

Review

Occurrence, Function, and Biosynthesis of the Natural Auxin Phenylacetic Acid (PAA) in Plants

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Abstract: Auxins are a class of plant hormones playing crucial roles in plant growth and development and stress responses. Phenylacetic acid (PAA) is a phenylalanine-derived natural auxin found widely in plants. Although auxin activity of PAA in plants was identified several decades ago, PAA homeostasis and its function remain poorly understood, whereas indole-3-acetic acid (IAA), the most potent auxin, has been used for most auxin studies. Recent studies have revealed unique features of PAA distinctive from IAA and enzymes and intermediates of PAA biosynthesis pathway have been identified. Here, we summarize the occurrence and function of PAA in plants and highlight the recent progress made in PAA homeostasis, emphasizing PAA biosynthesis and a crosstalk between IAA and PAA metabolism.

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Table 1. Occurrence of PAA in plants, showing plant tissue, PAA and IAA contents (if available)

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Species Name	Plant tissue (PAA content)	Plant tissue (IAA content)	Reference
Arabidopsis (<i>Arabidopsis thaliana</i>)	Seedling (413 pmol/gFW);	Seedling (49 pmol/gFW);	
	Dry seed (3,250 pmol/gFW);	Dry seed (1,950 pmol/gFW);	
	Siliques (800 pmol/gFW);	Siliques (2,000 pmol/gFW);	
	Inflorescence (1,900 pmol/gFW);	Inflorescence (130 pmol/gFW);	[7–11]
	Cauline leaf (400 pmol/gFW);	Cauline leaf (30 pmol/gFW);	
	Rosette leaf (250 pmol/gFW);	Rosette leaf (33 pmol/gFW);	
Bean (<i>Phaseolus vulgaris</i>)	Stem (200 pmol/gFW);	Stem (50 pmol/gFW);	
	Root (1,100 pmol/gFW)	Root (130 pmol/gFW)	
Tomato (<i>Lycopersicon esculentum</i>)	Shoot	N/A	[4]
Pea (<i>Pisum sativum</i>)	Shoot (1,616 pmol/gFW)	Shoot (211 pmol/gFW)	[5,12]
	Shoot (632 pmol/gFW);	Shoot (126 pmol/gFW);	
	Root (347 pmol/gFW);	Root (115 pmol/gFW);	
	Cotyledon (451 pmol/gFW);	Cotyledon (13 pmol/gFW);	[5,6,12]
Sunflower (<i>Helianthus annuus</i>)	Epicotyl (427 pmol/gFW);	Epicotyl (46 pmol/gFW)	
	Shoot (1,484 pmol/gFW)	Shoot (245 pmol/gFW)	[5,12]
Tobacco (<i>Nicotiana tabacum</i>)	Shoot (1,234 pmol/gFW)	Shoot (228 pmol/gFW)	[5,12]
Cotton (<i>Gossypium hirsutum</i>)	Cotyledon	N/A	[16]
Nasturtium (<i>Tropaeolum majus</i>)	Root (12 pmol/gFW);	Root (679 pmol/gFW);	
	Hypocotyl (14 ng/gFW);	Hypocotyl (166 ng/gFW);	
	Shoot (12 pmol/gFW);	Shoot (103 pmol/gFW);	[13]
	Leaf stalk (13 pmol/gFW);	Leaf stalk (74 pmol/gFW);	
	Older leaf (11 pmol/gFW)	Older leaf (86 pmol/gFW)	
Sorghum (<i>Sorghum bicolor</i>)	Leaf (300 pmol/gFW)	N/A	[15]
Maize (<i>Zea mays</i>)	Shoot (903 pmol/gFW)	Shoot (143 pmol/gFW);	[5,12]
Barley (<i>Hordeum vulgare</i>)	Shoot (514 pmol/gFW);	Shoot (63 pmol/gFW);	[5,7,12]
	Young shoot (4,353 pmol/gFW)	Young shoot (30 pmol/gFW)	
Oat (<i>Avena sativa</i>)	Young shoot (3,860 pmol/gFW)	Young shoot (31 pmol/gFW)	[7]
Ostrich fern (<i>Matteuccia struthiopteris</i>)	Crozier (2,790 pmol/gFW);	Crozier (119 pmol/gFW);	
	Young rachis (1,470 pmol/gFW);	Young rachis (219 pmol/gFW);	
	Immature pinnae (4,860 pmol/gFW);	Immature pinnae (161 pmol/gFW);	[14]
	Mature pinnae (2,380 pmol/gFW);	Mature pinnae (67 pmol/gFW);	
	Fertile pinnae (2,490 pmol/gFW)	Fertile pinnae (70 pmol/gFW)	
Moss (<i>Physcomitrella patens</i>)	1,049 pmol/gFW	14 pmol/gFW	[7]
Liverwort (<i>Marchantia polymorpha</i>)	469 pmol/gFW	74 pmol/gFW	[7]

