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From Auxin Homeostasis to Understanding Plant Pathogen and Plant Symbiont Interaction: Editor's Research Interests

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Introduction

To introduce myself as the new Editor-in-Chief of the *Journal of Plant Growth Regulation* I wish to briefly describe my research interests. In the following, I present a short overview of current research projects in my laboratory. Although this article is written in review style and provides a short theoretical background, my aim was not to present a comprehensive review of the subject. Therefore, the literature I have cited should not be considered a complete list.

PLANT HORMONES - OF COURSE!

Plant hormones, as we all know, are important substances for growth and development of plants, but they are also important factors for the interaction of plants with microorganisms during pathogenesis or symbiosis. In my laboratory, we are mainly interested in the role of auxins in plant developmental processes as well as signaling molecules during pathogenesis and symbiosis.

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Auxin Homeostasis

Auxins are a class of plant hormones that, at low levels, control a plethora of developmental processes but inhibit plant growth at higher concentrations. Therefore the regulation of hormone concentration is crucial for the proper development of plants. The concentration of a given hormone can be regulated by 1) biosynthesis, 2) reversible inactivation, 3) degradation and 4) transport.

Over 95% of the total auxin in a plant can be found in the conjugated form, therefore the formation of auxin conjugates is one of the key regulatory pathways for the activation/inactivation of IAA (Hangarter and Good 1981; Cohen and Bandurski 1982; Bandurski and others 1995). Conjugates can be formed with amino acids or sugars, but the formation of conjugates with peptides and proteins has also been described (Bialek and Cohen 1986; Bandurski and others 1995; Walz and others 2002).

Amide conjugates account for the bulk of conjugated indole-3-acetic acid (IAA) in dicots studied to date. Various IAA conjugates, among them IAA-Aspartate, IAA-Glutamate, IAA-Alanine, and IAA-Leucine, have been identified as natural conjugates in several plant species including *Arabidopsis thaliana* (Cohen 1982; Östin and others 1992; Barratt and others 1999; Tam and others 2000; Kowalczyk and Sandberg 2001).

IAA amidohydrolases are thought to control the quantity of IAA that is released from the conjugated

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into the free form (Cohen and Bandurski 1982; Bandurski and others 1995). Several IAA amidohydrolases have been isolated from Arabidopsis thaliana (Bartel and Fink 1995; Davies and others 1999). Because auxin conjugate hydrolases have not been well characterized in other plant species, a homolog of the A. thaliana ILR1 hydrolase was isolated from the close relative Arabidopsis suecica and dubbed sILR1 (Campanella and others 2003). Examination of the enzymatic characteristics of sILR1, when overexpressed in E. coli, showed a different substrate specificity compared to ILR1, indicating probable differing functions. In contrast to ILR1, the sILR1 protein can utilize IAA-Alanine and IAA-Glycine as substrates more effectively than ILR1 but cannot cleave IAA-Phenylalanine or IAA-Leucine as substrates (Campanella and others 2003; LeClere and others 2002). Auxin conjugate hydrolases identified from a partially purified protein extract from Chinese cabbage seedlings also showed preference for IAA-Alanine but an additional activity, which was able to cleave IAA-Aspartate, was discovered in root extracts infected with the clubroot pathogen Plasmodiophora brassicae (see below; Ludwig-Müller and others 1996). To learn more about the structure - substrate relationship we have begun to clone and characterize more hydrolase genes/ proteins from different plant species including monocots such as wheat and the model legume Medicago truncatula.

In addition to the small molecular weight conjugates, IAA conjugated to peptides and proteins may play a role in auxin homeostasis. Recently, Walz and others (2002) suggested that IAA-amino acid conjugates are present at low levels whereas IAA bound to peptides and proteins account for the majority of IAA-amide conjugates. A gene for a bean (Phaseolus vulgaris) 42 kDa protein with IAA covalently attached has been isolated. The protein shows homology to a seed protein from *Glycine max*. However, the physiological role of such a protein is yet unclear. Two possibilities have been proposed: 1) storage form of IAA in seeds and 2) a novel protein modification by the plant hormone. Functional analysis of the gene will shed light on this question. To this end, we have begun to transform model plants (Arabidopsis, Medicago truncatula) with this gene from bean and also to isolate IAA-modified proteins from Arabidopsis.

