

Microproteins of Plants: Small but Potent Regulators of Plant Growth

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Abstract

MicroProteins (miPs) are proteins with a single domain that are less than 20 kDa in size. This space permits microProteins to collaborate with viable areas of transformative related proteins and adjust the vital physiological pathways in a few creatures. Starting from the first report of a microProtein in quite a while, various microProteins have been distinguished in plants by computational methodologies. Nonetheless, a couple of up-and-comers have been practically described, basically in Arabidopsis. The new progress of manufactured microProteins in tweaking physiological exercises in crops makes these proteins fascinating contender for crop designing. Here, we exhaustively sum up the blend, method of activity, and practical jobs of microProteins in plants. We also talk about different ways to find plant microProteins. Also, we examine novel ways to deal with plan engineered microProteins that can be utilized to target proteins directing plant development and improvement. We at long last feature the possibilities and difficulties of using microProteins in future harvest improvement programs.

Keywords: Biomolecules; Plant science; Plant improvement

Introduction

Microproteins are a class of small proteins that play important roles in various biological processes [1]. They are characterized by their small size, typically consisting of less than 100 amino acids, and their ability to interact with larger proteins or regulatory molecules to modulate cellular functions. In recent years, microproteins in plants have gained significant attention due to their diverse functions and potential applications in crop improvement and biotechnology.

Plant microproteins are involved in a wide range of physiological processes, including development, signal transduction, stress responses, and defense mechanisms. Despite their small size, these proteins can have significant impacts on plant growth and adaptation to changing environmental conditions. They often act as regulatory elements in complex molecular networks, modulating the activity of larger proteins or acting as molecular switches.

The discovery and characterization of plant microproteins have been facilitated by advancements in genomic and proteomic technologies [2]. High-throughput sequencing and mass spectrometry techniques have enabled the identification and quantification of microproteins in plant tissues. Additionally, genetic and biochemical approaches have helped elucidate their functions and mechanisms of action.

One of the well-known examples of plant microproteins is the small signaling peptide family. These peptides are involved in intercellular communication and play crucial roles in plant development, such as root growth, stomatal regulation, and flower development. Another example is the microProtein 1 (miP1) family, which regulates flowering time in Arabidopsis thaliana.

The study of plant microproteins is still in its early stages, and many more microproteins and their functions are yet to be discovered [3]. Understanding the roles and mechanisms of action of these small proteins could have significant implications for improving crop yields, enhancing stress tolerance, and designing novel biotechnological applications in agriculture.

In summary, microproteins are small but functionally important proteins in plants. Their roles in various biological processes make them intriguing targets for further research and exploration. By unraveling their functions and mechanisms, scientists aim to uncover new ways to manipulate plant traits and enhance crop productivity.

Through both in-silico and functional studies, numerous putative and functional small proteins from plants have been identified. Be that as it may, a couple of them have been described as microProteins in view of their size, construction, beginning, and useful systems. Numerous proteins that are ordered as miPs, were recognized as interfacing accomplices of practical proteins, generally transcriptional controllers. The first miP recognized in quite a while was the DNA restricting Inhibitor (Id) protein [4]. Id was separated around thirty years prior from a cDNA library got from murine erythroleukemia cells. It is a protein with a tiny helix loop helix (HLH) domain of 16 kDa that interacts with the muscle differentiation regulator MyoD (Myoblast Determination Protein 1), a transcriptional regulator. The first miP family detailed in quite a while was the group of proteins. Through its leucine zipper domain, ZPR interacts with and regulates other proteins that contain leucine zippers post-translationally to alter plant development. It oversees formative cycles like undeveloped cell support in shoot apical meristem (SAM) and leaf improvement by connecting with HD-ZIPIII/Fire up. Before ZPRs, a miP known as TRYPTYCHON (TRY) was discovered and functionally characterized, but it was not considered a miP at the time. Afterward, in light of its size and capability, it was delegated a microProtein.

