

Production and Metabolism of Indole Acetic Acid (IAA) by Root Nodule Bacteria (*Rhizobium*): A Review

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The production of indole acetic acid (IAA) by the root nodule bacteria is considered to have many important physiological implications. The biosynthesis, enzymatic oxidation and metabolism of IAA in *Rhizobium* have been reviewed. The existence of two different types of IAA biosynthesis pathways in plants and two different types of IAA biosynthesis pathways in *Rhizobium* and factors influencing the biosynthesis of its have described. The biological activity of the oxidation products of IAA and production of IAA in culture has also been discussed. Role of ACC deaminase on IAA metabolism, and VAM induced IAA production and role of IAA in legume-*Rhizobium* symbiosis are also critically reviewed. Isolation, identification and estimation of IAA by rhizobacteria have also been included with 140 references. The IAA content in the nodule and supply to the host may be taken as the second line of symbiosis in the root nodule-*Rhizobium* association.

Key words: Indole Acetic Acid (IAA), Root nodule, Rhizobacteria, Legume-*Rhizobium* symbiosis.

Indole acetic acid (IAA), earlier known as heteroauxin, was isolated from urine¹, cultures of yeast plasmolysate², *Rhizopus suinus*³ and a large number of higher plants⁴. The term auxin (Greek 'auxein', "to increase") was first used by Went (1928)⁵, who discovered that some unidentified compound probably caused curvature of Oat coleoptiles towards light⁶. Since the 1930's when K. V. Thimann (1935)³ first observed the synthesis of IAA in the mould *Rhizopus suinus*, which had been fed the amino acid tryptophan⁷.

Many physiological activities of plants are regulated by a variety of plant growth regulators and phytohormones. A large amount of information

regarding phytohormones, nitrogen fixation, nodules (development, morphogenesis and physiology) and hormone production by microorganisms had enriched the literature from time to time. Among which IAA is play a critical role in nodule and nodule bacteria for the nodule development and symbiotic relationship. IAA has been implicated in virtually all aspects of plant growth and development^{8,9}.

Recently advancement in understanding the IAA signaling pathway in plants has been established. The advancement in plant IAA signaling has also intensified research on the various aspects of bacterial IAA synthesis, including its role in bacteria-plant interactions. The role of IAA in plant-microorganisms interactions appears diverse in different bacterial species. The detail biochemical pathways of bacterial IAA synthesis and their regulation have provided some

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clues on the possible interactions between plants and IAA producing bacteria. The present review mainly includes the IAA bioproduction and metabolism by Rhizobacteria and their role in physiology of root and nodule in legume plants.

Metabolism of IAA

Biosynthesis of IAA

German botanist Julius Van Sachs (1832-1897) proposed that chemical messenger is responsible for formation and growth of different plant organs. After that Charles Darwin performed phototropism experiment in which demonstrated the presence of a transported signal originating from the plant apex, able to promote differential cell elongation in the seedling lower parts resulting in its bending toward the light source¹⁰. This signal was subsequently isolated and named auxin by Went (1935)¹¹. Since the 1930's when K.V. Thimann first observed the synthesis of IAA in the mould *Rhizopus suinus*, which had been fed the amino acid tryptophan⁷.

Several pathways are known regarding IAA biosynthesis. In higher plants, synthesis of IAA occurs in three steps, beginning with the conversion of tryptophan involving donation of the amino group to a α -keto acid by a transamination reaction to form indole-3-pyruvic acid and then decarboxylation of indole-3-pyruvate to form indole-3-acetaldehyde, oxidized to IAA in the last step^{6,7} (Fig- I)¹². Indole-3-acetaldehyde may also be reversibly reduced to indole-3-ethanol. The second pathway involved an initial decarboxylation of tryptophan to tryptamine⁷. Tryptamine was converted to indole-3-acetaldehyde by amine oxidase, which was in turn oxidized to IAA (Fig -I)¹². However, mutants of maize deficient in tryptophan synthesis formed large amounts of IAA, although tryptophan synthesis was blocked. Possibly there were alternative pathways for IAA synthesis in different plants¹³. Ostin *et al.* (1999)¹⁴ reported the presence of tryptophan independent pathway of IAA synthesis in maize (Fig -II)¹². Biosynthesis of IAA via indole-3-pyruvate (IPA) and indole-3-acetaldehyde pathways were found to occur in *Rhizobium meliloti*¹⁵ and in *Bradyrhizobium* sp.¹⁶. *Rhizobium leguminosarum* bv. *phaseoli* was shown to convert tryptophan to indole-3-ethanol (Ieth), IAA and indole-3-methanol (IM); Ieth to IAA and IM; and IAA to IM¹⁷. Kobayashi *et al.* (1995)¹⁸

proposed a pathway; common in plant associated bacteria, in which indole-3-acetonitrile (IAN) was converted to indole-3-acetamide (IAM) by nitrile hydratase and IAM was then converted to IAA by amidase in *Rhizobium* spp. Fast growing *Rhizobium* spp. and *Bradyrhizobium* sp. produced IAA as well as a number of IAA precursors in free living state^{17,19}.

The biosynthesis of IAA is not restricted to only root nodule bacteria, it also exist in different bacteria including plant growth promoting Rhizobacteria. However there are different IAA biosynthesis pathway exist in different bacteria²⁰. The overview of bacterial IAA biosynthesis pathways is given in Figure-III²⁰. Tryptophan has been identified as a main precursor for IAA biosynthesis in bacteria. There are following two types of IAA biosynthetic pathway exist in different species of *Rhizobium*.

Indole-3-acetamide (IAM) pathway

Indole-3-acetamide (IAM) pathway is a two step pathway where tryptophan is first converted to IAM by the enzyme tryptophan – 2-monoxygenase encoded by the *iaaM* gene. Later IAM is converted to IAA by the enzyme IAM hydrolase encoded by the gene *iaaH* (Fig – III). The gene *iaaM* and *iaaH* have been cloned and characterized in *Rhizobium* sp. and *Bradyrhizobium* sp. The IAM pathway was described previously as bacterial specific pathway, but Pollmann (2002, 2003)^{21,22} first stated that this pathway also operated in plant *Arabidopsis thaliana*.

