. MF B, PCG F, AK K, FG H, AL N, HBC M, et al. MicroRNAs and new biotechnological tools for its modulation and improving stress tolerance in plants. *Plant Biotechnol J* [Internet]. 2019 Aug 1 [cited 2021 Oct 18];17(8):1482–500. Available from: <https://pubmed.ncbi.nlm.nih.gov/30947398/>
14. Sen, T. D. ., & Thakur, T. . (2021). Some Ethnomedicinal Plants of Western Himalayas Useful in Making Local Alcoholic Drinks. *Journal of Scientific Research in Medical and Biological Sciences*, 2(3), 75-103. <https://doi.org/10.47631/jsrmb.v2i3.309>
15. Zerín, T., Islam, A., Gulnàhar, S., Farjana, N. E., Begum, M. A. ., & Sadia, H.-E. (2021). Identification and Antibiotic Susceptibility of Blood Culture Isolates from Rajshahi, Bangladesh. *Journal of Scientific Research in Medical and Biological Sciences*, 2(2), 1-10. <https://doi.org/10.47631/jsrmb.v2i2.264>