In light of their starting point, microProteins are named cis-miPs and trans-miPs. Cis-miPs are encoded by mRNA isoforms through elective grafting as well as substitute interpretation start and stop site choices. Trans-miPs, on the other hand, evolved as a result of genome amplification and a subsequent event of domain loss. Large numbers of the miPs are integrated by the interpretation of smORFs (little Open Understanding Edges) situated on lncRNAs [5]. An enormous number of smORFs have been found in creatures across realms including

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microscopic organisms, plants, and creatures; also, may comprise around 5-10% of the absolute genome of a living being. smORFs made an interpretation of items were accepted to have no pertinent capability. In any case, the disclosure of utilitarian deciphered results of under 100 amino acids like MIPS, opened another part in understanding the genome of a life form all the more profoundly.

Ethylene in root improvement

Ethylene affects root improvement. To start with, ethylene restrained the multiplication of cells in the apical meristem of the root. In addition, ethylene prevents cell development in the root's elongation zone. Past examinations on the ethylene impacts on the division of cells in roots, notwithstanding, have shown blended results [6]. As per past exploration, ethylene has no impact on the multiplication of cells in the apical meristem of the root yet controls cell extension in the zone of prolongation in the root. In the mean time, one more investigation discovered that ethylene repressed the expansion of cells in the root meristem, thus antagonistically controlling root meristem size. Ethylene treatment restrained parallel root commencement in tomatoes. The restraint of parallel root creation was forestalled by expanded ethylene amalgamation or flagging, suggesting that ethylene smothered horizontal root arrangement.

Ethylene in leaf senescence

Ethylene is quite possibly of the most fundamental chemical in its guideline of leaf senescence for plant species like maize (*Zea mays*) and rice (*Oryza sativa*). During the underlying phases of senescence beginning, ethylene biosynthesis sped up. Ethylene has been found to assume a part in sorting out the deterioration of cells and enacting the supplements back from maturing passes on to different pieces of plants at the sub-atomic level. As per, leaf cells played out an organized destroying and successive system that includes a few cycles [7]. For instance, protein debasement, nucleic corrosive decrease, film disturbance, peroxidation, and leaf shade deterioration. The leaf senescence in rice was advanced by the Ethylene Reaction Element 101 (OsERF101) that demonstrations all along and during the improvement of the leaf senescence. OsERF101 encoded a TF that was normal, which then prompted the degree of OsERF101 records in rice leaves rising dramatically during dull prompted senescence (DIS), and that implies that the maturing of passes on is because of dimness. Consequently, this inferred that OsERF101 is a record factor that is connected with senescence.

Ethylene in the guideline of plant reactions to biotic pressure conditions

Biotic pressure incorporates assaults by different microorganisms like microbes, growths, and nematodes. Plants have developed unique mechanisms to combat stress, such as the release of stress-responsive hormones like ethylene, as these conditions can reduce plant output. Past examinations depicted in sand pear (*Pyrus pyrifolia*), ethylene played a significant capability in the aversion to *Alternaria alternata*. To better comprehend this topic, the previous study utilized two cultivars—sensitive cultivars (Sucui1) and tolerant cultivars (Cuiguan). Plant obstruction was associated with low ethylene advancement, while growth improvement was initiated by high ethylene creation. Ethylene and catalase (Feline) action was found to have areas of strength for a. It was discovered that sensitive cultivars (Sucui1) had favorable conditions for both the growth of *A. alternata* and the induction of programmed cell death (PCD). These conditions included a high level of hydrogen peroxidase, weak CAT development, and high ethylene

biosynthesis. Ethylene has likewise been shown to be significant in the development of endophytic growths, for example, *Atractylodes lancea*. The development of parasite can prompt the development of sesquiterpenoids in plants by the creation of another endophytic organism, *Gilmaniella* sp. Ethylene additionally connected with various plant chemicals like salicylic corrosive and jasmonic corrosive to improve the sesquiterpene creation upstream.