Although IAA is considered the major native auxin in higher plants and therefore also the most studied auxin (Normanly and others 1995), other substances with auxin activity, including 4-chloro-indole-3-acetic acid, IBA, and phenylacetic acid (PAA), occur in plants (Ludwig-Müller 1999a).

Recently we have shown the occurrence of IAA, IBA and PAA in nasturtium (Tropaeolum majus L.) (Ludwig-Müller and Cohen 2002). Although IBA is a very prominent auxin in horticultural practice, it was only recently recognized as a native compound in various species such as maize (Zea mays L.) and Arabidopsis thaliana (reviewed in Ludwig-Müller 2000a). It was demonstrated that IAA is converted to IBA in vivo using dark-grown maize seedlings (Ludwig-Müller and Epstein 1991). The same reaction occurs in Arabidopsis thaliana seedlings and mature plants (Ludwig-Müller and Epstein 1994) and two varieties of sterile cultured Grevillea (Ludwig-Müller 2003), but not in apple cuttings and stem slices (van der Krieken an others 1992, 1993). IBA may be formed by the acetylation of IAA with acetyl-CoA in the carboxyl group, because in labeling experiments the carboxy-14C was retained (Ludwig-Müller and Epstein 1991).

The in vitro conversion of IAA to IBA in maize seedlings is catalyzed by a microsomal membrane preparation, which forms IBA in the presence of acetyl CoA and ATP (Ludwig-Müller and others 1995a). The formation of IBA from IAA is not only found in maize, but in a wide variety of other plants (Ludwig-Müller and Hilgenberg 1995). The enzyme involved in the conversion of IAA to IBA in maize, termed IBA synthetase, has been characterized and partially purified. The regulation of IBA synthesis in maize has been studied under different conditions. Induction of IBA synthetase activity was found 1) after exposing the plants to drought and osmotic stress (NaCl and sorbitol) and 2) treatment with abscisic acid (ABA) (Ludwig-Müller and others 1995b), 3) after application of herbicides of the cyclohexanedione type (Ludwig-Müller and others 2000a) and 4) after inoculation with the arbuscular mycorrhizal (AM) fungus Glomus intraradices (see below; Ludwig-Müller and others 1997a).

Several reports show that IBA is also metabolized to conjugates. However, contrary to the conjugation patterns of IAA in dicots, the occurrence of substantial amounts of IBA glucose in addition to IBA amide conjugates was described in several dicotyledonous plant species after feeding with labeled or unlabeled IBA (Ludwig-Müller and Epstein 1993; Ludwig-Müller 2000a). We have now begun to characterize the enzymes/genes involved in IBA hydrolysis.

Secondary Plant Metabolites and Auxin Synthesis

The biosynthesis of IAA in Brassicaceae (for example, *Arabidopsis thaliana*) is closely connected to the

synthesis of a group of secondary plant metabolites, the glucosinolates. Glucosinolates are secondary plant products synthesized by members of the Brassicaceae but also occurring in several other plant families (Rodman 1991). They can be grouped into three different classes, depending on the amino acid from which they are derived: 1) aliphatic/alkenyl glucosinolates derived from methionine, 2) aromatic glucosinolates derived from phenylalanine and tyrosine, and 3) indole glucosinolates derived from tryptophan (Bennett and Wallsgrove 1994; Bennett and others 1995). The glucosinolates have been implicated in plant defense against bacterial and fungal pathogens as well as insect predators (Bennett and Wallsgrove 1994), but they may also play a role in host/pathogen recognition.

Indole-3-methylglucosinolate is thought to be an intermediate as well as a storage form for IAA in Brassicaceae. However, other pathways to IAA bypassing the glucosinolates have been described (Hull and others 2000). During a screen for Arabidopsis thaliana mutants defective in glucosinolate synthesis, six mutants with different glucosinolate patterns compared to the wild type were isolated (Haughn and others 1991). Four of these six had altered levels of alkenyl glucosinolates, whereas one mutant showed, in addition, low leaf indole glucosinolate concentrations (TU8). This mutant was used to study IAA synthesis during seedling and plant development as well as after pathogen infection (Ludwig-Müller and others 1999). The line TU8 shows traits of an auxin-deficient shoot phenotype (shorter stems, altered branching pattern) as well as rosette size. However, IAA synthesis and metabolism were essentially unaffected in the TU8 mutant during early development (Ludwig-Müller and others 1999).