Indole-3-pyruvate (IPyA) pathway

Indole-3-pyruvate (IPyA) pathway is considered as major pathway for biosynthesis in plants. But the key genes or enzymes have not been identified yet in plants. In the first step tryptophan is converted into IPyA by the enzyme aminotransferase through transamination. The second step is rate limiting step where IPyA is decarboxylated to indole-3-acetaldehyde (IAAld) by indole-3-pyruvate decarboxylase. In the last step IAAld is oxidized in IAA (Fig- III)²⁰. This pathway has been described in a broad range of bacteria like *Bradyrhizobium*, *Rhizobium*, *Azospirillum*, *Enterobacter cloacae* and cyanobacteria.

Factors influence IAA biosynthesis in bacteria

There are several factors alters the levels

of IAA biosynthesis and / or the IAA biosynthesis gene expression in bacteria. But it is not possible to integrate these factors into a comprehensive regulatory scheme of IAA biosynthesis in bacteria. This may be due to the diversity of regulation of IAA biosynthesis across bacteria and also lack of integrated studies following IAA expression in different bacteria and different environments.

Environmental factors modulating IAA biosynthesis

IAA biosynthesis in different bacteria is related to environmental stress including pH²³, osmotic and matrix stress²⁴ and carbon limitation^{23, 25}. Although the diversity of stress factors associated with modulating IAA expression in different bacteria, a common feature can be identified. The expression of IAA biosynthesis genes are in a fine tuned to encounter environmental stresses associated with the soil and plant environment. A typical rhizosphere environment is acidic pH due to proton extrusion through membranes of root cells. Similarly, matrix potential is an important condition in the environment of epiphytic bacteria²⁴.

Another class of factors regulating bacterial IAA production are contains of plant extracts. In the symbiotic bacteria *Rhizobium* sp., flavonoids produced by the host plant stimulate IAA production in a NodD1-, NodD2-, and SyrM2-dependent manner. NodD1, NodD2 and SyrM2 form a regulatory cascade that coordinates the expression of genes under influence of flavonoids²⁶. In *Xanthomonas axonopodis* IAA production increased in the presence of plant leaf extracts from *Citrus cinensis*. The question as to which specific compound is responsible for this induction remains unclear²⁷.

Tryptophan is an important molecule that alter the level of IAA and identified as the main precursor for IAA. The addition of exogenous tryptophan was shown to increase the IAA production in various bacteria^{28, 29}. There are two sources of tryptophan in rhizosphere viz. one from degrading root and microbial cells³⁰ and other from root exudates³¹. Although the amount of tryptophan in root exudates is rather low, exogenous tryptophan can be efficiently absorbed by bacteria. The K_m value indicate that the affinity of the transporter for tryptophan is low and the affinity of bacteria for tryptophan is high which makes

them good scavengers for tryptophan even at low concentration³². Besides the role of the precursor tryptophan in the regulation of IAA production, IAA biosynthesis can also be modulated by the end-product IAA and by its intermediates¹⁸.

Genetic factors modulating IAA biosynthesis

There are different genetic factors have been involved in level of IAA biosynthesis in bacteria firstly, the location of IAA biosynthesis gene in the genome, either plasmid³³ or chromosomal³⁴ has been shown to modulate the level of IAA production. Secondly, the mode of expression, constitutive or induced of IAA biosynthesis genes was observed to differ across biosynthesis pathways and across bacterial species. Further, RpoS – transcriptional regulators, regulates transcription of genes in response to stress conditions and starvation and the two component system GacS/GacA controls the expression of genes^{35, 36}.

Role of ACC deaminase on IAA metabolism in *Rhizobium*

The enzyme ACC deaminase cleaves ACC, the immediate precursor of ethylene in plants, to form ammonia and α -ketobutyrate. This multimeric enzyme is a common component of many soil microorganisms, both bacteria and fungi. The pioneering work in elaborating the biochemical properties of ACC deaminase is largely the results of studies carried out by Honma and his co-worker^{37, 38}. ACC deaminase is a multimeric enzyme (homodimeric or homotrimeric) with a subunit molecular mass of approximately 35-42 kDa. It is a sulfhydryl enzyme in which one molecule of the essential co-factor pyridoxal phosphate (PLP) is tightly bound to each subunit. Interestingly, the enzyme ACC deaminase is cytoplasmically localized³⁹ so that the substrate ACC must be exuded by plant tissues⁴⁰ and subsequently taken up by an ACC deaminase-containing microorganism before it is cleaved⁴¹. The PLP-dependent enzymes catalyze a wide variety of biochemical reactions, many of which are involved in the metabolism of amino acids. In most of these reactions two basic chemical properties of the PLP have been conserved: (i) PLP forms an external aldimine between its aldehyde group and the α -amino group of the substrates and (ii) PLP acts as an electron sink, withdrawing electrons from the substrate⁴². In higher plants, the

enzyme S-adenosyl-L-methionine (SAM) synthetase catalyzes the conversion of methionine to SAM⁴³; ACC synthase catalyzes the hydrolysis of SAM to ACC and 5' methylthioadenosine⁴⁴; and ACC oxidase catalyzes the conversion of ACC to ethylene, carbon dioxide, and hydrogen cyanide⁴².

The plant hormone ethylene plays an important role in root initiation and elongation, nodulation, senescence, abscission and ripening as well as in stress signaling⁴⁵. During periods of environmental stress, plants produce high levels of "stress ethylene". Moreover, much of the growth inhibition that occurs as a consequence of an environmental stress is the result of the response of the plant to the increased levels of stress ethylene which exacerbates the response to the stressor. In addition, inhibitors of ethylene synthesis can significantly decrease the severity of some environmental stresses. Thus, if ACC deaminase-containing bacteria can lower plant ethylene levels,

treatment of plants with these organisms should provide some protection against the inhibitory effects of these stresses.

