

Plant 9-lox oxylipin metabolism in response to arbuscular mycorrhiza

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The establishment of an Arbuscular Mycorrhizal symbiotic interaction (MA) is a successful strategy to substantially promote plant growth, development and fitness. Numerous studies have supported the hypothesis that plant hormones play an important role in the recognition and establishment of symbiosis. Particular attention has been devoted to jasmonic acid (JA) and its derivatives, the jasmonates, which are believed to play a major role in AM symbiosis. Jasmonates belong to a diverse class of lipid metabolites known as oxylipins that include other biologically active molecules. Recent transcriptional analyses revealed upregulation of the oxylipin pathway during AM symbiosis in mycorrhizal tomato roots and point a key regulatory feature for oxylipins during AM symbiosis in tomato, particularly these derived from the action of 9-lipoxygenases (9-LOX). In this mini-review we highlight recent progress understanding the function of oxylipins in the establishment of the AM symbiosis and hypothesize that the activation of the 9-LOX pathway might be part of the activation of host defense responses which will then contribute to both, the control of AM fungal spread and the increased resistance to fungal pathogens in mycorrhizal plants.

Arbuscular mycorrhizal (AM) symbiosis is a mutually beneficial interaction among most of the higher plants, including the majority of agricultural crop species, and soil fungi of the phylum *Glomeromycota*.¹ This symbiosis is present in most ecosystems and is of tremendous significance in agricultural ecosystems. Arbuscular mycorrhizal fungus (AMF) play a major role in nutrient cycling, particularly phosphate, and promotes plant growth by improve the nutrient status and the water absorption of their host.¹ The plant, in turn, supplies the fungus with carbohydrates. This exchange of nutrients is performed in the cortical cells of the root by fungal structures called arbuscules.² In addition, the fungus renders the plant more resistant to biotic and abiotic stress.^{1,3} During mycorrhization, plant cells undergo the structural and functional changes necessary for establishing symbiosis, suggesting that there is a high degree of interaction between both partners at the cellular, molecular and genetic levels. In this regard, plant hormones appear to play an important role in the recognition and establishment of symbiosis.

Plant hormones are essential molecules for signaling changes occurring in the plant's growth, development and morphological adaptation processes in response to environmental conditions as well as in defense responses to pathogen and abiotic stress factors. In AM, phytohormones play an important role in the recognition and extension of fungus within the roots of host plants. In the first phase, once the host plant recognizes AMF, transcriptional reprogramming occurs in plant cells intended for accommodating the fungus within the cell.⁴ Subsequently, transcriptional reprogramming is used to control fungal growth inside the roots. This transcriptional reprogramming appears to be mediated by plant hormones. Thus, changes are detected in the relatively abundant plant hormones during mycorrhization, most of which are thought to be involved in the symbiotic process.^{5,6} Salicylic acid (SA) and ethylene (Et) are known to play a negative regulatory role during mycorrhization,⁷⁻⁹ while abscisic acid (ABA) is necessary for the proper functioning of the symbiosis and the formation of arbuscules.¹⁰⁻¹² Particular attention has been devoted to jasmonic acid (JA) and its derivatives, jasmonates, which are believed to play a major role in AM symbiosis.¹³ Experiments involving exogenous application of JA have shown a dose-response effect. Low concentrations of JA boosted colonization,¹⁴ while high doses produced inhibitory effects.¹⁵ Moreover, mycorrhization experiments with the JA-deficient tomato plant mutant *spr2*, lacking the chloroplastic fatty acid desaturase involved in JA biosynthesis,¹⁶ have shown a reduction in colonization,^{17,18} while studies with the JA-insensitive tomato mutant *jai-1*, defective in the function of the tomato homolog of COI1 in Arabidopsis,¹⁹ have pointed out an increased colonization respect to wild-type tomato plants,²⁰ suggesting an intricate regulatory role for JA in AM symbiosis. This regulatory role played by JA may be due to the complex biosynthetic pathway and signaling of JA and its derivatives. Jasmonates belong to a diverse class of lipid metabolites known as oxylipins which include other biologically active molecules.^{21,22}

Plant Oxylipins

Oxylipins are a group of biologically active molecules with different structures and functions which are derived from the oxidative metabolism of fatty acids. They are generated by the coordinated action of lipases, lipoxygenases (LOXs) and a group of cytochrome P450 (CYP74) specialized in metabolizing hydroperoxy fatty acids.²³ The synthesis of most plant oxylipins is initiated

