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Hairy roots as a model to investigate the role of suberin in the Phytophthora sojae-soybean pathosystem

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Graduate Program in Biology
A thesis submitted in partial fulfillment of the requirements for the degree in Master of Science
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HAIRY ROOTS AS A MODEL TO INVESTIGATE THE ROLE OF
PHYTOPHTHORA-SOYBEAN PATHOSYSTEM

(Spine title: Suberin analysis of soybean hairy r

(Thesis format: Monograph)

by

PooSharma

Graduate Program in Biology

A thesus submitted in partial fulfillment
of the requirements for the degree of
Master of Science

The School of Graduate and Postdoctoral Studies
The University of Western Ontario
London, Ontario, Canada

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THE UNIVERSITY OF WESTERN ONTARIO
School of Graduate and Postdoctoral Studies

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ABSTRACT

Part of the resistance mechanism of soybean (*Glycine max*) to the root-knot disease caused by *Phytophthora sojae* is the formation of root suberization. To investigate the role of suberization in the resistance to root-knot disease, hairy roots, formed as a result of *Agrobacterium rhizogenes* infection, as a model to be used as a reliable soybean root system for *in vitro* and *in vivo* studies were cultured and demonstrated to be highly resistant to root-knot disease. The anatomy and suberin deposition in soybean hairy roots were compared with those of wild-type roots. The hairy roots contained a very similar amount of suberin to that of wild-type roots. Suberin was identified using gas chromatography-mass spectrometry. The suberin composition in both epidermal and endodermal cells along the root axis was similar. Finally, the response of soybean hairy roots to *P. sojae* infection was investigated and compared with that of wild-type roots.

Keywords

Suberin, Glycine, *Phytophthora sojae*, *Agrobacterium rhizogenes*, transformation.

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CHAPTER 1: INTRODUCTION

1.1 Soybean

Soybean (*Glycine max* Meisn.), legume that is intricately linked to human life. Due to its high protein and oil content, soybean is used for human consumption, animal feed and various industrial products. Soybean production have allowed the cultivation to spread throughout Canada from Ontario since the mid 1970s. To this day, soybean production as noted in the 2006 Agricultural Census (Doré & Garneau, 2009) today, soybean is grown almost exclusively in Ontario, Prince Edward Island, Quebec, Alberta and approximately 2% of the land area over the world (Canadian Grain Commission, 2012). In other parts of the world, important agricultural crops such as soybean are also affected by Phytophthora blight outbreaks which are a serious problem in the United States (Kaufmann and Gerdemann, 1958) and continue to plague soybean producing countries (Wraight, Detrahçe et al., 2003).

1.2 Phytophthora life cycle and infection process

Phytophthora is a saprophytic and one of 80 species from the group Oomycetes. Phytophthora oomycetes differ from true fungi in that hyphae are aseptate and cell walls containing cellulose as opposed to chitin, with zoospores having two anterior tinsel flagella and a posterior whiplash flagellum throughout much of their life cycle (Dick, 1969; Heffer Link, 2003).

P. sojae has a very narrow host range, infecting mainly soybean amount-2 billion dollars and maintenance costs are several Riberio, 1996; Wrather et al., 2001a,b). Oomycete pathogens mainly because they infect underground plant parts and where difficult and uneconomical (Tyler, 2007).

Zoospores, or flagellated spores, are the infective spore water in the spring when the soil is moist and warm, zoospores form 30 zoospores, which are attracted to soybean root exudates (Morris and Ward, 1992). Once at the root surface outer epidermal waxy cuticle, germinate, and the emerging hypha penetrate epidermis and into the cortex. As hyphae grow between cortical cells, pathogen can feed on host structures called appressoria on the outer surface of root epidermal cell walls allow the formation of which penetrate root cell walls; haustoria penetrate the epidermal cell pathogen (Tyler 2002) feeding is obligate, however, feeding leads to weakening of the host cell which eventually leads to necrosis. In some situations the above ground plant parts to wilt and die because they cannot take up and transport water and nutrients. Once the roots are colonized, hyphae form haploid antheridia and oogonia leading to the formation of diploid overwintering oospores, which can germinate to produce hyphae that can produce sporangia. The initial infection process involves physical penetration of the

plant resistance involves physical barriers, namely epidermal cells and the spread of lignin in the root.

1.3 Plant defense pathways and the genetics of resistance

Pathogens such as Phytophthora cause a substantial crop loss annually and they lead to an alteration of host metabolism (Danko and Dehne, 2004). To combat microorganisms, plants have two kinds of defense: constitutive and inducible. Constitutive defenses include physical barriers such as suberized and lignified cell walls and chemical compounds such as isoflavonoids. Inducible defenses include the production of a pathogen-associated molecular pattern (PAMP) or pathogen-associated molecular pattern (PAMP) receptor (PAMP) (formerly known as horizontal or basal resistance) and immunity (formerly known as resistance) (Boller and Felix, 2009). In the former case, a microbial protein such as flagellin might be recognized by the host and induce a specific response, such as the production of an avirulence gene product) might be recognized and induce localized necrosis may result, whereas, here, recognition of the presence of a pathogen and induction of a series of responses can lead to the hypersensitive response (HR) or a related systemic response called systemic acquired silencing (SAR) gains increased immunity from initial infection through the up-regulation (reviewed in Coll. et al., 2011)