1pmol/gFW is uniformly used as the unit of approximate amount of PAA

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N/A ; not available in the same paper

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3. Biological Function of PAA

Auxin activity of PAA was identified through three classical auxin activity tests: pea test, cylinder test, and oat bending test [17]. All three tests revealed PAA has less than 10% of IAA activity [17]. One of the most representative functions of PAA is the promotion of root growth and development [6,8,13,18,19]. PAA induced root formation in tomato, sunflower, marigold, artichoke, buckwheat, dahlia, and tobacco when applied to the stem [20]. PAA application promoted the formation of adventitious roots of cress hypocotyls, sugar-beet seedlings, and pea epicotyls [21]. Furthermore, leaf explants of *Ajuga bracteosa* on growth media supplemented with PAA increased frequency of root induction and

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biomass [19]. *Arabidopsis* seedlings treated with PAA increased the formation of lateral
61 roots, although PAA showed 10- to 20-fold lower activity than IAA [7]. However, some
62 studies showed stronger activity of PAA than IAA. In pea seedlings, PAA induced more
63 lateral root primordia and emerged lateral roots and longer lengths of lateral roots com-
64 compared to those of IAA [6,18].

65 PAA impacts aerial parts of plants as well [7,11,22,23]. Daily exogenous application
66 of PAA on tomato plants for 2 weeks significantly increased tomato height [22]. PAA ap-
67 plication led to epinastic leaves of artichokes [20], stimulated the elongation of wheat col-
68 eoptile and moss gametophore [7,23], and promoted elongation of the *Phaseolus* internode
69 [24]. *Arabidopsis* plants with increased PAA production showed elongated hypocotyls
70 and epinastic leaves, similar to what was observed in high-IAA *Arabidopsis* plants [11].
Supplementation of PAA induced callus formation in tobacco, sunflower, chickpea, and
lentil, but the optimal concentration of PAA for tobacco callus induction was 3-4 times
higher than IAA [25,26]. Similar to IAA, PAA application to leafless cotyledon retarded
the petiole abscission in cotton and inhibits ethylene evolution [16].

71 PAA itself has anti-microbial and anti-fungal activities and exogenous application of
72 PAA enhances tolerance to pathogen infection, whereas increased IAA in plants enhances
73 susceptibility to pathogens [27–29]. For example, exogenous application of PAA on citrus
74 inhibits the incidence of fungus molds caused by *Penicillium digitatum* and *P. italicum* [30].
75 Herbivore infestation in maize, poplar, and plumeria increases PAA production [31–33].
76 Application of PAA in oilseed rape enhances the prevention of *Sclerotinia sclerotiorum* and
77 *in vitro* treatment with PAA demonstrated adverse effects through the disruption of cell
78 wall and cytoplasm in mycelia [34]. However, any biological role of PAA in plant defense
79 remains unknown.

80 The first step of auxin action starts from auxin sensing by auxin receptors (TIR1 and
81 AFBs), which results in degradation of transcription repressors Aux/IAAs [35]. Shimizu-
82 Mitao and Kakimoto showed PAA-dependent degradation of Aux/IAA [35]. Interaction
83 of Aux/IAAs with auxin receptors TIR1 or AFB2 leads to degradation of Aux/IAA [35].
84 They showed that PAA induced Aux/IAA degradation with lower activity than IAA [35].
85 Sugawara *et al.* showed that PAA application rescued growth defects of IAA deficient
86 plants yuc quadruple mutants (*yucQ*) [7]. In the same study, a yeast two-hybrid assay and
87 a pull-down assay revealed that PAA promoted the interaction of auxin receptors and
88 Aux/IAA *in vitro*, suggesting that sensing and signaling modes of PAA are similar to IAA
89 [7].