Ethylene in the guideline of plant reactions to abiotic stress conditions

Exogenously applied ethylene can guard the photosynthesis cycle because of weighty metal pressure in *Brassica juncea* plants. Abiotic stresses like outrageous temperature (excessively low or high), weighty metals, UV radiation and inadequate or exorbitant water can change plant development and improvement. Due to an increase in the production of reactive oxygen species (ROS), heavy metal stress led to oxidative stress in this instance. Expanded degrees of ROS obstructed an assortment of cell, metabolic, and physiological pathways in plants. A past report directed found that the use of ethylene by ethephon animated the course of photosynthesis in two cultivars [8]. *juncea* and prompted a higher movement of nitrate reductase. The superior photosynthesis from the organization of ethephon could be credited to higher ACC synthase protein movement. Moreover, a few different examinations have exhibited that ethylene has a capability in dry spell pressure. For instance, when maize was subjected to drought stress, there was an inverse relationship between the levels of ethylene and the elongation of the root. The downregulation of the biosynthetic pathway of ethylene expanded yield in *Zea mays* that filled in water-pushed conditions. This finding recommended that ethylene took part in plants' guideline during dry spell pressure.

Phenolic compounds

A previous study found that ethylene effectively promoted the total phenolic compounds in *Catharanthus roseus* leaves, particularly C6C3 phenolic acid derivatives and C6C1 simple phenolic compounds. This, on the other hand, was not the case with the flavonoids or C6C3C6 compounds, whose results demonstrated a significant inhibitory trend. Consequently, ethylene can also accumulate flavonoids on its own or in combination with auxin. Auxin is a plant chemical that animates cell lengthening in shoots and is significant in plant development guideline. Ethylene balances the creation of chalcone isomerase, chalcone synthase, and flavonol synthase by directing the flavonol biosynthesis by means of the myeloblastosis (MYB12) record factor agreeing [9]. The treatment with ethylene antecedent, 1-aminocyclopropane-1-carboxylic corrosive (ACC) expanded the declaration of phenolic biosynthesis qualities, for example, anthranilate synthase (AS), isochorismate synthase (ICS), cytochrome P450 hydroxylation (C4H) and phenylalanine alkali lyase (Buddy).

Another study found that using 1-aminocyclopropane-1-carboxylic acid (ACC), an ethylene precursor, increased the total catechin content of oolong tea (*Camellia sinensis* L.) seedlings. Concurring, catechins are the most bountiful and significant phenolic constituents in tea plants. The all out catechin focus, including epigallocatechin and epicatechin portion, was viewed as more noteworthy in oolong tea seedlings following treatment with ACC, as estimated utilizing elite execution fluid chromatography. Following ACC openness, the amassing of phenolic substances including flavonoids, anthocyanins, and all out polyphenols was expanded. These discoveries propose that ethylene flagging was connected with the flavonoid creation pathway in oolong tea seedlings and managed catechin designation levels.

Alkaloids

Ethylene which goes about as a development controller impacted the improvement of alkaloids in plants. Ethylene was found to can increment or diminishing the quantity of alkaloids in culture media. Ethylene goes about as a go-between flagging atom in the blend of elicitors which produces terpenoid indole alkaloids (TIAs), concurring. In the past, it was found that the phytohormones ethylene and cytokinin raised the levels of alkaloid accumulation in periwinkle callus or cell suspension cultures [10]. When exogenously provided with cytokinin or ethylene (gave by ethephon), the centralization of indole alkaloids, for example, serpentine and ajmalicine expanded emphatically in cells that were subcultured in a sans d medium. Serpentine is an indole alkaloid tracked down in the *Rauvolfia serpentine* plant, while ajmalicine indole alkaloids are found in the *Catharanthus roseus* plant. *Leucojum aestivum*'s levels of Amaryllidaceae alkaloids like galanthamine and lycorine increased as ethylene levels decreased, according to the study.

Besides, guidelines of exogenous ethylene on terpenoid indole alkaloids creation and inner cadmium (Album) gathering in therapeutic plants (*Catharanthus roseus* L.) under Compact disc stress were additionally explored. The outcomes uncovered that ethylene treatment raised Album gathering level, and simultaneously the treatment expanded different TIAs. Illustration of TIAs that were expanded in this treatment was vindoline, catharanthine, and vinblastine. These are just a few of the crucial TIAs that aid *Catharanthus roseus* L., like in the defense system. Furthermore, TIAs pathway protein quality articulations at the transcriptional level showed an addition.