In soybean, resistance is based on both qualitative and quantitative genes, where the former is triggered and the latter is inherited as partial resistance. Qualitative resistance, also known as field resistance, is based on a few major genes, including *Rps* genes, 15 of which have been identified (Anderson and Polzin et al., 1994; Dorrance et al., 2003; Smith and Tetrick, 2004; 2010). The effectiveness of these genes relies on the presence of a corresponding avirulence gene in the pathogen whose product can be recognized by the plant's R protein. However, recognizing a pathogen as avirulent is not always successful for a long time because this pathogen has a short life cycle and can overcome resistance genes in a relatively short period (Burnham et al., 2003; Dorrance et al., 2003). Quantitative resistance is targeted against a broad range of structural and/or antimicrobial targets and is inherited quantitatively (Dorrance et al., 2003; Ranathunge et al., 2010). As the incidence of *P. vitivora* continues to increase in area production, it is essential to increase and incorporate partial resistance cultivars for effective disease management.

1.4 Suberin: physiological roles and structure

Suberin functions as a barrier to water loss and also as a barrier to pathogen attack and ingress mainly because of its molecular structure. Suberization of cell walls occurs mainly in the epidermis and part of the endodermis) and exodermis of underground plant parts.

molecule is characterized by a poly(aliphatic) domain (SPAD) and a poly(cyclic) domain (SPPD) (Figure 1), which differ in their location and are covalently linked to one another. The SPPD is hypothesized to be located in the primary cell wall, whereas the SPAD, often appearing as rings (known as suberin lamellae), is found between the primary cell wall and the plasma membrane (reviewed by Bernards, 2002).

A) SPPD

B) SPD

Figure: The hypothesized structure of the upper (phenolic) domain covalently attached to the primary cell wall (aliphatic) domain between primary cell wall and plasma membrane by a SPPD via ester linkages appearing as dark and light bands (C = carbohydrate, S = sugar from Bernards, 2002).

The SPAD is made up of aliphatic monomers specific to example hydroxy fatty acids, and diolic acids generally form the major aliphatic substituents, and can be found in a wide range of plants (Pereria, 1997; Barr-Timmmons, 2010). Other components include other fatty acids, glycerol and hydroxy acids (e.g. p-coumaric and ferulic acids) (Grac Pereria, 1997). The SPPD comprises a covalently linked network of polymers from hydroxycinnamic acids and alcohols (hydroxy cinnamyl alcohols) (Kollatukudy, 1984; Zeier and Schreiber 1997; Mat 2009).

In epidermal cells, suberin is deposited in radial and tangential walls enclosing the cells (reviewed in Bernards, 2002 and Enstone 2002). In the endodermis, suberization is characterized in three distinct stages in the root tip both aliphatic and phenolic suberin is found in the radial walls of endodermal cells and forms the Casparian band which can be visualized with the use of lipophilic dyes. Within the Casparian band, the deposition of suberin on radial walls of endodermal cells results in a contiguous wall layer that resembles a fishnet surrounding the stele when the underlying cortex is removed (Figure 2). Further along the root axis additional suberin layers are deposited in all walls of endodermal cells (Casperian band), however not in all endodermal cells, finally, iii) far from the root tip further deposition of suberin in radial and tangential walls results in thickenings of endodermal cells (Wilson and Peterson, 1984).

Similarly, heavier, although (non., diffuse) suberin deposition
epidermal cells along the root axis, moving away from the

Figure 2 Longitudinal scanning electron micrograph of
 minial. Suberin forms a net like base. Arrow shows
 arrow shows suberized cell walls remaining after cell
 enzymatically digested). Bar = 100µm (modified from Schr
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1.5 Suberin and resistance

The physical nature of suberin is the principal factor in the inhibition of pathogen penetration into plant tissues that can be demonstrated in soybean root poly(aliphatic) suberin and partial resistance to *P. sojae*. That is, the soybean cultivar Conrad, with lower rates of infection in the field compared to cultivar OX7 had lower amounts of both preformed aliphatic suberin and field level resistance. Specifically, the fatty acid and dicarboxylic acids of the SPAD were directly correlated with soybean field level resistance. Furthermore, Ranathunge et al. (2007) showed that *P. sojae* hyphal penetration and growth was inhibited to a greater extent in OX7 compared to 6OX7. Hyphal progress was especially impaired at the endodermal layers.

The role of the phenolic suberin in resistance to pathogens is also important as it not only anchors the suberin molecule to the cell wall via hydroxycinnamic acid monomers but also serves as a barrier to pathogen entry (Lai and Collier, 1998; Pomar et al., 2004; Bajji et al., 2005). Collectively, these findings suggest that the barrier and some of the molecules that make up its core, is important when studying constitutive defense mechanisms, increased to shift soybean resistance.

1.6 Manipulating suberin levels part of enhanced partial re

In essence, suberin not only acts to prevent water loss restricts pathogen growths at the suberinized epidermal cell wall. In one word based upon the above mentioned hypothesis, the role of suberin in plant partial resistance against pathogens can be considered as a strategy to manipulate suberin levels in the plant, to increase resistance. This may be achieved, for example, by enhancing synthesizing enzymes, which can lead to increased deposition of the hydroxy acids which form much of the SPAD, which is linked to an inhibition of pathogen ingress. Thus, it would lead to the hydroxylation of fatty acids expressed by an attempt to enhance suberin biosynthesis in roots.