90 It is noteworthy that PAA does not engage in polar auxin transport [7,16,36–38]. La-
91 beled PAA transport assay using pea epicotyls revealed that the transport of PAA barely
92 occurs in both the basipetal and acropetal direction [36]. PAA applied to the apical bud of
93 intact pea plants did not move in the long-distance basipetal transport [38]. Auxin polar
94 transport inhibitor naphthylphthalamic acid (NPA) inhibited IAA transport, but NPA did
95 not affect PAA gradient patterns in cotton, pea, and maize [7,16,37]. Unlike IAA, PAA did
96 not form concentration gradients in response to gravitropic stimulation via active and
97 directional transport in maize [7]. However, PAA inhibited IAA polar transport in internode
98 segments and long-distance movement of the pea apical bud [38].

99 4. PAA Homeostasis

100 As auxins regulate a vast array of processes, changes in content or distribution of
101 auxins can have profound effects on plant growth and development and in extreme cases
102 can lead to severe dwarfism or sterility [39–42]. Auxin homeostasis refers to the spatio-
103 temporal distribution of auxin throughout plant tissues and organs which governs plant
104 growth and development. Although several processes, including auxin transport, conju-
105 gation and degradation influence auxin homeostasis, *de novo* biosynthesis directly affects
106 local concentration of auxins.

107 4.1 PAA Biosynthesis

The main route of IAA biosynthesis from tryptophan in plants is the YUCCA pathway [43–52] (Figure 1a). The first step of this pathway is the conversion of tryptophan to indole-3-pyruvate (IPA) by enzymes belonging to the Tryptophan Aminotransferase of *Arabidopsis* (TAA) family [53–56]. Then, flavin-containing monooxygenases belonging the YUCCA (YUC) family convert IPA to IAA [42,55,57–60]. This pathway is also believed to contribute towards PAA biosynthesis (Figure 1b), as several studies have shown that TAA and YUC enzymes can convert phenylalanine to phenylpyruvate (PPA) and PPA to PAA *in vitro*, respectively [7,54,59,61,62]. YUCCA overexpression increases endogenous PAA or PAA conjugate content [7]. However, TAA and YUC mutants sometimes show little or no change in PAA content despite significant alterations to IAA content. For example, the maize YUC1-deficient mutant *de18* has an over 90% reduction in free and total IAA contents while PAA content is not significantly affected, and the *tar2-1* pea mutant displays a near complete loss of free IAA but no change in PAA levels [61]. Similarly in *Arabidopsis* the *yuc1yuc2yuc6* triple and *yuc3yuc5yuc7yuc8yuc9* quintuple mutants have wild-type levels of PAA but 40–50% reductions in IAA content [7]. However the TAA1 deficient mutant *wei8-1* displays a 20% and 80% reduction in PAA and IAA, respectively [7]. These findings suggest that these enzymes may function in PAA biosynthesis in plants, but may not be major players in PAA biosynthesis in some species [35].