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by the addition of an oxygen molecule at carbon 9 or 13 of the linoleic or linolenic acid.²⁴ This reaction is catalyzed by LOXs (non-heme iron dioxygenases) and generates either a 9-LOX or 13-LOX pathway, depending on where the oxygenation takes place. The LOX-derived hydroperoxy acids can be metabolized by the following enzymes: allene oxide synthase (AOS), divinyl ether synthase (DES), hydroperoxide lyase (HPL), alkyl hydroperoxide reductase, peroxygenase, epoxy alcohol synthase or LOX itself, thus giving rise to different groups of oxylipins.^{25,26} One of the most commonly studied groups is the AOS branch of the 13-LOX pathway that leads to the family of jasmonates including JA/MeJA and its precursor, 12-OPDA. However, in recent years, the 9-LOX pathway has been studied due to its essential role in plant defense against microbial pathogens.^{27,28}

13-LOX Oxylipins are involved in several physiological plant development processes, such as growth, fertility^{29,30} and tuberization in potato.³¹ Additionally, these oxylipins play an important role in plant adaptation to adverse environmental conditions³² and in defensive responses to fungal and bacterial pathogens.^{33,34} In this regard, others oxylipins, apart from the 13-LOX derived, are known to play an antimicrobial role in relation to bacteria, oomycetes and fungal pathogens,^{35,36} and are capable of activate the expression of genes involved in pathogenesis²⁸ and regulate cell death.³⁷ It is therefore not surprising that oxylipins are important in relation to regulating symbiotic processes, particularly AM symbiosis.

Jasmonates and Arbuscular Mycorrhiza

In general, much research on oxylipins has focused on the jasmonate family of molecules. It is therefore understandable that, until recently, the study of the regulatory role played by oxylipins in mycorrhization has also focused on jasmonates. AM colonization appears to be related to endogenous JA levels. In this respect, Hause et al. observed an induction of genes involved in JA biosynthesis in cells harboring arbuscules in barley roots.³⁸ Similar results were obtained by Isayenkov et al. in relation to *Medicago truncatula*.³⁹ They silenced the gene coding for the enzyme allene oxide cyclase of the 13-LOX pathway in hairy roots of *M. truncatula*, observing a reduction in JA levels and consequently in the degree of mycorrhization, mainly in relation to arbuscular mycorrhizal formation. However, this reduction in the level of arbuscules did not affect their structure. It is possible that one of the mechanisms by which JA regulates the mycorrhization process and the formation of arbuscules is through the regulation of the carbohydrate metabolism and transport in the plant. In this regard, the degree of mycorrhizal colonization in tomato plants correlated with changes in the transcriptional regulation of genes involved in sucrose hydrolysis and transport, cell wall invertase activity and mycorrhizal-specific fatty acid content in roots.¹⁷ These results were confirmed in tomato plants deficient in JA synthesis (*spr-2*), which showed a reduced level of colonization. Exogenous application of JA enabled a partial recovery in the level of mycorrhization and the expression of genes involved in carbon partitioning in the plant.¹⁷ Moreover, induction of genes involved in the biosynthesis of JA has been observed in sink

tissues.^{40,41} Cells harbouring arbuscules act in fact as sink tissues for carbohydrates in mycorrhizal plants. Thus, a model has been proposed in which the induced biosynthesis of JA in mycorrhizal roots is linked to the sink phenomenon.³⁸ In addition, the expression of sink-specific and defense-related genes is a characteristic of sink tissue⁴² which may contribute to the enhanced defense status of the plant.

Jasmonates were labeled as secondary metabolites, but now it has become clear that they themselves act as elicitors of the production of secondary metabolites across the plant kingdom, from angiosperms to gymnosperms. Among the classes of metabolites that are induced by JAs are free and conjugated forms of polyamines, quinones, terpenoids, alkaloids, phenylpropanoids, glucosinolates, and antioxidants.^{43,44} Therefore JA involvement in the mycorrhization process may be also mediated through the induction of the biosynthesis of secondary metabolites such as flavonoids and terpenes, which are known to play a significant role in mycorrhizal symbioses.⁴⁵ In this sense, it is well known that application of jasmonates leads to increases in phenylalanine ammonia lyase (PAL) mRNA accumulation⁴⁶ and in PAL enzyme activity,⁴⁷ suggesting that JA may play a role in regulating flavonoids involved in the process of mycorrhization.