1.7 SPAD monomer synthesizing enzymes

Fatty hydroxylase is a part of the cytochrome P-450 monooxygenase family of enzymes that catalyze the hydroxylation of the terminal carbon of fatty acids (Serrano et al., 2003; Pinot and Beisson, 2006). More specifically, the CYP86A and CYP94B monooxygenase members that can catalyze the hydroxylation of fatty acids, respectively, from fatty acids in a NADPH-dependent reaction (Serrano et al., 2009). According to Serra et al. (2009), RNAi knockdown of a CYP86A gene in potato leads to lower retention of water by the epidermal cells (WT) because of a changed suberin composition in the potato tuber.

genes, and numerous other related pseudogenes, and the expression of these has been shown in soybean roots (Koteles, 2012).

1.8 Soybean transformation

In order to begin to work on changing gene expression of GmFAE1 genes, a method of plant transformation must be selected. The insertion of suberin biosynthetic genes of interest into the genome for analysis of their changed expression in suberin composition affected root growth. Traditional transformation techniques using *Soybean* & *Rhizobium radiobacter* (Young et al., 2001) are a bacterium that can be engineered to carry foreign genes. However, transformation efficiency and long plant regeneration times make transformation is not always feasible (Cao et al., 2009; Tsai et al., 2001). An alternative strategy is *Agrobacterium tumefaciens* (Young et al., 2001) *Rhizobium rhizogenes* (Young et al., 2001) mediated transformation and generation of transgenic hairy roots.

1.9 *Agrobacterium rhizogenes* hairy roots

Agrobacterium rhizogenes is a soil-dwelling bacterium of the family Rhizobiaceae that leads to extensive adventitious root growth (root syndrome) at the site of infection (Ribeiro et al., 2003). Hairy root formation is dependent upon the successful transformation of plant cells with bacterial genes. Although the transformation mechanism is a

tumefaciens mediated transformation to adventitious root formation rather than the formation of undifferentiated cells (Nilsson and Olsson, 1997). Ri (root inducing) plasmids (T-DNA) are of several hundred base pairs in length and contain a T-DNA region that may contain auxin biosynthetic genes as well as genes that lead to increased sensitivity of the plant tissue (White et al., 1991). Expression of the particular gene of interest in hairy roots leads to increased sensitivity to endogenous auxin which is essential for root formation. Consequently, hairy root genes lead to adventitious root formation (White et al., 1985). These oncogenes lead to neoplastic growth (adventitious root growth), and lead to the formation of opines. The purpose of this is to provide a growth substrate (opines) for bacteria, thus giving bacteria a competitive advantage over other species of bacteria in the rhizosphere (White et al., 1997). The engineered T-DNA can be used to knock down or over express native plant genes, or to introduce genes from bacteria, the relative proportion of transformed cells that differentiate into adventitious roots is greater than in non-transformed tissue since transformed cells differentiate into adventitious roots. It is important to note that hairy roots are transformed because of local phytohormones that induce cell differentiation into root tissue.

Since hairy roots are neoplastic and adventitious in nature (unlike roots in the traditional sense), it might be anticipated that

deposition might be affected. Hairy root cultures have been more than 100 species, their anatomy and structure have been studied by all countries (Cancha and Vargas, 1999) by Caliform (Solzica californica) and Poppy (Papaver rhoeas) (Park and Chini, 2000) and tomato (Solanum lycopersicum) (Picu et al., 2004) in cell arrangement structure between transgenic roots have sometimes. In particular, poppy hairy roots had a loose cortical arrangement whereas tomato hairy roots had a higher number of vascular bundles. This suggests that hairy roots differ between species. Thus, to study the anatomy and chemistry of hairy root cultures of transgenic plants to understand the impact those differences may have on functional

Soybean hairy roots can be induced and cultured (Chou et al., 2000). Induction of hairy roots involves wounding plant material, such as hypocotyls, stems or young leaves, and simultaneously infecting with Agrobacterium strains. Usually within a few days root growth begins and small roots appear at the site of inoculation. Once established, roots can be cultured in solid or liquid nutrient media. The stability and ease of regeneration are important to plant biologists. (2009) have found that transgenic hairy roots retain morphological stability in culture and thus can be cultured relatively easily and stably. Thus, studying plant gene expression in hairy roots is simpler and more efficient than in plant tissue culture, as a fast growth rate, is stable and can be viewed in a flask.

Hairy roots have been a wide variety of plant biology topics including gene expression (Ding et al., 1999), nodule development (Ding et al., 2001). They have also been used to study the reactions between plant roots and microbes. For instance, an approach has been used to study the interaction of soybean roots with *Fusarium oxysporum* (Mandal and Mitra, 2004). In this system, hairy roots can be used to study plant root and pathogen interactions. In particular, glyceollin and coumestrol synthesis was measured by liquid chromatography in two different cultivars of soybean after infection with *F. oxysporum* (Liszovaya et al., 2004).

1.10 Rationale: why hairy roots?

Since *Phytophthora sojae* pathogen transformation leads to the hairy root phenotype, it seems that using soybean hairy root system is an excellent option. In this hairy root transformation system, suberin levels can be manipulated by using appropriate constructs to alter the expression of suberin biosynthetic genes. This system further allows the study of suberin's role in the pathogen growth within soybean roots. Generating a whole root system where some cells and cells that may or may not be transformed can take place. However, transformed hairy roots are generated within a few weeks.

pathogen preferentially attacks roots, a whole plant need not be infected. As mentioned earlier, the aliphatic domain of suberin is closely associated with the partial resistance in roots. Therefore, it becomes imperative to study whether or not the deposition of suberin in hairy roots mimics that in WT. For this reason, hairy roots must be investigated more carefully by using a hairy root model to study the role of suberin in soybean partial resistance. This study fits into my thesis objectives.