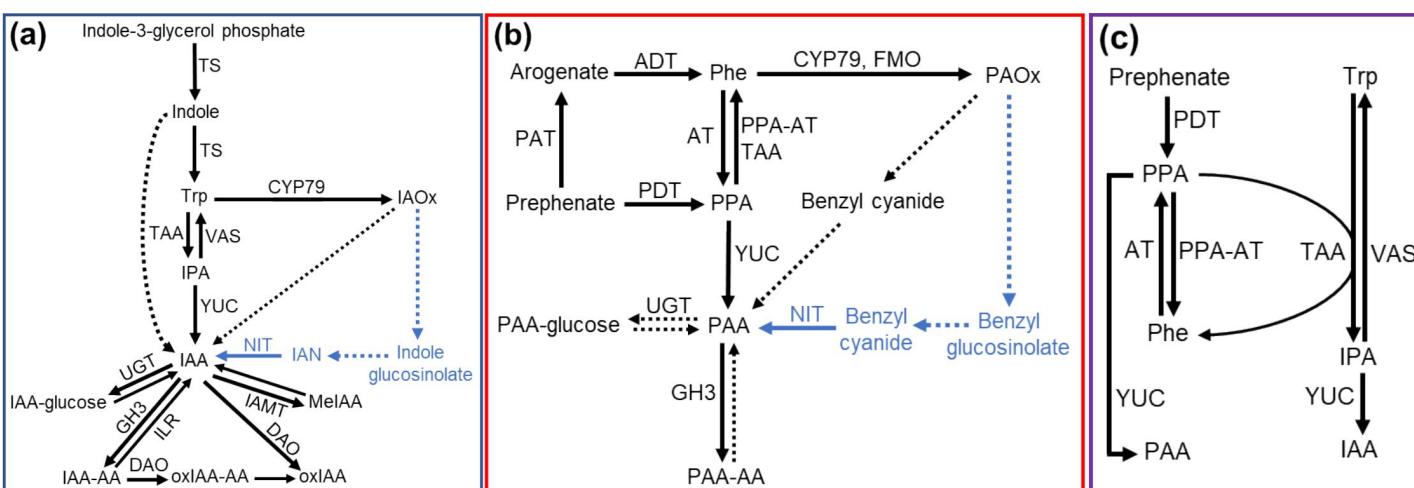


Figure 1. Schematic diagrams of IAA biosynthesis (a), PAA biosynthesis (b), and a link between IAA and PAA metabolism in plants (c). The pathways only include steps and enzymes that are demonstrated via genetic evidence. Solid arrows represent single reactions catalyzed by known enzymes, and dotted arrows represent predicted single or multiple steps. Blue arrows and metabolites represent pathways and metabolites present only in Brassicales species. IAA, indole-3-acetic acid; IAA-AA, amino acid-conjugated IAA; IAN, indole-3-acetonitrile; IAOx, indole-3-acetaldoxime; IPA, indole-3-pyruvate; MeIAA, methyl-conjugated IAA; oxIAA, 2-oxindole-3-acetic acid; ox-IAA-AA, amino-acid conjugated oxIAA; PAA, phenylacetic acid; PAA-AA, amino-acid conjugated PAA; PAOx, phenylacetaldoxime; Phe, phenylalanine; PPA, phenylpyruvate; Trp, tryptophan; AT, amino transferase; CYP79, cytochrome P450 monooxygenase of the 79 family; DAO, dioxygenase for auxin oxidation; FMO, flavin-containing monooxygenase; GH3, Gretchen Hagen 3 auxin-amido synthetase; ILR, IAA-Leu Resistant IAA-Amino hydrolase; IAMT, IAA carboxymethyltransferase; NIT, nitrilase; PAT, prephenate aminotransferase; PDT, prephenate dehydratase; PPA-AT, phenylpyruvate aminotransferase; TAA, tryptophan aminotransferase of *Arabidopsis*; TS, tryptophan synthase; UGT, UDP-glucuronosyltransferase; YUC, YUCCA family of flavin-containing monooxygenase; VAS; methionine aminotransferase

In plants and prokaryotes, phenylalanine biosynthesis from prephenate occurs through two routes: transamination of prephenate to arogenate which is subsequently decarboxylated and dehydrated into phenylalanine, or decarboxylation and dehydration of prephenate to form phenylpyruvate (PPA) which is converted to phenylalanine through transamination [63–65] (Figure 1c). Generally, the PPA pathway is more commonly found in prokaryotes while the arogenate pathway is the major route of phenylalanine

biosynthesis in plants; however, there is evidence for both pathways existing and making significant contributions in several plant and bacterial species [63–65]. Thus, modification of PPA metabolism may impact PAA biosynthesis not only directly by being converted to PAA but also indirectly by affecting phenylalanine pools in plants (Figure 1c).

Aoi *et al.* demonstrated that arogenate dehydratase (ADT), the enzyme that catalyzes the conversion of arogenate to phenylalanine, affects PAA biosynthesis, as overexpression or knockout of *ADT*s results in increased or decreased PAA content, respectively [10]. As arogenate serves as a precursor of phenylalanine, increased ADT activity results in increases in phenylalanine-derived metabolites such as PAA. They also detected changes in PPA levels upon modulation of ADT activity that followed the trends measured for PAA content (i.e. *ADT* overexpression resulted in increased levels of PAA and PPA) [10], supporting the role of PPA as a precursor of PAA.

