

A REVIEW ON PLANT HORMONES PRODUCING MICROORGANISMS

Anurag Verma*; **Vaibhav Rastogi****; **Prabhakar Viswakarma*****

Deepak Singh****

*Professor & Principal,

Department of Pharmacy, Teerthanker Mahaveer University,
Moradabad, Uttar Pradesh, INDIA

**Department of Pharmacy, Teerthanker Mahaveer University,
Moradabad, Uttar Pradesh, INDIA

Email id: vaibhavr.pharmacy@tmu.ac.in

***Department of Pharmacy, Teerthanker Mahaveer University,
Moradabad, Uttar Pradesh, INDIA

**** Lecturer,

Department of Pharmacy, Teerthanker Mahaveer University,
Moradabad, Uttar Pradesh, INDIA

DOI: 10.5958/2249-7137.2021.02498.8

ABSTRACT

Plant hormones, also known as phytohormones, are divided into five categories: auxins, abscisic acid, cytokines, gibberellins, or ethylene. Many more phytohormones have now been discovered. The capacity to generate phytohormones is found in a wide range of microbial species, with the greatest information gathered on the synthesis and function of auxin. The function of various phytohormones in the interaction with the plant is addressed in this chapter, as well as microbial biosynthesis, control, and regulation of microbial production. Microbial phytohormone synthesis is a powerful method for changing plant physiology, resulting in a variety of effects ranging from disease to plant growth stimulation. However, there is currently a paucity of genetic evidence for the involvement of several phytohormones in microbe-plants interactions, casting doubt on the relevance of microbial synthesis. Plant studies in an agronomic context, along with targeted methods focused on genetic evidence for the function of phytohormones, will enable uncovering the significance and potential of this interesting microbial feature.

KEYWORDS: *Auxins, Cytokinins, Ethylene, Microbe, Plant Hormones.*

1. INTRODUCTION

Hormones are chemical substances generated in tiny quantities in a specific tissue that govern and regulate different processes in the receptive tissue such as growth, metabolism, or reproduction. Plants generate a variety of hormones, also known as phytohormones, but their structures are relatively basic compared to animal hormones, as well as the components are not synthesized and stored in specialized glands. Auxins, abscisic cytokinins, gibberellins, acid, or ethylene are the five classic phytohormone classes. Phytohormones such as strigolactones,

salicylic acids, brassinosteroids, jasmonate, polyamines, as well as nitric oxide have just lately been identified [1].

The physiological activities of these hormones have been researched extensively in recent decades, but the molecular processes by which they exert their effects have only lately been discovered. The dose-response curve for auxins illustrates how changes in hormone concentrations may dramatically affect growth and development of plants both in a positive and negative manner. Furthermore, since most phytohormones do not operate alone on a specific growth or developmental component, hormonal balances across various classes may be critical. The conjugation of the active hormone to other molecules like as sugars and amino acids, which (reversibly) inactivates the hormone, is another neglected component of phytohormonal activity [2].

1.1. Microbes and Phytohormones:

Many soil as well as plant-associated bacteria and fungi have also been shown to produce phytohormones in the supernatant of their culture media. Phytohormones do not cause normal hormonal or significant physiological changes in these species. Changes in root architecture and plant growth promotion have been related to microbial phytohormone production. However, depending on the phytohormone and the investigated microbial strain, the degree of evidence for their participation may vary greatly. The presence of a phytohormone in a microbial culture's supernatant is insufficient to establish a functional role for this molecule in its interaction with the plant. The association of plant growth responses with hormone levels measured in the culture media or on/in colonized plant tissues may be used as further proof. The final evidence is inoculation with a bacterial mutant strain that is deficient in phytohormonal production, demonstrating the phytohormone's participation directly. Many microorganisms produce phytohormones, which may be detected in their culture media. However, several of the reported instances lack the required follow-up studies to prove their involvement in plant growth enhancement [3], [4].

1.1.1. Auxins:

In the subapical area of the stem, this group of phytohormones may cause cell elongation. Auxins are involved in virtually every aspect of plant growth and development, including shoots and roots elongation, cell division stimulation, lateral and adventitious root initiation, apical dominance, vascular tissue differentiation, gravitropism, and phototropism, to name a few (Davies 2010). Indole-3-acetic acid is the most common auxin found in nature (IAA). Other active auxins include indole-3-butyric acid and phenylacetic acid, but their biosynthesis routes and functions have not been well investigated.