1.11 Objectives

1. Establish soybean hairy root cultures from soybean cuttings.
2. Confirm that established hairy roots are representative of investigating the expression of the gene using PCR.
3. Study the anatomy and suberin deposition pattern in established hairy root cultures using histochemical techniques.
4. Characterize the aliphatic suberin (quantitatively and qualitatively) in hairy roots.
5. Investigate the infection by *Phytophthora sojae* in hairy roots and compare to WT roots.

By fulfilling these objectives, I hope to gain a clear picture of the structure and functional similarity of hairy roots to WT roots, thus establishing a hairy root model tool to investigate the role of suberin in the defense system.

CHAPTER 2: MATERIALS AND METHODS

2.1 Plant materials

Seeds of *Glycine max* var. Conrad and Firmex 760 grown plants (year of culture 2009) were obtained from Agriculture and Agri-Food Canada (London, Ontario). Seeds were surface sterilized by 10% available bleach, Clorox Co. (Brampton, Canada) for 20 minutes and rinsed with sterile water. Surface sterilized seeds were then placed in petri dishes. Petri dishes were sealed using parafilm and placed in a 25°C incubator (light/dark) period. Once the cotyledons were excised and to generate hairy roots as described below.

2.2 Agrobacterium strain

Agrobacterium strain LBA9402, a gift from Dr. Patrick (National Research Council Canada) was used to generate hairy roots. Media were maintained in YIM (4HR) (0.8 mM MgSO₄ 1.7 mM NaCl, 1 mM mannitol, 0.4 g yeast extract, and 15 mM NaOH) at 4°C in the dark.

2.3 Generation of hairy roots

Hairy roots were generated using a protocol developed by Cho et al. with slight modifications. Briefly, soybean cotyledons were inoculated on the abaxial side by wounding the major vein using a scalpel.

coated Avicel with zooglone for 24 h. Explants were grown overnight on medium at 30 °C inoculated explants were placed on a medium containing MS (Sigma) (4 g L⁻¹), sucrose (3%) and cefotaxime (500 mg L⁻¹), adjusted to pH 5.8 with NaOH. The antibiotic is used to prevent the growth of rhizoglyphs but not the site of inoculation. The inoculated explants were placed in a 16 h light/8 h dark period, 25 °C).

2.4 Maintenance of roots

Once hairy roots emerged (approx. 5 cm length) they were excised from the parent explants and placed on a medium with same concentration of cefotaxime but without bacterial growth. They were plated on MS medium without antibiotic. Plates with hairy roots were placed in an incubator at 25 °C in a 16 h light/8 h dark period. The first 4 cm of root was subcultured every few weeks onto a fresh plate as described above to propagate and maintain the hairy roots.

2.5 PCR analysis

In order to confirm the origin of adventitious root growth, DNA was amplified from genomic DNA obtained from established hairy roots by polymerase chain reaction. Genomic DNA was extracted from both Conrad and modified (CTAB-trimethyl Ammonium Bromide) protocol and Yang (2004) by briefly, roots were ground

in liquid. A sterile mortar and pestle and approximately 100 mg of fresh root tissue was suspended in 600 µL of CTAB buffer (1.0 M NaCl, 0.1 M Tris-HCl pH 8.0, 20 mM EDTA pH 8.0, 2% CTAB) along with 0.2% v/v mercaptoethanol and 2 µL of β-mercaptoethanol. The suspension was heated at 65°C for 1 hour. To the suspension 600 µL of Chloroform:Isoamylalcohol (24:1) was added and centrifugation at 13,000 rpm for 12 min. The supernatant was transferred to a fresh microcentrifuge tube and 0.7 volumes of isopropanol were added. The mixture was cooled at 4°C for 30 minutes and centrifuged again at 13,000 rpm for 12 min. The supernatant was discarded and the pellet was washed with 700 µL of ethanol and centrifuged again at 13,000 rpm. The pellet was completely dried using a vacuum oven at 40°C. The DNA was suspended in 50 µL of DNAse free water.

The *OsG* gene was amplified using primers described by Zeng et al. (2011). The forward primer (F) sequence is 5'-GCTCTTGCAGTGCTAGCAATAGTAGGGTGCAGCTACCTACTC-3' and the reverse primer (R) sequence is 5'-CTGAGGCGAGGTCAGTGGCAGT-3'. A 430 bp fragment was amplified from hairy and root WT roots from cultivars was used as a control (Water roots control). PCR reactions were run in 25 µL of PCR buffer (Applied Biosystems) containing 1.5 µL MgCl₂ (50 mM), 2.5 µL 10 X PCR buffer mixture (100 mM), 0.3 µL dNTP (50 mM), 100 ng of genomic DNA or bacterial preparation and 0.15 µL of Taq polymerase. The enzyme and primers were obtained from Applied Biosystems. The PCR reaction was conducted at a duration of 94°C for 30 s, 55°C for 45 s, 72°C for 1 min, repeated 35 cycles. The annealing temperature was 55°C and final extension was 72°C for 10 min.