Another PAA biosynthesis pathway is the aldoxime pathway using phenylalanine-derived aldoxime, phenylacetaldoxime (PAOx), as an intermediate [8,10,11,15,66]. Aldoximes such as indole-3-acetaldoxime (IAOx) and PAOx as well as aldoximes derived from other amino acids are well characterized as precursors of various specialized metabolites such as glucosinolates, cyanogenic glycosides, and camalexin as well as nitrogenous volatiles [31,33,67–72]. Several studies have shown that IAA can be made from IAOx in Brassicales and monocots [11,73–75] (Figure 1a). Similarly, it was shown that PAOx is a precursor of PAA in Arabidopsis and monocots [8,11,15] (Figure 1b). Arabidopsis plants overproducing PAOx increase PAA and display altered morphology such as epinasty leaves and elongated hypocotyls similar to shown in plants with increased IAA [8,11,42]. Maize and sorghum plants fed with labeled PAOx produce labeled PAA [11,15]. These findings indicate a wider distribution of the aldoxime-derived auxin biosynthesis pathway throughout the plant kingdom rather than limited to Brassicales.

The first step of the aldoxime pathway is the production of IAOx or PAOx by cytochrome P450 monooxygenases of the 79 family (CYP79s) [8,11,15,32,66]. In addition to CYP79 enzymes, flavin-containing monooxygenases (FMOs) in two fern species have been shown to catalyze conversion of phenylalanine to PAOx [76]. Aldoximes contribute to auxin pools through two routes (Figure 1a, 1b). In Brassicales plants, both IAOx and PAOx are precursors of family-specific glucosinolates. Glucosinolates and their degradation enzyme beta-thiol-glucosidases known as myrosinases are stored in separate cellular and subcellular compartments [77–80]. Upon herbivore or pathogen attack, however, these compartments are compromised, resulting in glucosinolate hydrolysis by myrosinases and the rapid release of toxic metabolites such as isothiocyanates, nitriles and epithionitriles [81–83]. Glucosinolate turnover has also been shown to occur *in vivo* without tissue damage or disruption [84–87]. Nitriles such as indole-3-acetonitrile (IAN) and benzyl cyanide are byproducts of glucosinolate degradation. These nitriles can then be acted upon by nitrilase enzymes to generate IAA and PAA [13,88–92]. On the other hand, aldoximes can be converted to auxins through the aldoxime-derived auxin pathway, which is glucosinolate-independent and is present in both Brassicales and non-Brassicales species as maize and sorghum [11,15]. A recent study demonstrated that benzyl cyanide serves as an intermediate of PAOx-derived PAA biosynthesis in maize and sorghum [15]. Application of benzyl cyanide increases PAA in maize and sorghum and both species convert labeled benzyl cyanide to labeled PAA [15], suggesting that nitriles may be key intermediates in both routes of the aldoxime pathway (Figure 1a, 1b). Unlike the YUCCA pathway, the aldoxime-derived auxin pathways do not appear to be the main route of auxin biosynthesis under normal growth conditions. For example, the Arabidopsis IAOx deficient mutant, *cyp79b2 cyp79b3* (*b2b3*) double mutant, grows normally under optimal temperatures [73], and the CYP79A2 gene encoding the PAOx production enzyme is barely expressed in the vegetative tissue of Arabidopsis ecotype Col-0 [11]. However, at high temperature and under salt stress, the *b2b3* mutant displays a low auxin growth phenotype [73,93], suggesting that the aldoxime pathway contributes significantly towards stress-induced auxin production. Indeed, many CYP79 enzymes have their expression

induced by stressors such as herbivory or by treatment with stress hormones such as jasmonic acid [31,32,68,72,94]. Given that aldoximes often serve as precursors of defense metabolites, the aldoxime pathway may play a role in modulating plant growth during the defense response.