1.1.2. Microbes' IAA Biosynthetic Pathways:

Until far, only six biosynthetic routes in microorganisms have been identified, with the majority of them predicated on the presence of metabolic intermediates in the culture. Because there is no genetic evidence for many pathways, the existence and significance of these pathways must be discovered. The aromatic amino acid tryptophan is used as a precursor in most routes. Despite the many routes, there seem to be two main microbial pathways based on both abundance and genetic evidence: one through intermediate indole-3-acetamide (IAM) and the other via intermediate indole-3-pyruvate (IIP) (IPyA). Tryptophan is transformed to IAM by a tryptophan

monooxygenase, which is subsequently catalyzed to IAA by an IAM hydrolase in the IAM route. The Many phytopathogenic bacteria, as well as certain rhizobia, have been studied extensively. Other microbial routes for IAA production have been suggested in addition to the two mentioned above, although genetic evidence for the majority of these processes is missing. Tryptophan is decarboxylated by a tryptophan decarboxylase before being converted to IAAlD by an amine oxidase in the tryptamine route. A route through indole-3-acetonitrile has been proposed, based on the conversion of indole-3-acetonitrile to IAA directly or via IAM by nitrilases or nitrile hydratase in plants. It's worth noting that several IAA biosynthesis routes may exist in a single organism, as shown by *Pantoea agglomerans*, whose genome encodes both the IAM and the IPy A pathways. Microbes have storage products and conjugates similar to plants, but their function is unknown [5].

Biosynthesis of IAA is regulated. IAA biosynthesis in bacteria is carefully controlled because it is expensive to manufacture, owing to the high expense of synthesizing tryptophan. Pathogenic *Agrobacterium* strains are the only exception. Strong (plant-specific) constitutive promoters regulate the IAA biosynthesis genes. The tryptophan pool of the plant is utilized to generate large quantities of IAA, inducing gall development in conjunction with a high level of cytokinins, since this DNA region is transmitted to the plant following infection (Jameson 2000). Expression is mainly related to other virulence factors such as the type III secretion system in other phytopathogens (those that do not transfer DNA to plants) (TTSS). Auxin biosynthesis is decreased in a TTSS mutant in *Ralstonia solanacearum*, whereas the expression of TTSS genes is reduced in an IAA mutant in *Erwinia chrysanthemum*. mutation in biosynthesis Microbial IAA's Impact on Plants and Microbes [6].

Auxin synthesis (usually in conjunction with abnormal cytokinin production) by phytopathogens has a significant impact on plants (gall and tumor formation). The connection between bacterial IAA and plant disease is explicitly shown when auxin production is inactivated, resulting in decreased or no gall development. Both the IAM and IPyA pathways are found in the gall-inducing bacteria *P. agglomerans* pv. *Gypsophilae*, enabling researchers to investigate their roles. The IAM route is inactivated, resulting in a substantial reduction in gall size without compromising colonization capacity, while the IPyA pathway is inactivated, resulting in no significant reduction in gall size but a loss in epiphytic fitness as assessed by colonization capacity [7].

Auxins impact not just plants, but also microorganisms, causing physiological changes as well as altered gene expression. IAA has been found to shut off gene production in *Agrobacterium tumefaciens*, which may be a signal for the bacterium to complete a successful plant transformation. In yeast, IAA causes adhesion and filamentation via the surface protein FLO11, which is mediated by YAP-1. It was proposed that IAA may arise at wounding areas on plants and function as an appealing signal for yeast. IAA protects cells in *Escherichia coli* from harmful stress conditions. Genes encoding cell envelope components and stress-resistance proteins are also elevated in response to IAA therapy. IAA seems to function as a signal molecule in beneficial bacteria, causing gene expression to change in response to the presence of the plant environment. IAA-regulated genes are involved in flavonoid signal processing, root attachment, and motility switching in *Rhizobium* [8].

Degradation of Auxin The enzyme responsible for IAA degradation are encoded by the *iac* locus in *P. putida*. IAA is degraded to catechol, which may then be degraded to -ketoadipeate in a three-step process. In addition, a MarR-type *iac* gene expression repressor was discovered, which is likely released in the presence of IAA. Despite this genetic understanding of IAA degradation, the ecological role of auxin degradation in plants interactions is unclear, however it has been speculated that this activity may disrupt plant auxin homeostasis for the bacterium's advantage. Auxin breakdown by bacteria, on the other hand, may offer a nutritional advantage [9].