Besides, ethylene has been recognized to control alkaloid contents in the tobacco (*Nicotiana tabacum* L.) alkaloid digestion through record factor (TF) [11]. Nicotine, nornicotine, anatabine, and anabasine are the four main alkaloids that can be found in tobacco. In tobacco, overexpression significantly increases alkaloid accumulation, particularly in anatabine. NtERF91 helped the declaration of numerous nicotine biosynthesis qualities, and it likewise changed the alkaloid gathering design, prompting a critical ascent in anatabine testimony. Nicotine biosynthesis gene expression was triggered and alkaloid metabolism was controlled by NtERF91 in tobacco, particularly in the increase in anatabine accumulation.

Conclusion

Ethylene has been found to play a vital part in the guideline and change of plant improvement and security. Ethylene modulation in plant development promotes seed germination, root development, and leaf senescence. Besides, ethylene can safeguard plants from both abiotic and biotic stressors, permitting them to develop. Broad examinations in understanding the connection between plant chemicals, warm

and water pressure are vital in the flow peculiarity of environmental change. Also, ethylene guideline in optional metabolites, for example, phenolic compounds, alkaloids, glucosinolate, and terpenoids supports expanding or restraining auxiliary metabolite content levels in plants. Despite the significance of ethylene in plants that has been described, there are only a few published studies on how ethylene regulates secondary metabolism, so more research can be done in this area. All in all, the writing upholds the guideline and regulation of ethylene in plant improvement and auxiliary digestion, in light of the relative multitude of discoveries evaluated.

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Conflict of Interest

None

References

1. Alghamdi SS, Faiifi SAA, Migdadi H, Khan MA, Harty EHE, et al. (2012) Molecular diversity assessment using sequence related amplified polymorphism (SRAP) markers in *Vicia faba* L. *Int J Mol Sci* 13: 16457-16471.
2. Bai WN, Wang WT, Zhang DY (2014) Contrasts between the phylogeographic patterns of chloroplast and nuclear DNA highlight a role for pollen-mediated gene flow in preventing population divergence in an East Asian temperate tree. *Mol Phylogenet Evol* 81: 37-48.
3. McGuigan K (2006) Studying phenotypic evolution using multivariate quantitative genetics. *Mol Ecol* 15: 883-96.
4. Brown JE, Beresford NA, Hevrøy TH (2019) Exploring taxonomic and phylogenetic relationships to predict radiocaesium transfer to marine biota. *Sci Total Environ* 649: 916-928.
5. Konovalenko L, Bradshaw C, Andersson E, Lindqvist D, Kautsky U, et al. (2016) Evaluation of factors influencing accumulation of stable Sr and Cs in lake and coastal fish. *J Environ Radioact* 160: 64-79.
6. Babu KN, Sheeja TE, Minoo D, Rajesh MK, Samsudeen K, et al. (2021) Random amplified polymorphic DNA (RAPD) and derived techniques. *Methods Mol Biol* 2222: 219-247.
7. Apraku BB, Oliveira ALG, Petrol CD (2021) Genetic diversity and population structure of early and extra-early maturing maize germplasm adapted to sub-Saharan Africa. *BMC Plant Biol* 21: 96.
8. Prasanna BM (2012) Diversity in global maize germplasm: characterization and utilization. *J Biosci* 37: 843-55.
9. Hamouda M (2019) Molecular analysis of genetic diversity in population of *Silybum marianum* (L.) Gaertn in Egypt. *J Genet Eng Biotechnol* 17: 12.
10. Souframanien J, Gopalakrishna T (2004) A comparative analysis of genetic diversity in blackgram genotypes using RAPD and ISSR markers. *Theor Appl Genet* 109: 1687-93.
11. Chenuil A (2006) Choosing the right molecular genetic markers for studying biodiversity: from molecular evolution to practical aspects. *Genetica* 127: 101-120.