The ACC deaminase- containing plant growth-promoting bacteria bind to the surface of either the seed or root of a developing plant-some endophytic bacteria are also located inside of the plant root (Fig.-IV)⁴¹. In response to root exudates, including the amino acid tryptophan, the bacteria synthesize indoleacetic acid (IAA). Plant cells take up some of the IAA that is secreted by the bacteria and, together with the endogenous plant IAA, can stimulate plant cell proliferation and/or elongation as well as induce the synthesis of the enzyme ACC synthase. Some of the ACC, already present or newly synthesized by the plant, is exuded and taken up by the ACC deaminase-containing bacteria. This ACC is cleaved by ACC deaminase to form ammonia and alpha-ketobutyrate, both of which are readily metabolized by the bacteria. As a

Table 1. IAA content in root nodules of some legumes and IAA production by their symbionts

Name of the Plant	Name of the symbiont	Max IAA present in root nodules (µg/g)	Max IAA produced by the symbiont (µg/ml)	Reported by
<i>Pongamia pinnata</i>	<i>Rhizobium sp.</i>	206	-	Sinha <i>et al.</i> (1981) ¹¹⁸
<i>Phaseolus aureus</i>	<i>Rhizobium sp.</i> (P5)	7.0	169.29	Dangar (1987) ¹¹⁹
<i>Pterocarpus marsupium</i>	<i>Rhizobium sp.</i> (M9)	11.5	160.18	
<i>Lens esculenta</i>	<i>Rhizobium sp.</i> (L1)	14.5	187.47	
<i>Butea monosperma</i>	<i>Rhizobium sp.</i> (B3)	21.0	188.99	
<i>Erythrina indica</i>	<i>Rhizobium sp.</i>	65.0	152	Bhowmick (1987) ¹²⁰
<i>Sesbania grandiflora</i>	<i>Rhizobium sp.</i>	50.0	152.0	
<i>Pterocarpus santalinus</i>	<i>Rhizobium sp.</i>	46.86	131	
<i>Samanea saman</i>	<i>Rhizobium sp.</i>	5.4	83.0	Chattopadhyay (1989) ¹²¹
<i>Dalbergia sisso</i>	<i>Rhizobium sp.</i>	4.2	89.5	
<i>Crotalaria juncea</i>	<i>Rhizobium sp.</i>	3.8	53.5	
<i>Arachis hypogaea</i>	<i>Rhizobium sp.</i>	2.5	102.2	Roy (1990) ¹²²
<i>Clitoria ternatea</i>	<i>Rhizobium sp.</i>	3.77	47.1	
<i>Erythrina indica</i>	<i>Rhizobium sp.</i>	42.0	82.0	
<i>Mimosa pudica</i>	<i>Rhizobium sp.</i>	2.27	60.0	
<i>Dalbergia lanceolaria</i>	<i>Rhizobium sp.</i>	7.42±0.09	82.7±2.0	Ghosh (1999) ¹²³
<i>Aschynomene aspera</i>	<i>Rhizobium sp.</i>	25.4±0.04	50.9±1.0	
<i>Roystonea regia</i>	<i>Rhizobium sp.</i>	16.90±0.95	122.0±2.0	
<i>Melilotus alba</i>	<i>Rhizobium sp.</i>	13.1±0.35	298.3±3.0	Datta (2000) ¹²⁴
<i>Dolichos biflorus</i>	<i>Rhizobium sp.</i>	5.3±0.11	309.7±2.75	
<i>Cajanus cajan</i>	<i>Rhizobium sp.</i>	6.7±0.15	168.0±1.55	
<i>Phaseolus mungo</i>	<i>Rhizobium sp.</i>	22.2	162	Ghosh <i>et al.</i> (2008) ²⁹
<i>Crotalaria saltiana</i>	<i>Rhizobium sp.</i>		212.5	Mazumdar <i>et al.</i> (2008) ¹³⁸
<i>Vigna mungo</i>	<i>Rhizobium sp.</i>	-	-	Mondal <i>et al.</i> (2009) ¹³⁹

consequence of lowering the level of ACC within a plant, the amount of ethylene that can form is reduced. Thus, the net result of the interaction of ACC deaminase-containing plant growth-promoting bacteria with plant cells is that the bacteria act as a sink for ACC. Direct consequences of this interaction are significantly increased plant root and shoot length, an increase in biomass, and protection of plants from inhibitory effects of ethylene synthesized as a direct consequence of a variety of biotic and abiotic stresses. In practice, ACC deaminase-containing plant growth promoting bacteria have been used to protect plants against growth inhibition caused by: flooding, both in the laboratory⁴⁶ and in the field⁴⁷; the presence of organic toxicants such as polyaromatic hydrocarbons (PAHs), polycyclic biphenyls (PCBs) and total petroleum hydrocarbons (TPHs) both in the laboratory^{48,49}; the presence of a variety of different metals including nickel, lead, zinc, copper, cadmium, cobalt and arsenic, both in the laboratory⁵⁰ and high salt⁵¹; phytopathogens⁵²;

drought⁵³; and infection of plant roots by various strains of Rhizobia⁵⁴.

While it is well known that IAA can activate the transcription of ACC synthase⁵⁵, it is less well known that ethylene may inhibit IAA transport and signal transduction⁵⁶. This feedback loop of ethylene inhibition of IAA synthesis and/or functioning limits the amount of ACC synthase, ACC and, ultimately, ethylene following every stressful event of the plant. When an ACC deaminase-containing plant growth-promoting bacterium lowers the ethylene concentration in plant roots, this relieves the ethylene repression of auxin response factor synthesis, and indirectly increases plant growth⁵⁷. Thus, ACC deaminase-containing plant growth-promoting bacteria facilitate plant growth by (i) decreasing ethylene inhibition of various plant processes and (ii) permitting IAA stimulation of cell proliferation and elongation without the negative effects of increasing ACC synthase and plant ethylene levels.