The PCR products were run on a 1.0% agarose gel at a voltage of 100 V and stained with ethidium bromide. Gel bands were visualized on a UV transilluminator (Universal Hood II, S76S/01511).

A relatively easy method of determining whether or not a plant was transformed was also employed, which allowed for a more confident analysis. In vitro grown cotyledons (obtained as described above) were divided into two groups. One group was mock inoculated as described above, whereas, the second group was inoculated with the Agrobacterium strain. On days 10, 15, and 20 the presence or absence of hairy root formation was noted.

2.6 Histochemical analysis

In order to view the pattern of suberin deposition and the presence of fluorescent dyes were employed. Sections of hairy roots (cultivar 4-12 in length) were cut at intervals of 0.5 cm along the length of the root. Sections were viewed using a Zeiss Axioimager Z1 Microscope. The presence of a band in the endodermis was determined using Toluidine Blue (TBO) (Sigma) according to Lulai and Morgan (1992). free hand cross sections were stained with fresh TBO (0.05% in 0.1 M phosphate buffer, pH 6.5) for 1 minute followed by a 10% methanol wash. Stained sections were then rinsed several times in water. Sections were viewed with blue light (490 nm) through a dichroic mirror (510 nm) and a 515 nm long pass filter. Suberin deposition was visualized as a yellow fluorescence. Images were captured with a Nikon Coolpix 3. Suberin lamellae were

viewed using fluorol yellow (FY) (Brundrett et al., 1991). The sections were then placed in 0.01% (w/v) FY in 90% glycerol for 1 hour. These sections were then rinsed several times in fresh 75% glycerol and viewed (filter 560 nm, dichroic mirror 585 nm, barrier filter 600 nm) with a Nikon Axiophot 2. Under these conditions, staining of suberin lamellae gave a bright yellow fluorescence. Suberin was also detected using Sudan Red VII B (fast red B) dissolved in 0.1% (w/v) in 1:1 polyethylene glycol for 2 hours (Brundrett et al., 1991). The sections were rinsed with clear water in 75% glycerol and viewed with bright field illumination with a Nikon Axiophot 2. Suberized cell walls stain pink.

2.7 GGMS analysis

Suberin is a polymeric network and in order to quantify it in plant tissue, it has to be depolymerised. Both roots and isolated epidermal and endodermal tissues were analysed. For whole shooty roots of 14 sc (m) 2 were inflorescence and ground a powder in a mortar and pestle.

To isolate epidermal and endodermal tissue separate root inoculations were used, for example, from both cultivars. Roots of 14 cm length were separated into 3 segments of 4-8 cm. Any lateral branching was removed. Root cross-sections were made; the epidermis was removed; three separate

for any root sections that were dried. This was done so that the surface area of the roots could be calculated and suberin area per mm^2 value. The epidermis was then removed using a wire which was pulled through the, which stepped the epidermis and few cells left behind the endodermis, stele and a few cortical cells. removed, it was frozen using liquid nitrogen. Ground tissue was placed in a microcentrifuge tube kept frozen at -80°C until extraction. Root sections were made of endodermis and its diameter measurements were made at different locations. The endodermal tissue was also removed from the epidermis and placed in a separate microcentrifuge tube.

In order to quantify the suberin in the root tissue was first extracted in chloroform:methanol (Meyer et al., 2011). Briefly, frozen hairy root tissue from both tissue layers and cellulose thimbles and extracted in chloroform:methanol (2:1) for 3.5 hours. The solution was removed and the thimbles were cleaned and the remaining tissue was extracted for 3.5 hours in fresh chloroform:methanol (2:1). This solution was added to the and the tissue was extracted in 100% chloroform overnight. The third aliquot was combined with the previous extracts and removed from the thimbles, weighed and placed in 5 mL solvent. The components were obtained by drying the chloroform:methanol mixtures using a rotary evaporator. The amount of suberin was determined by the weight of the residue.

bottom flasks, the solutions were removed using a glass pipette and weighed clean glass vials. A 10 mL of a 1:1 (v/v) chloroform:methanol was added and the mixture was evaporated using a steady stream of nitrogen and the mass was weighed the vials again.

Suberin monomers were obtained by using a methylation protocol according to M. S. S. (2011) (2011). Separated hairy roots (approximately 6 mg for intact hairy roots) were incubated with HCl (Supelco, 3 N dimethyl sulfoxide) in 100% methanol at 80°C for 24 hours. Once samples were brought to room temperature, deionized water was added to stop the reaction after which 10 µL of a 100 µg/mL standard was added. Samples were extracted three times with hexane and the vial was sealed. The upper layer was then removed and a clean screw cap glass vial and extraction with hexane was performed. Hexane solubles were dried under a steady stream of nitrogen and 10 µL of pyridine and 10 µL of TMS-OH were added and incubated at 70°C for 40 minutes to derivatize remaining hydroxyl and carboxylic acid groups. The final sample was transferred to a clean vial. Concentrations of esterified monomers and any TMS derivatives were analyzed on a GC Chromatograph equipped with a flame ionization detector (GC/FID) and an ion trap mass spectrometer were connected to a GC/FID. A 5 µm DB-5MS column (WCOT silica 30 m X 0.25 mm). One µL samples were injected.