On the other hand, it has also been suggested that JA is involved in regulating AM fungus colonization mediated by the induction of the expression of genes coding for defense-related proteins. Mutant JA-insensitive (*jai-1*) tomato plants showed increased susceptibility to AM colonization.²⁰ *Jai-1* plant mutants are deficient in systemic wound-inducible expression of proteinase inhibitor (PI) genes and also lack PI expression in response to MeJA application.⁴⁸ Exogenous application of MeJA to tomato plants reduced mycorrhization and mainly affected the fungal phosphate metabolism and arbuscular formation, showing that AM colonization may be controlled by the JA signaling pathway.²⁰

9-LOX Oxylipin Pathway and Arbuscular Mycorrhiza

Few studies are available on the changes that occur in the 9-LOX oxylipin pathway during AM formation. Two recent microarray analyses of mycorrhizal tomato roots showed significant upregulation of genes involved in the metabolism of 9-LOX oxylipins.^{49,50} However, in the case of *M. truncatula*, the analysis of fatty acid profiles of non-mycorrhizal roots and in roots colonized by *G. intraradices* did not show significant differences between the 9-LOX and 13-LOX products of linoleic and α -linolenic acid, except in relation to JA (a 13-LOX oxylipin) which reached high levels in mycorrhizal roots.⁵¹ Therefore, it would be plausible to assert that the 9-LOX pathway plays a more important role in Solanaceae plants than in other plant families.

The LOXA and AOS3 genes involved in the 9-LOX metabolism were induced in tomato roots with a well-established colonization by *G. intraradices*, and their expression appears to be dependent on a certain degree of AM fungal colonization.¹⁸ In addition, the induction of these genes in mycorrhizal tomato roots only occurred on the colonized part of the mycorrhizal split-root plants. Moreover, the 9-LOX pathway is known to play

a defensive role in relation to microbial pathogens in plants.^{27,28,52} This suggests that the activation of the 9-LOX pathway could be a mechanism for controlling AMF development in the roots of Solanaceae plants. However, tomato plants deficient in the synthesis and/or perception of JA (*spr-2*, *def-1* and *jai-1*) did not show an upregulation of *LOXA* and *AOS3* genes, indicating that this strategy for controlling fungal spread in roots is at least partly dependent on JA pathway activation.¹⁸ Unlike *M. truncatula*, the content of OPDA (a mixture of 10- and 12-OPDA) in mycorrhizal tomato plants has been shown to increase compared with non-mycorrhizal plants and was not accompanied by any increase in free JA.⁵¹ Thus, it is possible that OPDA and other oxylipins, though not free JA, play an important role in orchestrating plant responses to AM fungi in Solanaceae.⁵¹ 12-OPDA is known to play a role in plant defense signaling,⁵³ with a similar role being suggested for 10-OPDA.⁵⁴ These results show that 9-LOX pathway may be involved in regulating the mycorrhization process.

The expression pattern during AM formation of *LeDES*, a gene coding for a 9-LOX desaturase which catalyzes the biosynthesis of colnelenic and colneleic acids, is the subject of some controversy. Although *LeDES* has been described by López-Ráez et al. as a mycorrhizal upregulated tomato gene in a microarray of tomato roots,⁵⁰ two other transcriptional analyses did not demonstrate any upregulation.^{49,55} The transcriptional regulation of *LeDES* during mycorrhization may not be directly dependent on the degree of colonization, as seems to be the case with *LOXA* and *AOS3*.

It has been suggested that the bioprotective effect of mycorrhization against fungal pathogens and the autoregulation of mycorrhization possibly are two sides of the same medal.⁵⁶ It seems plausible that mycorrhizal plants develop only one mechanism to repulse further colonization by fungi, not discriminating between AMF and soil-borne pathogenic fungi, and the activation of 9-LOX metabolism take part of this mechanism. As reported with respect to *Phytophthora parasitica*⁵⁷ and other fungal pathogens,^{25,28} it is conceivable that the 9-LOX pathway plays a defensive role and restricts fungal spread in roots. In several studies a local bioprotective effect has been linked with a high

degree of AM root colonization, whereas intermediate and low levels of AM root colonization showed no bioprotective effect. Apparently a critical level of AM root colonization is needed to provide bioprotection for mycorrhizal plants, and similarly the upregulation of the expression of genes involved in the 9-LOX metabolism in mycorrhizal roots seems to depend on a particular degree of AM-fungal colonization. It is therefore conceivable that the activation pathway of 9-LOX oxylipins could be responsible for the increased resistance to fungal pathogens in mycorrhizal plants.