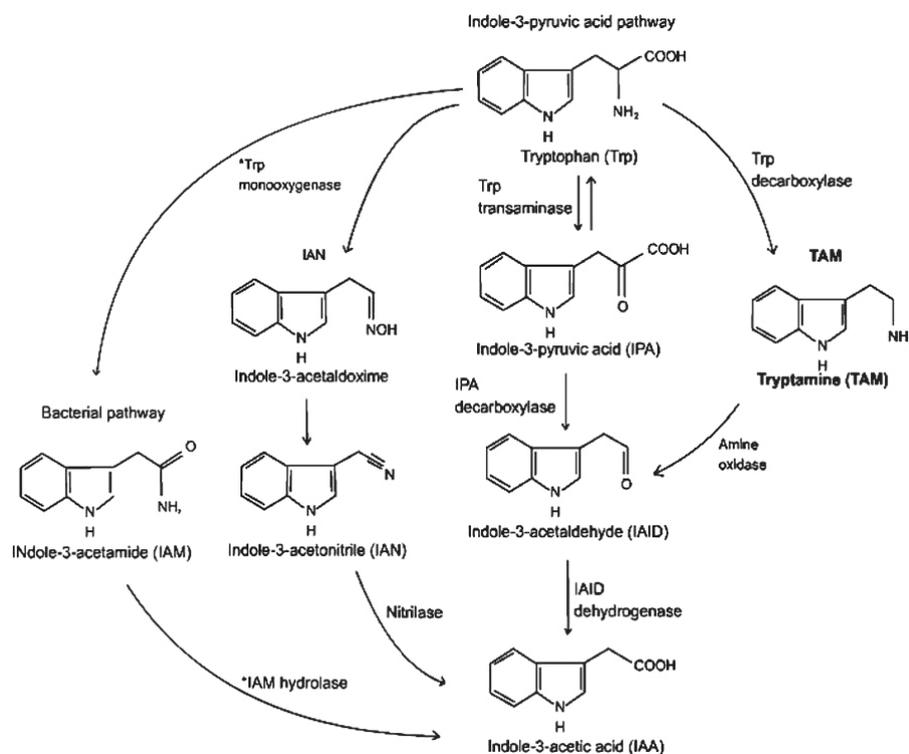


Fig. 1. Tryptophan-dependent pathways of IAA biosynthesis in plants and bacteria. The enzymes that are present only in bacteria are marked with an asterisk (After Bartel 1997).

VAM induced IAA production in root nodule

The nitrogen-fixing interaction between bacterial members of Rhizobiaceae and legumes are the two most commonly studied symbioses⁵⁸. The association between *Rhizobium* sp., legumes and that between vesicular arbuscular mycorrhizal fungi (VAM)⁵⁹ and most of the land plants display a remarkable degree of similarity. Both the events of symbiosis involve the recognition of the host for entry and coexistence within the plant roots, with the development of a specialized interface that always separates the two partners and at which nutrient exchange occurs.

Development of both the fungal and bacterial symbioses can be explained as an analogous progression of events like attraction, recognition, contact, entry, growth, development, and differentiation. The wide spread occurrence of VAM fungi in nodulated legumes and the mycorrhizal role in improving nodulation and *Rhizobium* activity within the nodules are universally recognized⁶⁰. The beneficial effect of VAM in symbiotic activity of *Rhizobium* and in nodulation and N₂ fixation is due to the relatively high phosphorus demand during N₂ fixation process by *Rhizobium* which is mitigated with

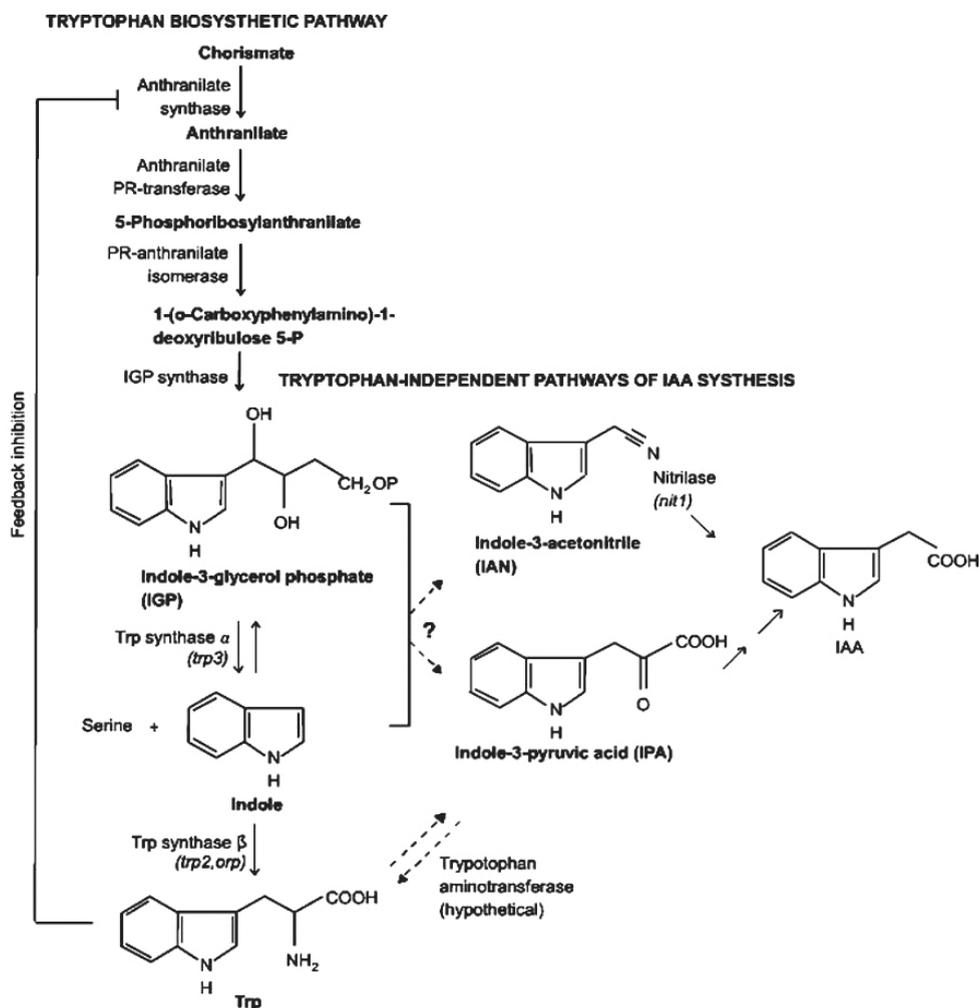


Fig. 2. Tryptophan-dependent pathways of IAA biosynthesis in plants. The tryptophan (Trp) biosynthetic pathway is shown on the left. Mutants are indicated in parentheses as uncertain (indole-3-glycerol phosphate or indole), and IAN and IPA are two possible intermediates. PR, phosphoribosyl (After Bartel 1997)