Besides PPA, PAOx, and benzyl cyanide, several other metabolites have been implicated in PAA biosynthesis, although where they fit within the known biosynthetic pathways is unclear. Several labeled feeding experiments have demonstrated that phenylalacetalddehyde (PAAld) is derived from phenylalanine metabolism and produced along with labeled PAA [5,95]. PAAld biosynthesis from PPA has been shown to occur in rose through the actions of phenylpyruvate decarboxylases [96]. Also, in rose as well as other species PAAld has been shown to be directly synthesized from phenylalanine by the action of aromatic aldehyde synthases or aromatic amino acid decarboxylases [96–100]. Once PAAld is synthesized, it can potentially be acted upon by aldehyde oxidases to generate PAA which have been demonstrated to have activity for PAAld in maize [101]. Another metabolite, 4-phenylbutyric acid (4PBA), was recently shown to display an auxin-like effect during plant regeneration via conversion to PAA using a mechanism independent of IBR3-catalyzed oxidation [102]. Further study showing altered PAA contents upon removal of intermediate biosynthesis enzymes may reveal the role(s) that these metabolites play in PAA biosynthesis.

4.2 PAA Inactivation

Another major facet of auxin homeostasis is the conversion of active auxins to inactive forms. Inactivation of auxin not only supports the formation of auxin gradients and maintenance of auxin levels but is also necessary to prevent cytotoxic levels of auxins from accumulating in cells. IAA inactivation proceeds through two pathways: reversible IAA conjugation (to glucose, methyl, or amino acids) and irreversible IAA conjugation (to amino acids) and oxidation, with recent findings demonstrating that amino acid-conjugated IAA is oxidized and then subsequently hydrolyzed to form oxidized IAA [103,104]. As with biosynthesis, knowledge of PAA inactivation is limited compared to our understanding of IAA inactivation. Multiple studies have demonstrated that some Gretchen Hagen 3 IAA-amido synthetase (GH3) and UDP-glucuronosyltransferase (UGT) enzymes have activity towards PAA to generate PAA conjugates such as PAA-asp and PAA-glu and PAA-glucose, respectively [7,105–108] (Figure 1b).

4.3 Metabolic Interaction between IAA and PAA

More recent studies have shown a link between IAA and PAA metabolism. The homeostasis of IAA and PAA was shown to be maintained through modulation of auxin conjugation, with the accumulation of PAA resulting in the induction of GH3 or UGT genes that preferentially act upon IAA and vice versa [8,9]. Lynch *et al.* showed that PPA can, in addition to its previously defined and proposed impacts of PAA biosynthesis, impact IAA biosynthesis by serving as amino acceptor in the TAA-catalyzed conversion of tryptophan to IPA [109]. This interaction not only promotes the production of IAA but may also impact PAA biosynthesis, as increasing flux through the PPA route of phenylalanine biosynthesis was shown to decrease steady state levels of phenylalanine [109] (Figure 1c). Perez *et al.* demonstrated that accumulation of PAA results in transcriptional downregulation of genes related to tryptophan and IAA biosynthesis in *Arabidopsis* [11], demonstrating a complex regulatory network for maintaining auxin homeostasis.

5. Conclusions

In the past decades, several biochemical and genetic studies have identified key metabolites, enzymes and pathways that contribute towards IAA metabolism. While many questions remain regarding PAA homeostasis, recent studies have greatly expanded our understanding on how PAA is synthesized and inactivated. The role of PPA as a metabolite linking together phenylalanine, IAA and PAA biosynthesis has been supported by

genetic studies and suggests that PPA-derived PAA biosynthesis is more complex than the corresponding IAA biosynthetic pathway. Meanwhile, the occurrence of PAOx as a PAA precursor in Brassicales and monocots suggests that this hidden pathway may be distributed widely in the plant kingdom and contribute towards PAA homeostasis wherever PAOx is produced. Additionally, the identification of PAA-amino acid and PAA-glucose conjugates within Arabidopsis has provided mechanisms for PAA inactivation which may be shared among other species, and may employ similar pathways used in IAA inactivation. Future investigation is needed to reveal other potential PAA biosynthesis and inactivation pathways as well as the physiological roles of these pathways.	255 256 257 258 259 260 261 262 263 264
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