Hairy roots were incubated directly in zoospore suspension and 20 hours. -hFarrad cross sections were made 1 cm from the root tip for microscopy. *Phytophthora* described by Ranathunge et al., 200 were cleared using 10% KOH stained with 2% toluidine blue water for 2 (Sigma Aldrich) and stained with a solution of 1:1:1 of glycerol and KOH for 5 min. Cross sections were mounted in 75 and viewed under bright light using the microscope described taken using CamICc1.

2.9 Statistical analysis

Student's t test was used to compare poly(aliphatic) suberin of intact hairy roots from both cultivars. Analysis of Variance compare mean amount of poly(aliphatic) suberin of isolated cultivars. ANOVA was also done to compare mean amount of suberin distributed by chain length in intact hairy roots of both cultivars. waxes of isolated hairy roots from both cultivars. In the case of significance denoted by ANOVA, tukey's post hoc test was used to determine. All analysis was done using SigmaStat® 3.5.

CHAPTER 3: RESULTS AND DISCUSSION

3.1 Hairy root generation

Hairy roots from *C. xanthocoma* were generated in the lab using a protocol of Cho et al. (2000) where inoculation with *Agrobacterium rhizogenes* 14929s surmounting inoculation became successful and approximately one week inoculation callus growth appeared. Hairy roots originated from the callus region in 14 days (Figure 3.1). Previous studies report similar timeline for hairy root generation in different al., 2009; Fernandez et al., 2010). Although many roots were generated from 14 days root growth was also noticed before a time range. This could be attributed to the inherent differences which in turn affect the level of endogenous auxin in the tissue. This affects the hairy root growth is abundant (Takahashi, 1997). Furthermore, the insecticide also affect the amount and frame of hairy root (Seki et al., 2005). Hairy roots in the medium growth rates of approximately 2k.

Figure 3 Time course of hairy roots on *Agrobacterium tumefaciens* (A) and *Agrobacterium rhizogenes* (B) on wounded *Chenopodium album* 7 days pi, C, roots emerging from callus 10 days pi and D, Two-week-old hairy roots in nutrient rich agar medium (50 mg sucrose and 50 mg cefotaxime mg^{-1}).

Cotyledons obtained from in vitro germination of soybean root production, proved to be a more efficient system rather than cotyledons from soybean plants germinated in greenhouse. Cotyledons from greenhouse soybean followed by inoculation with bacteria resulted in necrosis and eventually embryonic leaf death before any hairy root formation.

Once putative hairy root cultures were established it was determined whether or not they originated transformation. For this analysis was done using genomic DNA isolated from hairy roots along with WT roots. The presence of *B. p. (430 P)* *R. n. p. i. g. a.* on a gel (Figure 4) confirmed the hairy root genotype. This is important because in order to manipulate suberin levels in a system is required that will alter the soybean genome, and hormonal changes. However, successful generation of hairy roots visually. That is, cotyledons wounded with a scalpel but not inoculated with rhizogenic bacteria do not produce any roots whereas those inoculated with rhizogenic bacteria produce hairy root formation at the site of inoculation (data not shown). It is the necessity of conducting PCR analysis on hairy roots, because genetically transformed hairy roots only has the hairy root plant tissue with a native soybean binary vector also transform a secondary plasmid, thus is efficient as a binary vector system through the use of a binary vector system transformed soybean as well as gene encoding a protein product which fluoresces under any generated hairy root which fluoresces red is truly transformed.

reported that 34% of roots generated *in vitro* were transformed and were initiated due to hormonal effects.

Figure 1 PCR analysis of genomic DNA Ausrihig pgrifnges for the A. rhizogew whole bacterial DNA preparation (6 WT) and Conrad WT = genomic DNA itsplatiendvfiton weildinated soybean (negative control) and Conrad HR genonX7 DNA isolated from soybean hairy roots PCR run on 1% agarose gel. Selected ladder (bp) are labeled on the left hand side of the gel. T 430 bp.

One major reason why hairy roots form the basis of an system is that they are cultured on nutrient rich media almost in true for WT roots (Fernandez et al., 2009). Morphologically WT roots, however there were some differences, namely the (Figure 3), which is where hairy roots obtain their name. Ex and a fast growth rate can be attributed to increased sensitivity (as mentioned above) or the increased sensitivity of hairy roots which influences growth (Shen et al. 1988, Van Sluys and 1991, Mallol et al. 2001, Peres et al. 2001, Lee et al. 2004).

It was observed that hairy roots grow aerially, i.e. roots emerge callus and display negative geotropism (Fitzgerald et al. 2006). suggested that fewer amyloplasts are found in hairy roots possibly leading to a weak gravitational response (Kim et al. 2009). Furthermore, large air spaces were observed in the hairy roots (Figure 5). Teakle et al. (2011) reported that roots growing in areas, such as agar, develop an aerenchymatous morphology in root tissue under limiting conditions. These features were found in both COX760.

3.2 Hairy root anatomy

Hairy roots are anatomically similar to WT roots as can be seen. However in addition to the air spaces found in hairy roots, the vascular anatomy of hairy roots seems different than WT. In particular, in some

three xylem poles whereas, WT roots have four (Figure 5). (1957), auxin levels can increase in roots from decapitated roots placed in auxin medium. Thus, since higher levels of endogenous auxin (or are more sensitive to) that the number of xylem poles in hairy roots.