Conclusions

Research to date shows that oxylipins play an important role in the colonization and establishment of AM. In particular, JA clearly seems to play a key role in arbuscular formation, possibly through the regulation of the carbohydrate metabolism and transport in the plant, the induction of secondary metabolites such as flavonoids and/or through the activation of genes coding for defense-related proteins. However, not much is known about the regulatory role of 9-LOX pathway in the process of mycorrhization (Fig. 1). Recent studies have shown a late activation of the 9-LOX pathway during the establishment of AM symbiosis in Solanaceae, which could be related to a mechanism for controlling AMF development in roots, although we cannot rule out an involvement of the 9-LOX metabolism in the bioprotective effect of mycorrhization against fungal pathogens. Further research is required in areas such as the use of plant mutants in the biosynthesis and perception of oxylipins in order to clarify the role played by the 9-LOX pathway.

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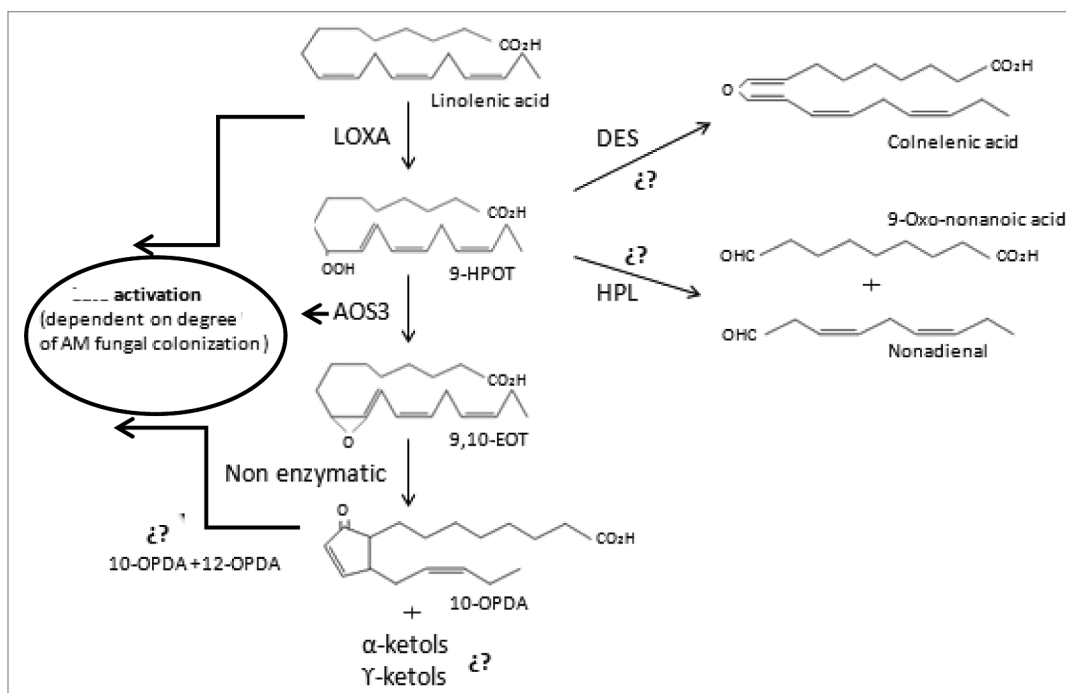


Figure 1. The 9-LOX metabolism of linolenic acid in response to AM fungal colonization in tomato roots. LOXA and AOS3 are induced when the AM colonization is well-established in roots. OPDA (a mixture of 10- and 12-OPDA) increased in response to AM colonization at this stage. The role of DES is controversial and its induction no dependent directly on the degree of colonization. The role of HPL and ketols are not known during AM colonization. LOX, lipoxygenase; AOS, allene oxide synthase; DES, divinyl ether synthase; HPL, hydroperoxide lyase; 9-HPOT, 9-hydroperoxy linolenic acid; 9-10-EOT, 9-10-epoxy octadecatrienoic acid; 10-OPDA, 10-oxo phytodienoic acid.

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