Phosphorous supplied by the mycorrhizal fungus. However, nutrients other than P, such as Zn, Cu, Mo, and Ca can affect the infectivity and symbiotic efficacy of *Rhizobium*. Enhanced uptake of different nutrients like P, K, N, Ca⁶¹, Zn and S⁶² by the VAM fungi has been demonstrated using radioactive isotopes. Therefore, enhanced uptake of these elements could also be involved in the synergistic interaction of VAM fungus and *Rhizobium* conversely. Supply of Nitrogen by N₂ fixation, as carried out by rhizobial activity, could be critical to maintain a balanced physiological status in the host plant, which is important for mycorrhiza formation and functioning⁶³. Dual effect of VAM fungus, *Glomus fasciculatum* and the nitrogen-fixing bacteria, *Rhizobium* sp. on the nodulation of roots of *V. mungo* was studied. It was recorded that the roots which were inoculated simultaneously with both the symbionts i.e., *G. fasciculatum* and *Rhizobium* exhibited greater amount of IAA production than the non-inoculated roots⁶⁴.

Enzymatic oxidation IAA, inhibitors and co-factors of the enzyme

IAA in aqueous solution is readily degraded by a variety of agents, including acids, ultraviolet rays and ionizing radiation, visible light, and in the presence of sensitizing pigments such as riboflavin. The most prevalent form of IAA degradation, however, appears due to oxygen and peroxides either separately or in combination, in the presence of a suitable redox system⁷. It became clear that plants synthesize, inactivate, and catabolize IAA by multiple pathways and multiple genes could encode a particular enzyme within a pathway⁶⁵. IAA is destroyed by two basic oxidative processes: enzymatic reactions and photooxidation⁶⁶. There are two pathways of enzymatic IAA catabolism (Fig V). The first involved oxidation by oxygen and loss of the carboxyl group as carbon dioxide. The products were variable, but 3-methyleneoxindole (Meox) was usually a principal one⁶ and other reported products of oxidation of IAA were 3-

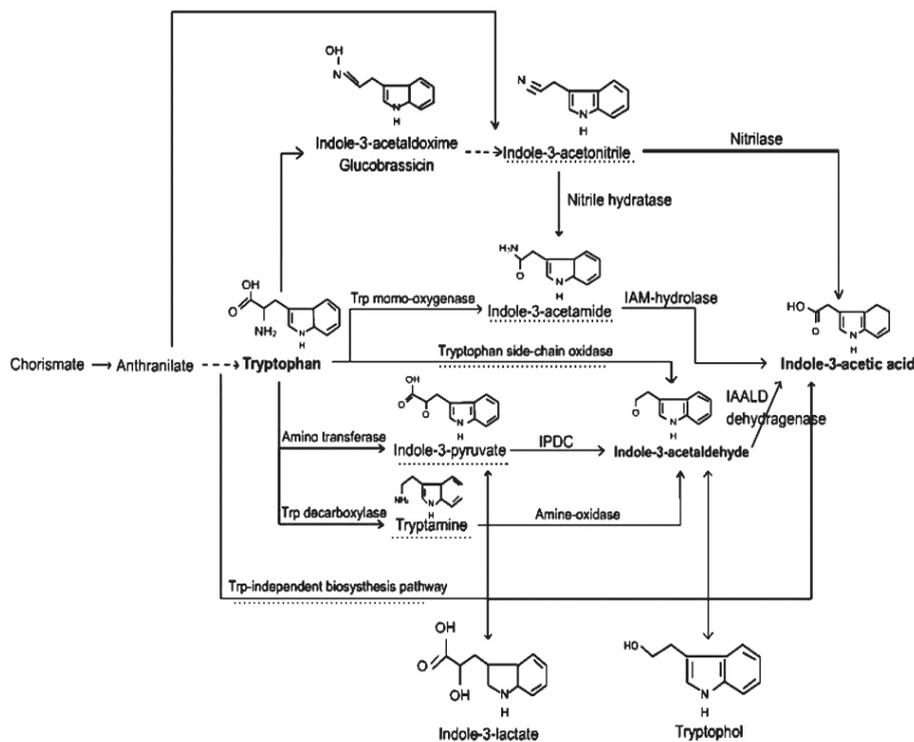


Fig. 3. Overview of the different pathways to synthesize IAA in bacteria. The intermediate referring to the name of pathway of the pathway itself is underlined with a dashed line. IAALD, indole-3-acetaldehyde; IAM, indole-3-acetamide; IPDC, indole-3-pyruvate decarboxylase, Trp, tryptophan (after Spaepen et al 2007)

hydroxymethyl oxindole (HMO), indole-3-carboxylic acid⁶⁶, oxindole-3-acetic acid (OxIAA), indole-3-acetyl aspartic acid (IAAsp) and indole-3-acetyl glutamate (IAGlu)⁶⁷. Formation of indole-3-methanol was also reported by Gazaryan *et al.* (1999)⁶⁸. The enzyme that catalyzed this reaction was IAA oxidase. In plants Meox was formed by enzymatic conversion of HMO⁶⁹. Meox was enzymatically converted into 3-methyl oxindole⁷⁰. Level of IAA is regulated in tissues by synthesis, formation of conjugated auxin, or by degradation.

The enzyme peroxidase, in concert with a flavoprotein, was shown to catalyze the oxidation of IAA releasing CO₂. Oxidative decarboxylation of IAA is now known to be catalyzed by peroxidases from a variety of plant sources. There are dissimilar requirements for enzymes from different sources and even multiple isozymes within a single species⁷. The ratio of the various products depended on several factors including enzyme substrate ratio, co-factors and pH of the reaction²⁵. IAA oxidase from higher plants required Mn⁺².