I also noted that hairy roots did not appear to have the same mechanical strength as WT roots. This was especially evidenced during sectioning of hairy roots. This is a characteristic of hairy roots, which are prone to breaking. This is also characteristic of hairy roots, which have air spaces present in the cortex (Figure 5) may also contribute to their mechanical integrity. Additionally, due to the influence of the moist medium in which hairy roots are first grown and then transferred to liquid culture conditions can weaken the epidermal cell walls making them more prone to damage. Hairy roots are widely grown in liquid cultures and used as tools and models for many questions involving plant growth. It seems that while media may have a certain robustness it does not preclude their use as an experimental



Figure C5: Cross section of a *Ox760* (top image) and a *Ox760* (bottom image) stained with farrus. Left hand side shows the cortex and central stele.

3.3 Hairy root suberin histochemical analysis

In order to use hairy roots to test the hypothesis that soybean pathosystem, it is imperative that suberin deposition resembles that of WT roots. Through the use of fluorescence microscopy, it was shown that cell wall suberin histochemistry of hairy roots (Figure 6B). Previous research using WT roots documented that clover root has a state I endodermis, in other words, a suberized barrier and solute transport between the cortex and the stele in the root (Thomas et al., 2007). In a transverse section, the Casparian band is evident as points of fluorescence in endodermal cell walls stained with a fluorescent dye, and this same pattern can be seen in hairy roots (Figure 6C). At the root tip, endodermal cell walls of hairy roots were more suberized than in WT roots. However, not every endodermal cell was suberized resulting in a characteristic suberin deposition pattern where regions of no lamellae were present (Figure 6C). This may be to allow the passage of water and solutes into the stele even at these young stages (Charko et al., 1975; and Robards, Peterson and Enstone, 1996; Waduwara et al., 2008). Importantly, hairy roots still had a Casparian band. Normally as roots mature, suberin deposition also increases (Paterson, 1978). In hairy roots we found increased suberin deposition in epidermal cell walls distal to the tip along the length of the root (Figure 6E; this was evident in greater staining of epidermal cell walls close to the root tip at approximately 10 cm and this was also observed in WT roots (Thomas et al., 2007).

Figure 5 Suberin deposition patterns in soybean hairy roots (A, C, E, G) and nodules (B, D, F, H) (system of Dr. Raymond Thomas), free hairy root cross-sections. stained with toluidine blue 0 and neutral red, 2 cm from the root tip. C patches of cells with suberin lamellae (arrows) are present stained with FY, > 8 cm from the root tip. E to H, Sections stained with FY, > 8 cm from the root tip. lamellar suberin is present in all nodules (arrows) on root tip, F 4-6 cm, G 8 cm and H 24 cm

Hairy roots from both cultivars displayed similar suberin in root axis and similar morphology and anatomy compared to important because use of a root model hinges on the tenet actual system are comparable.

3.4 Hairy root suberin analysis

After establishing suberization patterns of hairy roots, poly(aliphatic) suberized tissues (some measured 1.2 cm long, see materials and methods for details) were analyzed for amount and amount.

3.4. Quantitative analysis

Quantitative analysis of hairy roots had an order of suberin compared to Conrad (Figure 7). Although this difference is in contrast to published work Conrad had applied a relatively amount of aliphatic suberin (Thomas et al., 2007), this difference to both cultivars responding differently to the genetic transformation and/or the medium in which they are grown. It is clear that suberin deposition is influenced by these environments. It has been shown that has greater partial resistance to higher amounts of suberin in suberizing tissues (Dorrance et al., 2003; Thomas et al., 2008; Ranathunge et al., 2008). Anderson (1982) found that a 2% mortality rate was observed in susceptible cultivar Ar

had 40% mortality rates. However, interestingly, the percentage of plants that survived in the fields changes between years, leading to the fact that a change in the environment can influence level of suberin deposition and thus resistance to pathogens. In other words, hairy roots may be more plastic to a changing environment, thus have higher suberin levels compared to control plants. This may be due to the medium as opposed to growing in soil may contribute to this. The insertion of the hairy root may also influence expression of genes, (Baker et al., 2010) thus cause hairy roots to have a different phenotype.

Figure 7 Quantification of poly(aliphatic) suberin and intact so
 Conrad) hairy Tissue was subjected to esterification to rele
 poly(aliphatic) suberin. Total poly(aliphatic) suberin was me
 data are expressed on basis of amount of tissue (mg) trans
 average \pm SE of three replicates. No significant difference

Quantitative differences in aliphatic suberin were found in hairy roots when the endodermis and epidermis were analyzed. Differences were not always statistically significant, but suberin was highest farthest away from the endodermis. Two important aspects of suberin deposition in hairy root dermal poly(aliphatic) suberin is higher in hairy roots than in hairy root cultivars, and 2) poly(aliphatic) suberin amounts increased. Furthermore, there are quantitative differences between WT (publ. al., 2007) and hairy roots, where hairy roots have aliphatic suberin approximately 8 times lower than WT. In other words, amounts of aliphatic suberin in hairy roots are a per m comparable to roots in the case of this important because when developing a root model system it is necessary to understand the model may have from the original system. With this data and histochemical data it is possible to determine appropriate in vitro model compared to Conrad.