The development of the clubroot disease of the Brassicaceae (see below) is closely linked to the synthesis of plant hormones such as auxins and cytokinins. Increased cell division and elongation result in the formation of typical root galls (Ludwig-Müller 1999b). The breakdown of indole glucosinolates, which could lead to the release of relatively large amounts of auxin, may be one factor responsible for clubroot symptoms (Butcher and others 1974). This implies that plants with reduced levels of indole glucosinolates should have reduced disease symptoms. It was shown that the mutation TU8 decreased the size of root galls after infection with Plasmodiophora brassicae and that the IAA and indole-3-acetonitrile (a precursor of IAA) and indole glucosinolate levels were lower in clubs of the mutant compared to the wild type (Ludwig-Müller and others 1999). Thus, indole glucosinolates and auxin may be pathogenicity factors involved in gall formation.

In a different investigation we were able to show that levels of nitrilase, the enzyme catalyzing the conversion of indole-3-acetonitrile to IAA, were increased in infected roots of *Arabidopsis* and that the nitrilase protein was closely associated with pathogenic structures (Grsic-Rausch and others 2000). In addition, a nitrilase mutant and plants transformed with one of the nitrilase genes in the antisense direction showed delayed club development (Grsic-Rausch and others 2000; Neuhaus and others 2000).

Links Between Auxin and Stress Physiology?

In addition to the phenotypes described above, the TU8 mutant was found to be remarkably less thermotolerant than wild-type plants upon exposure to elevated temperatures. Although a moderate temperature increase only affected shoot growth, exposure to severe heat stress led to a dramatic decay of mutant plants. Survival above optimal temperature conditions is mainly dependent and accompanied by a massive accumulation of heat stress proteins (Hsps), most of which belong to a group of proteins termed molecular chaperones (Ellis and van der Vries 1991). The main task of these proteins is to assist in the refolding of partially unfolded or denatured proteins occurring under elevated temperatures (Forreiter and Nover 1998). Deficiency in expression of chaperones often results in increased thermosensitivity or death of the organism even under normal growth conditions (Lindquist 1986; Nover 1991).

This led us to investigate the expression of heat stress proteins (Hsps) in the mutant under heat stress and control conditions. Although the expression for small Hsps, Hsp70 and Hsp104 was not affected in the TU8 mutant, a remarkable reduction in Hsp90 compared to wild type was found after exposure to elevated temperatures (Ludwig-Müller and others 2000b). Immunolocalization showed that cytosolic Hsp90 is affected. Transient expression of Hsp90 in mutant protoplasts increased their survival rate at higher temperatures to near the equivalent of wild type protoplasts. These data suggest that the reduced level of Hsp90 in TU8 mutants may be the primary cause for the observed reduction in thermostability.

The function of Hsp90 in plants is not yet entirely clear. It has been shown that Hsp90 in yeast and animal cells is involved in the maturation of steroid receptors and several kinases. Our goal is to identify the TU8 gene by map-based cloning and to reveal its







Figure 1. The infection of Brassicaceae with the obligate biotrophic protist *Plasmodiophora brassicae*. (A) Infection of a young *Brassica campestris* plant. (B) Infection of *Arabidopsis thaliana*. (C) Resting spores of the pathogen in a hypertrophied host root cell. Scanning electron microscopy was done in collaboration with Manfred Ruppel, Goethe-Universität Frankfurt, Germany.

function (Wenke and Ludwig-Müller 2002). We are also interested in the extent to which Hsp90 is involved in the apparent mutant phenotype of TU8 plants and whether Hsp90 plays a role in the plant signal transduction network together with plant hormones.

Other indications for an involvement of temperature stress in auxin homeostasis comes from the work of Oetiker and Aeschbacher (1997), who showed that temperature-sensitive cells of henbane (*Hyoscyamus muticus* L.) grow like the wild type at 26°C but die rapidly at 33°C unless auxin is added to the medium. In addition, the conjugates formed from IAA differed in the wild type and temperature-sensitive variant. Although the wild type converted IAA mainly to IAAsp, the variant produced mainly IAA-glucose.