The reaction catalysed by IAA oxidase was accelerated by monophenol (e.g. 2, 4-dichlorophenol) and inhibited by orthodiphenols such as catechol and pyrogallol. Flavonols acted in the same way, as kaempferol promoted and quercetin inhibited IAA oxidase. Rigaud and Puppo (1975)⁷¹ reported an IAA oxidase activity in preparations of soybean bacteroids and in cytosol from root nodules. In a study with beech and horseradish, for example, 20 peroxidase isozymes were found, and all had IAA-oxidase activity⁷². Synthetic auxins and conjugated auxins were also resistant to IAA oxidases. The horseradish peroxidase system catalyzed oxidative decarboxylation without added cofactors, although manganese ion, simple monophenols, and m-diphenols increased the reaction rate. On the other hand, p-diphenols, o-diphenols and polyphenols generally inhibited IAA oxidation⁷. Hare (1964)⁷³ reported that IAA oxidase and peroxidase activities were found by the same enzyme. Presence of both peroxidase and non peroxidative forms of IAA-oxidase were also reported⁷⁴. Several IAA oxidase isozymes were present, and all or nearly all were identical to the peroxidases⁶.

IAA could be oxidized via two mechanisms: a conventional hydrogen-peroxide-dependent pathway, and other one that was hydrogen-peroxide independent and required oxygen. Only plant peroxidases were able to catalyze the reaction of IAA oxidation with molecular oxygen⁷⁵. Presence of hydrogen peroxide-independent pathway was also demonstrated in peanut by Gazaryan *et al.* (1999)⁶⁸.

A second pathway for degradation of IAA had been found to occur in dicots and monocots⁷⁶. In this pathway the carboxyl group of IAA was not removed, but carbon 2 of the heterocyclic ring was oxidized to form oxindole-3-acetic acid. Also, dioxindole-3-acetic acid exists in various species, and it had been oxidized both at carbons 2 and 3 of the heterocyclic ring. Details of this degradative pathway are still unknown⁶. Besides enzymatic oxidation, IAA could be oxidized by photooxidation. Riboflavin, eosin and other fluorescent dyes were effective catalyst for photooxidation of IAA. Products of photooxidation of IAA were like that of enzymatic reaction⁶⁶. IAA oxidase activity is generally higher in older, non growing tissues than then it is in

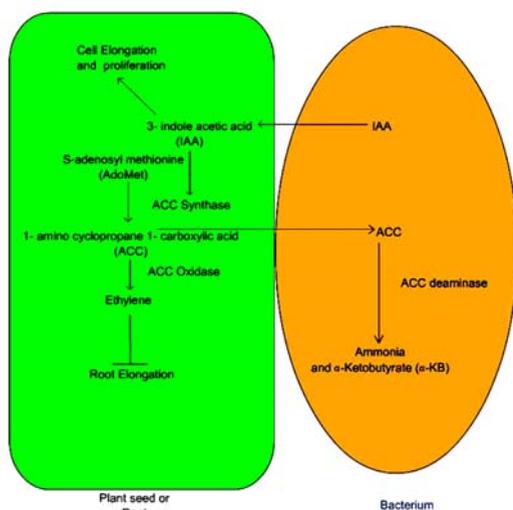


Fig. 4. Schematic representation of how a plant growth promoting bacterium bound to either a seed or a plant root lowers the ethylene concentration and there by prevents ethylene inhibition of root elongation. The arrows indicate chemical or physical steps in the mechanisms and the symbol indicates inhibition of root elongation by ethylene (Adopted from Glicet al. and J. Thear. Biol 1998)

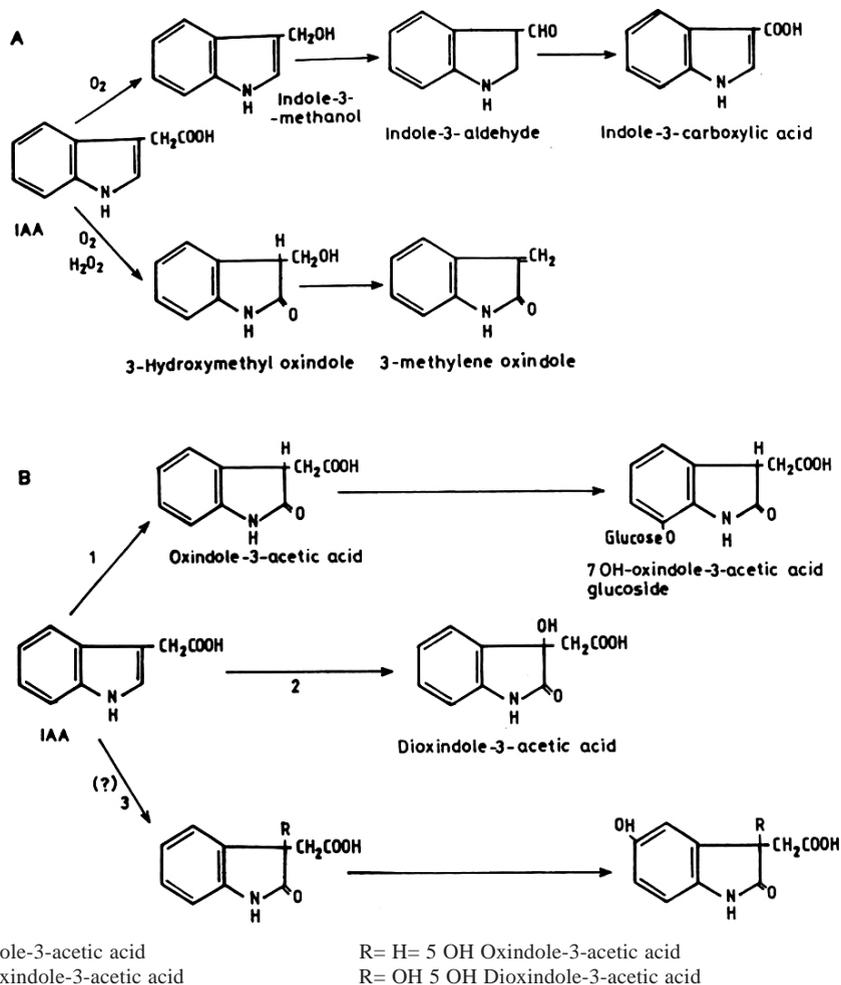
younger, actively growing tissues, which have a high auxin requirement⁷.