1.2. Ethylene, Cytokinins, Gibberellins, Abscisic Acid are Plant Hormones:

Cytokinin Biosynthesis and Function The majority of naturally occurring cytokinins (CK) are generated from adenine and are changed at the N6 position, including the ribosides, ribosides, and glycosides. In both plant roots and shoots, CKs stimulate cell proliferation and differentiation in meristematic tissues. They also play a role in senescence deferral, organ creation, root and root hair growth, and leaf expansion (Davies 2010). The transfer of an isoprenoid moiety (usually dimethylallyl pyrophosphate) to adenosine phosphate, mediated by adenosine phosphate-isopentenyl transferase, results in isopentenyl adenosine-5'-phosphate in plants.

Gibberellin Biosynthesis and Function Gibberellins (GAs) are a family of over 100 chemicals that are categorized as tetracyclic diterpenoid acids and have the backbone ent-gibberellane. During nearly all phases of plant development, GAs are engaged in developmental activities such as cell division and elongation (from seed germination to fruit growth). In addition, the function of Gas is influenced by the balance of other phytohormones. GA synthesis has been found in both fungus and bacteria, and biochemical routes have been suggested and/or unraveled. GA biosynthesis (beginning from the precursor GA12-aldehyde) has developed separately from plant routes in the fungal rice disease *Gibberella fujikuroi*, which is exploited to commercially generate GA3. It varies particularly at the stage when the 3- and 13-hydroxylation occurs. The biosynthetic genes in *G. fujikuroi* are grouped together in the genome. In bacteria, there is just a small amount of genetic evidence for GA production. In certain *Rhizobium* and *Bradyrhizobium* strains, operons comprising genes encoding for potential GA biosynthetic enzymes were discovered.

1.3. Abscisic Acid is a kind of astringent.

Abscisic acid (ABA) slows seed germination and promotes stomatal closure and fruit ripening. It also plays a role in bud dormancy as well as defensive responses to abiotic stressors including drought, salt stress, and metal toxicity. The "indirect pathway" is the method for ABA production in plants. In brief, the carotenoid lycopene is converted to violaxanthin, which is then split into xanthoxin by a dioxygenase. In two enzymatic processes, the latter chemical is transformed to ABA. Although the biosynthesis routes for *A. brasilense* and *B. japonicum* strains have been described, the biosynthetic pathways remain unclear. Bacterial ABA production may interfere with cytokinin levels in plants because ABA inhibits cytokinin biosynthesis. Furthermore, under stress circumstances, bacterial ABA synthesis may help plants maintain their internal ABA pool, reducing the detrimental consequences of the imposed stress.

1.4. Microbes Change Ethylene Levels:

Physiological and developmental processes like as seed germination, cell growth, senescence, and abscission are all affected by the gaseous phytohormone ethylene. It's also known as the ripening hormone since it causes fruit to mature. Ethylene also has a role in pathogen defense responses in plants. By working synergistically with jasmonate on one branch of the route leading to resistance to necrotrophic infections, it may influence the outcome of jasmonate-dependent defensive responses. Ethylene, on the other hand, inhibits the MYC branch of the jasmonate pathway, making you more vulnerable to insect assaults. In abiotic stress situations, ethylene plays a function. Elevated ethylene levels under stressful situations may have inhibitory effects.

1.5. Impact on the development of plants:

The synthesis of ethylene by bacterial infections such as *Pseudomonas*, *Xanthomonas*, and *Erwinia* has been documented. By causing hormonal imbalances in the plant, ethylene production contributes to bacterial pathogenicity. The metabolic routes proposed by bacteria differ from those proposed by plants. Methionine is the precursor in the first bacterial process, whereas 2-oxoglutarate is the precursor in the second. The potential ethylene biosynthesis routes and the function of ethylene production in illness are still poorly understood. Because ethylene accumulates in plants under stress (such as drought and wounding), lowering ethylene levels may help to relieve stress-induced growth retardation. Some helpful bacteria use one of these strategies.

Methionine is used to make ethylene in plants. S adenosylmethionine (SAM) is transformed to 1-aminocyclopropane-1-carboxylate (ACC) and 5'-deoxy-5'-methylthioadenosine by the activity of a SAM synthase and also an ACC synthase. Finally, ACC oxidase breaks down ACC into ethylene, carbon dioxide, and cyanide. Bacteria that reduce ethylene levels produce the enzyme ACC deaminase (AcdS), which converts the direct ethylene precursor ACC to -ketobutyrate and ammonia, reducing plant ethylene production.