PLASMODIOPHORA BRASSICAE

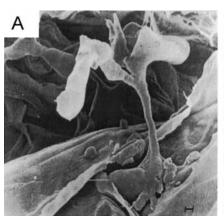
The clubroot disease of the Brassicaceae (Figure 1) is probably the most damaging plant disease within this family. About 10% of Brassica field plots worldwide are infected with clubroot and 100% losses were reported from fields infested with *Plasmodiophora brassicae*. As an obligate biotroph, *P. brassicae* completes its life cycle within the host roots (Figure 1C). Only the resting spores of the pathogen can be detected outside the plant tissue. It is difficult to control clubroot in the field because the spores, which are liberated from decomposing root tissue, can remain infectious for at least 15 years and the disease is difficult to control by either chemical or cultural means. Therefore, it is of great importance to understand the development of this disease.

Not only are widely used agricultural cultivars infected with the protist, but weed crucifers such as *Arabidopsis thaliana* are also suitable hosts (Figure 1A,B). Infection with *P. brassicae* induces cells to

first divide and during the later stages show signs of hypertrophy (Ingram and Tommerup 1972). The developing clubs form a strong metabolic sink within the host.

Clubroot symptoms clearly suggest that plant growth regulators are involved in disease development. Hyperplasia and hypertrophy, as well as the growth of leaf-like structures from the roots, indicate the involvement of auxins and cytokinins. In a number of studies it was shown that the concentrations of auxins and cytokinins are increased in infected tissue. Although it was demonstrated that the vegetative secondary plasmodia of the pathogen produce cytokinins (Müller and Hilgenberg 1986), the increase of IAA might be due to increased synthesis and turnover of putative host auxin precursors in infected roots (Searle and others 1982; Rausch and others 1983; see above). In addition, other plant hormones such as jasmonic acid may be involved in signal transduction and increased IAA biosynthesis (Grsic and others 1999). Another possible explanation for increased auxin concentrations is the hydrolysis of auxin conjugates in clubroots of Brassica (see above; Ludwig-Müller and others 1996). We were able to clone auxin conjugate hydrolases homologous to Arabidopsis hydrolases (Bartel and Fink 1995, Davies and others 1999) from P. brassicaeinfected Brassica rapa roots (Schuller and Ludwig-Müller 2002). Their expression during disease development is currently being analyzed to learn more about the role of auxin conjugate hydrolysis during this host/pathogen interaction. In addition, these auxin conjugate hydrolases will be further characterized with respect to their substrate specificity.

Different features for characterizing the host/ pathogen interaction in clubroot have been assessed in the past, namely the degree of colonization of root hairs (Sammuel and Garret 1945; Channon and others 1964), damage induced by the parasite



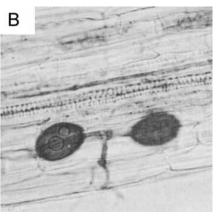


Figure 2. Colonization of maize (*Zea mays* L.) roots with the arbuscular mycorrhizal fungus *Glomus intraradices*. (**A**) Scanning electron micrograph of a young arbuscule (picture was taken in collaboration with Manfred Ruppel, Goethe-Universität Frankfurt, Germany). (**B**) Light microscopy picture of vesicles stained with toluidine blue (picture was taken in collaboration with Dr. Michael Kaldorf, Universität Leipzig, Germany).

measured by weight of shoots and roots or yield loss, and the extent of gall formation (Crute 1986). Most commonly, a subjective scale has been used to grade the size of galls on a population of plants (Buczacki and others 1975). However, different investigations used different methods. Therefore, we assessed the effect of various environmental factors. inoculum density and mutations in Arabidopsis and described symptom development by several criteria. The scoring systems we used included disease classes (Fuchs and Saristan 1996; Kobelt and others 2000) and a root index (the relation of root weight of inoculated plants to non-inoculated plants) (Ludwig-Müller and others 1999). Both disease index and root index gave comparable results and can be used for investigations of tolerance or resistance (Siemens and others 2002). Using these scoring systems under defined experimental conditions, a set of Arabidopsis mutants with defects in primary and hormone metabolism as well as developmental mutants, which could be involved in clubroot development, was investigated. However, this screen did not reveal many new candidates for tolerance against clubroot.