Although much is known about bacterial IAA producers (BIPs), little is known about bacteria that have the converse property i.e. the ability to destroy IAA. This is surprising given the early realization that, like BIPs, bacterial IAA degraders (BIDs) are abundantly associated with plants⁷⁷. Actually, BIDs were also considered a source of contamination, since their ability to destroy IAA obscured true levels of IAA in plant tissues⁷⁸. Ironically, there have been more studies dedicated to successfully eliminate BID activity

in measurements of plant IAA, e.g., by the use of antibiotics⁷⁷ than there have been serious attempts for trying to understand the abundance, origin, and significance of these bacteria and their unique ability to destroy IAA⁷⁹.

Effect of phenol and phenol metabolizing enzyme on IAA production

The degradation of IAA was catalysed by IAA oxidase. The enzyme IAA oxidase was accelerated by monophenol (e.g. 2, 4-dichlorophenol) and inhibited by orthodiphenols such as catechol and pyrogallol. More phenol in root nodules provided more di- and polyphenols



A) Oxidative decarboxylation pathway for IAA

B) Nondecarboxylation oxidative pathway for IAA in *Zea mays* (1), *Vicia faba* (2) and *Oryza sativa* (3) (after Moore, 1989).

Fig. 5. Pathways of IAA catabolism

as inhibitors of IAA oxidase⁶⁶ which superseded the activity of monophenols having some promotive effect on the enzyme. The levels of peroxidase and polyphenol oxidase generally changed inversely with the phenol level both in nodules and roots and these enzymes were less active in nodules, a condition which favoured the higher phenol level in root nodules⁸⁰. Flavonols acted in the same way, as kaempferol promoted and quercetin inhibited IAA oxidase. Rigaud and Puppo (1975)⁷¹ reported an IAA oxidase activity in preparations of soybean bacteroids and in cytosol from root nodules. In a study with beech and horseradish, for example, 20 peroxidase isozymes were found, and all had IAA-oxidase activity⁷². Synthetic auxins and conjugated auxins were also resistant to IAA oxidases. The horseradish peroxidase system catalyzed oxidative decarboxylation without added cofactors, although manganese ion, simple monophenols, and m-diphenols increased the reaction rate. On the other hand, p-diphenols, o-diphenols and polyphenols generally inhibited IAA oxidation⁷. The cause of difference of phenol levels in different parts would also be due to the variation in the metabolism and synthesis of phenols in different tissues by phenylalanine-ammonia lyase and tyrosine-ammonia lyase^{81, 82}.

Biological activity of the oxidation products of IAA

Many workers have shown the biological activities of the oxidation products of IAA. The elongation of wheat coleoptiles was stimulated by hydroxymethyl oxindole (HMO) has been reported earlier⁸³. HMO also stimulated ethylene evolution and increased protein and RNA content of wheat coleoptiles⁸⁴. Methylene oxindole (Meox), an oxidation product of IAA, stimulated growth by desensitization of regulatory proteins at low concentration, but it inhibited such process at high concentration⁸³. Meox was also reported to be 10 fold more effective than IAA as a plant auxin in promoting growth of pea and mung bean segment⁸³ and wheat coleoptiles⁸⁵. Frenkel *et al.* (1975)⁸⁶ reported that Meox promoted softening of the pears as well as increased evolution of ethylene in the same during ripening. HMO was reported to be more effective than IAA in inducing female flower buds^{87, 88} and ethylene evolution in

cucurbits⁸⁹. HMO and Meox increased the elongation of *Avena* coleoptiles⁹⁰.

On the contrary, auxin activity of Meox was not found in root initiation in pea stem cuttings, in extension of growth of etiolated pea segments and *Avena* first internode⁹¹, in coleoptiles and pea stem segments⁹², in xylem differentiation in explants of lettuce pith parenchyma cultures⁹³. Meox was found to be a potent bacteriostatic and a potent inhibitor of SH-containing enzymes⁶⁶. Lau *et al.* (1978)⁹⁴ reported that Meox and other oxidation products of IAA such as indole-3-carboxylic acid and dioxindole-3-acetic acid (DioxIAA) were unable to stimulate ethylene production. The oxindole-3-acetic acid (OxIAA), another oxidation product of IAA, was reported to be generally inactive in growth promotion^{94, 95}, although a contrary report has appeared⁹⁶.

Role of IAA in legume Rhizobium Symbiosis

Rhizobium spp. have shown to produce IAA and changes in IAA level in the host plant are a prerequisite for nodule organogenesis⁹⁷. IAA is involved in cell division, differentiation and vascular bundle formation in root and nodule also. But exact role of IAA in the different stages of *Rhizobium*-plant symbiosis remains unclear.

It was established that the specific nod inducers, flavonoids, stimulate the IAA production by *Rhizobium*⁹⁸. Moreover, in *Rhizobium* sp. NGR234 this flavonoid induction is dependent on the transcriptional regulators NodD1 and NodD2 also presence of the nod-box NB15 upstream of the y4wEFG operon required for IAA biosynthesis²⁶. In addition root nodules contain more IAA than nonnodulated roots^{80, 99, 100} and IAA might be important for maintaining root nodules¹⁰¹.

Nod factors initiate multiple responses that are essential for bacterial invasion of the legume plant host. One of the earliest plant responses to the correct Nod factor structure is an increase in the intracellular levels of calcium in root hairs, followed by strong calcium oscillations (spiking) and alterations to the root hair cytoskeleton. These responses are followed by curling of the root hairs, which traps rhizobial bacteria within what is known as a tight colonized curled root hair (CCRH). Simultaneously, Nod factor stimulates root cortex cells to reinitiate mitosis, a process that is dependent on the inhibition of auxin transport by rhizobia and plant

flavonoids. These cells will form the nodule primordium, and give rise to the cells that will receive the invading bacteria. In developing indeterminate nodules, infection threads grow through the developing meristematic zone to the underlying cell layers through which the wave of mitotic activity has already passed. These layers of invasion-competent cells have exited mitosis and become polyploid owing to cycles of genomic endoreduplication without cytokinesis. Plant cell endoreduplication is required for the formation of functional nodules, and is dependent on the degradation of mitotic cyclins by anaphase-promoting complex (APC), an E3 ubiquitin ligase. The advantages of cellular polyploidy are a higher transcription rate and a higher metabolic rate than cells with the normal $2n$ DNA content-characteristics that might be important for the invaded plant cells to support bacterial nitrogen fixation¹⁰².