3.4. Qualitative analysis

Next, it was also important to assess the monomeric composition of poly(aliphatic) suberin in hairy root and WT roots. Qualitatively, hairy root aliphatic suberin contained fatty acids, hydroxy fatty acids, and dioic acids as in WT roots (Shore et al., 2007). In the available isolated dermal tissue from hairy root, some suberin components were not detected at accurate detection levels and thus component analysis was not possible. However, it was found that although all fatty acids, hydroxy fatty acids, and dioic acids were not all chain lengths that are normally found in WT roots were found (Table 1). Generally 16 and 18 carbon chain lengths were found, whereas longer chain lengths of fatty acids and alcohols were more of suberin sizes, (reviewed in Bernards, 2002) were not considered an important feature to take note of. Hydroxy fatty acids were the most abundant and are similar to WT roots, making up 70% of total aliphatic suberin (Table 1). In 2007, it is interesting to note that hairy root has a high correlation with resistance to pathogens (Thomas et al., 2007). Again, hairy root not only has greater suberin composition, amounts are higher than WT roots. Interestingly, Conrad et al. (2007) found that although hairy root has this difference was not significant.

Table 1 shows the length distribution of hairy root aliphatics by substrate. The data are presented for intact hairy roots of both COX760⁻⁵ and COX760⁻⁵ hairy roots. The data are expressed as mg/mg of hairy root tissue subjected to transesterification and measured using GC-MS. The data are presented as averages of three replicates \pm SE. Means followed by different letters are significantly different (P = 0.006).

3.4.3 Soluble wax analysis

With respect to soluble wax components, the pattern of published data on WT roots (Thomas et al. 2007) for 60XF760 (where the soluble waxes increased, although the imbalances were not statistically significant) regardless of the lack of soluble wax contains unpolymerized alkanes, and although the actual amount of which in the hairy roots may vary between distances from the root tip. Earlier, soybean WT roots with higher amounts of insoluble wax were more resistant to infection, therefore, it can be expected that roots growing in an artificial medium may not have the same amount and may be considered more plastic to a changing environment.

Figure 9 Quantification of soluble waxes in isolated soybean hair
 Epidermal and endodermal tissues were isolated from soybean
 3 segments, 4, 8 and 28 cm. Soluble waxes were isolated by solvent
 Total suberin was measured using GC-MS. Data are expressed on
 root or endodermal surface area. Bars represent average \pm
 significant differences were found ($P = 0.235$).

3.5 Hairy root pathogen interactions

As a final step in investigating the appropriate effects of soybean WT analyzed the interaction between root- and pathogen hairy roots had higher levels of suberin, which were and had more structural integrity to Conrad, 6 hairy roots were used for this study. Hairy roots were exposed to zoospore suspension at different times that at 2 h zoospores attached to the epidermal cells in preparation for germination. This is in contrast to what was expected where zoospore attachment was observed at 2 h post-inoculation; however, zoospores had not attached to hairy roots (Figure 10A). Finally, within 22 h zoospores had penetrated the epidermal cells and growth was seen between cortical cells (Figure 10B, C). This is in contrast to what was reported wherein 24 h post-inoculation zoospores had penetrated the endodermis (Rahman et al., 2008). This difference could be due to the fact that hairy roots have gaps between cortical cells (Figure 5), which may impede the pathogen despite this it was observed that infection of hairy roots followed a similar pattern to that in WT roots, albeit it was slower. This is important to note as the effect of the change in suberin levels obtained through germination require a pathogenicity test, which in this case will not be used. With a baseline infection progress we can assess any change in infection that is manipulated.

Figure 1 Development of *Phytophthora sojae* in fresh and cross sections of long hairy roots taken from the root tip. After incubation zoospores attached and began to germinate. After incubation zoospore germinated and hyphae with dikaryon progressing between cortical cells (arrows). Bars = 50 μ m.

CHAPTER 4: CONCLUSIONS AND FUTURE DIRECTIONS

Through this experiment and flow work that hairy roots are similar to where root anatomy, suberin histochemistry, suberin composition and response to pathogen attack are concerned. Even though hairy root cultivars Conrad and Oxytropis with those found in WT roots, hairy root stable used a system mimicking WT roots since the anatomy, suberin composition and pathogen response has been documented experimentally. Various suberin levels can be manipulated by the expression of *GmMYB176*, changed. For this, RNA interference (RNAi) knockdown experiments which can down regulate transcription and hence the production of the SPAD. For example, Yi et al. (2010) have down regulated *GmMYB176* in soybean hairy roots via RNAi leading to decreased SPAD product. Conversely, SPAD levels could potentially be enhanced by upregulating *GmFAH* genes.

Lin et al. (2011) developed a new plant transformation vector for hairy roots, which can be used to study the relationship between hairy root growth and suberin formation. Transformed roots appear red under ultraviolet light due to the presence of suberin. Essentially, hairy roots have been engineered with the capacity to carry foreign genes separately. This can potentially be used to study the function of *GmMYB176* by using a strong promoter, such as Cauliflower mosaic virus promoter, to upregulate it.

Additionally, a different pathogenicity test could be employed. A test of the effect of changed suberin levels on hairy root resistance that relies on sectioning and a microscope, e.g. fluorescently labeled hairy roots with zoospore suspensions and monitoring root damage caused by *P. sojae* could be an alternate method of testing the effect of suberin manipulation. Such work has previously been done and further manipulation of other root specific genes have been manipulated.

In essence, if manipulated levels of suberin affect soybean hairy roots, then this will further support the hypothesis that suberin contributes to soybean partial resistance against this pathogen.

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APPENDICES

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