With *Arabidopsis thaliana* as a host plant for *Plasmodiophora brassicae* we have used the 22 K microarray (Affymetrix) to investigate host gene expression during the development of the disease (Ludwig-Müller and others 2003). Two time points, which were significantly different from each other, were chosen. At the early time point (10 days after inoculation) small secondary plasmodia of the pathogen are visible, but only about 20% of the host tissue is colonized, with limited change to host cell and root morphology. At a later time point (23 days after inoculation) different developmental stages of the pathogen are present. More than 60% of the host root cells were colonized and the root morphology was drastically altered. At both time

points more than 1000 genes were differentially expressed when mRNA from infected roots was compared with that from control roots of the same age. However, only a few genes showed similar expression patterns at both time points. Cytokinin oxidase was down-regulated at both time points, but much more strongly at the second time point. In addition, genes, which may function in IAA metabolism (such as members of the GH3 family) or signal transduction, were found to be up-regulated. The defense response of the host plant is modulated by P. brassicae as evidenced by the high number of down-regulated defense genes. We hypothesize that P. brassicae is able to circumvent the defense response of the host plant by a yet unknown mechanism.

Arbuscular Mycorrhizal Symbiosis

Arbuscular mycorrhiza (AM) is a unique symbiotic association between plant roots and a group of fungi from the order Glomales. This association often increases growth and yield of many crops by enhancing nutrient uptake, resistance to drought and salinity, and increasing tolerance to pathogens (Gianinazzi-Pearson 1996; Mosse 1957; Nelsen and Safir 1982: Smith and Gianinazzi-Pearson 1988). During colonization, distinct structures are formed by the AM fungi within the host roots (internal hyphae, arbuscules, vesicles; Walker 1992) (Figure 2). The complex cellular relationship between host roots and AM fungi requires a continuous exchange of signals, which leads to the proper development of mycorrhiza in the roots of a host plant (Gianinazzi-Pearson 1996). Plant hormones may be suitable candidates for the regulation of such a symbiosis. Little is known about the function of plant hormones during the colonization process although there is evidence that they are involved in signaling events between AM fungi and host plants (Barker and Tagu 2000; Ludwig-Müller 2000b). In addition, it has been suggested that phytohormones, such as IAA and cytokinins, released by mycorrhizal fungi may also contribute to the enhancement of plant growth (Frankenberger Jr. and Arshad 1995).

In maize roots colonized with a *Glomus* isolate, abscisic acid (ABA) levels were considerably higher in AM-colonized than in control roots, whereas the concentrations of zeatin riboside (with the exception of later stages of AM development) and indole-3-acetic acid (IAA) were similar for infected and non-infected roots (Danneberg and others 1992). Hyphae of *Glomus intraradices* were reported to contain ABA, thus contributing to the hormone concentration in colonized roots (Esch and others 1994).

Since stable isotope-labeled standards became available for the determination of plant hormones, it is possible to accurately measure auxin levels using gas chromatography-mass spectrometry (Cohen and others 1986; Sutter and Cohen 1992). With these sensitive techniques, the endogenous content of IAA and indole-3-butyric acid (IBA) in mycorrhizal and control roots of maize was re-investigated (Ludwig-Müller and others 1997a). For IAA, the results of Danneberg and others (1992) were confirmed. However, a comparison of IBA concentrations in mycorrhizal maize roots and controls showed significant differences (Ludwig-Müller and others 1997a). In younger roots, free IBA differed little between infected and control roots whereas amounts of conjugated IBA were higher in the infected tissue. In older roots, the free IBA content was lower in AM-infected roots than in controls, whereas the bound IBA fraction remained the same in infected and control tissues.

An altered phenotype of maize roots inoculated with Glomus was found in very young seedlings (10 days after inoculation). We were able to show that the phenotype induced by AM-fungal colonization could be mimicked by exogenous application of IBA and that a synthetic IBA analogue was able to suppress both the IBA-induced and AM-induced root phenotype of young maize plants. In accordance with these findings, the number of fungal structures also decreased in these treated roots (Kaldorf and Ludwig-Müller 2000). IBA is probably involved in lateral root formation to increase the sites for possible fungal infection because it was shown that the preferred sites for penetration were lateral roots compared to main roots (Karabaghli-Degron and others 1998). Changes in root morphology after colonization with arbuscular mycorrhizal fungi have been described for other plant species (see for example, Schellenbaum and others 1991; Yano and others 1996; Tisserant and others 1996). Clearly, our understanding of the role of plant hormones during mycorrhizal symbiosis is still limited, but the application of techniques such as reporter genes, microarrays and transgenic plants will allow us to further dissect the signaling pathways.

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