Recently, it has been demonstrated that a cytokinin receptor (*HITI* gene) was involved in the Nod factor signaling cascade in *Lotus japonicus* and *Medicago*^{103, 104}. Since the effect of cytokinins is dependent on the IAA/ cytokinin balance, these findings may give a new dimension to the role of IAA in nodule formation.

Bacterial IAA producers (BIPs) have the potentiality to interfere with any of these processes by input of IAA into the plant's auxin pool. The consequence for the plant is usually a function of (i) the amount of IAA that is produced and (ii) the sensitivity of the plant tissue to changes in IAA concentration. A root, for instance, is one of the plant's organs that are most sensitive to fluctuations in IAA, and its response to increasing amounts of exogenous IAA extends from elongation of the primary root, formation of lateral and adventitious roots, to growth cessation¹⁰⁵. Infection of the roots of legumes by *Rhizobium* spp. initiated a coordinated series of morphological and physiological events, which resulted in the formation of the organized structures of the root nodules. Presence of relatively large quantities of auxin in leguminous root nodules was reported by many workers^{101, 106, 107}. Root nodules contained higher amount of IAA than their corresponding roots^{108, 109}. It was also reported that the production of plant hormones such as auxins, cytokinins and gibberellins, which allow certain bacteria and fungi

to direct a plant's physiology toward their own advantage, is also a striking feature¹¹⁰.

IAA production by *Rhizobium* spp. in culture

Rhizobium sp. can produce a huge amount of IAA in culture rather than IAA produced in symbiotic condition (Table 1). *Rhizobium* spp. could utilize a wide range of carbohydrates as carbon source¹¹¹. Carbon of the incubation medium was a determining factor for the amount of IAA produced by *R. trifolii* in culture¹¹². Different carbon sources supplemented at 1% level promoted the bacterial growth and IAA production by a *Rhizobium* sp. to different extent and mannitol was the most effective promoter¹¹³. Nitrate was less preferred nitrogen source for some strains of *Rhizobium*, whereas glutamate, glutamine or NH_4^+ (except *R. trifolii*) was generally preferred as nitrogen source¹¹⁴. De and Basu (1996)¹¹⁵ reported that KNO_3 and NaNO_3 increased both growth and IAA production by a *Rhizobium* sp. isolated from *Tephrosia purpurea*.

Jordan (1984)¹¹¹ reported that biotin and other water soluble vitamins were required for growth of *Rhizobium* spp. But some *R. japonicum* strains were inhibited by biotin¹¹⁶. Growth of *Rhizobium* sp. might be promoted by biotin. Riboflavin could enhance the growth of a *Rhizobium* sp.¹¹⁷. Chakraborti *et al.* (1981)¹¹⁴ reported that out of the 31 strains of the cowpea rhizobia and 14 strains of *R. japonicum*, approx 50% of the population showed little or no response to any vitamin added individually or in mixture. For the slow growing strains, pantothenate and p-aminobenzoic acid are the most common vitamins or precursors of vitamins showing promoted growth, although some strains required the amine, biotin and choline.

Effects of IAA on Rhizobia

Very little information accumulated about the effect of IAA on microorganisms. IAA could enhance the incorporation of glycine in proteins¹²⁵ and also increase the formation of bacteroids¹²⁶ of *Rhizobium*. IAA was reported to increase the cell surface of *Rhizobium*¹²⁷. Nodules of plants inoculated with mutant *Bradyrhizobium japonicum* strains overproducing IAA contain higher amounts of IAA in comparison to nodules derived from wild-type bacteria¹²⁸, suggested a major contribution of bacteria to IAA accumulation in nodules. Recently it has been shown that IAA

induces cell defense systems^{129, 130} and TCA pathway^{131, 132}

Isolation, identification and estimation of IAA

IAA might exist either in free form or bound with sugars, nucleic acids, proteins, amino acids etc. in plants⁴. Bound auxin was now recognized as IAA that formed chemical conjugates. IAA-conjugates were themselves inactive but released free, active IAA upon solvent extraction, alkaline hydrolysis or *in vivo* enzymatic hydrolysis⁷. Bioassay was frequently used to measure partially purified hormones. Different bioassay techniques were used for measurement of auxin. The most common assay of IAA fall within three broad categories: a) biological assay or bioassay of straight growth measurement of *Avena*¹³³ or wheat coleoptile¹³⁴ and the curvature test of *Avena* coleoptile⁶ or *Cephalaria* sp. and *Raphanus sativus* hypocotyls¹³⁵; split pea curvature and root growth inhibition of lentil and wheat were also sometimes used for auxin bioassay¹³⁴, b) instrumental analysis - by the use of modern instruments of separation and quantization, including high performance liquid chromatography (HPLC), gas chromatography (GC) and nuclear magnetic resonance (NMR) along with thin layer chromatography (TLC), column chromatography, UV spectrophotometry and fluorometry which are followed by the use of mass spectrometry (MS) to obtain proof of structure and c) immuno assay⁶ - which are more rapid and extremely sensitive (about 10000 times more than any bioassay) detection method. Apart from these plant hormones can also be detected by immuno-affinity chromatography¹³⁶. The identification of IAA was done by checking the colour reactions with Ehrlich or Salkowski's reagent. Its property of being oxidized by IAA oxidase and peroxidase and the characteristics of its other biological activity were also used for identification¹³⁷.

CONCLUSION

The production of IAA by the nodule bacteria is considered to have important physiological implications as it seemed reasonable to suspect that IAA, alone or in conjunction with other plant hormones, might be involved in several stages of the symbiotic relationship and might be transported to other parts of the plant as Wheeler

et al. (1979)¹⁴⁰ showed that phytohormones from the nodules were transported to other parts of the plant. N₂ fixation and supply to the host was thought to be the only function of the root nodule-*Rhizobium* symbiosis.

The above data and the works of other authors show that, if the nitrogen fixation in the nodules and supply to the host can be considered as the first-line symbiosis, the IAA content in the nodule and supply to the host may be taken as the second line of symbiosis in the root nodule-*Rhizobium* association.

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