2. DISCUSSION

Drought, high temperature, salt, or heavy metal are among abiotic stressors that plants face. Abiotic stressors cause abnormalities in the genetic control of cellular processes, which have a detrimental effect on plant physiology as well as morphology. Plants use a variety of tolerance mechanisms or pathways to counteract the impacts of stressors that arise when their metabolism is disrupted. Phytohormones are one of the most essential growth regulators; they have a significant effect on plant metabolism and are also crucial in the activation of plant defense response systems in response to stress. Supplementation with exogenous phytohormones has been used to enhance growth and metabolism in stressed animals. Phytohormones generated by root-associated microorganisms have recently been shown to be significant metabolic engineering targets for developing host tolerance to abiotic stressors. Phytohormone biosynthesis routes have been discovered using a variety of genetic and biochemical techniques, and there are many reviews on the subject. We discuss current information on the role of phytohormones in improving abiotic stress tolerance and defense response in plants subjected to various stressors in this paper. We concentrate on recent breakthroughs in determining the functions of microbial phytohormones in stress tolerance, particularly in agricultural plants.

3. CONCLUSION

The synthesis of phytohormones by bacteria is a powerful method for microorganisms to influence plant physiology. The production and function of phytohormones in plant interaction are extensively researched and supported by genetic data, as described above. However, in so many cases, this is not the case, raising doubts about the phytohormone's role in microbe-plant interactions. More research is needed to determine if microbial production is a genuine effector in the relationship or just a by-product of microbial metabolism with no significant function. Plant trials in an agronomic context are also required. The imported organisms will have to compete with the indigenous microflora in these circumstances, which may explain the poor repeatability and high variability.

REFERENCES:

1. Qureshi O, Sohail H, Latos A, Strap JL. The effect of phytohormones on the growth, cellulose production and pellicle properties of *Gluconacetobacter xylinus* ATCC 53582. *Acetic Acid Bact.*, 2013;2(1). doi: 10.4081/aab.2013.s1.e7.
2. Sanchez L. et al. Rhamnolipids elicit defense responses and induce disease resistance against biotrophic, hemibiotrophic, and necrotrophic pathogens that require different signaling pathways in *Arabidopsis* and highlight a central role for salicylic acid. *Plant Physiol.*, 2012 Nov;160(3):1630-41. doi: 10.1104/pp.112.201913.
3. Demain AL, Fang A. The natural functions of secondary metabolites. *Advances in biochemical engineering/biotechnology*. 2000;69:1-39. doi: 10.1007/3-540-44964-7_1.
4. Lin HR, Shu HY, Lin GH. Biological roles of indole-3-acetic acid in *Acinetobacter baumannii*. *Microbiol. Res.*, 2018 Nov;216:30-39. doi: 10.1016/j.micres.2018.08.004.
5. Ravindran B, Wong JWC, Selvam A, Sekaran G. Influence of microbial diversity and plant growth hormones in compost and vermicompost from fermented tannery waste. *Bioresour. Technol.*, 2016, doi: 10.1016/j.biortech.2016.03.032.
6. Khalaf EM, Raizada MN. Taxonomic and functional diversity of cultured seed associated microbes of the cucurbit family. *BMC Microbiol.*, 2016;16: 131. doi: 10.1186/s12866-016-0743-2.
7. Asari S. et al. Analysis of plant growth-promoting properties of *Bacillus amyloliquefaciens* UCMB5113 using *Arabidopsis thaliana* as host plant. *Planta*, 2017;245:15–30. doi: 10.1007/s00425-016-2580-9.
8. Howden AJM, Preston GM. Nitrilase enzymes and their role in plant-microbe interactions. *Microbial Biotechnology*. 2009;2(4):441–451. doi: 10.1111/j.1751-7915.2009.00111.x.
9. Parthasarathy A, Cross PJ, Dobson RCJ, Adams LE, Savka MA, Hudson AO. A Three-Ring circus: Metabolism of the three proteogenic aromatic amino acids and their role in the health of plants and animals. *Frontiers in Molecular Biosciences*. 2018, doi: 10.3389/fmolb.2018.00029.