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ROLE OF HEME OXYGENASE IN MODULATING EXPRESSION OF ROS-
REGULATORY ENZYMES IN *Medicago truncatula*

A Thesis Presented

by

Parna Ghosh

to

The Faculty of the Graduate College

of

The University of Vermont

In Partial Fulfillment of the Requirements
for the Degree of Master of Science
Specializing in Cell and Molecular Biology

October, 2014

Accepted by the Faculty of the Graduate College, The University of Vermont, in partial fulfilment of the requirements for the degree of Master of Science, specializing in Cell and Molecular Biology.

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ABSTRACT

Heme Oxygenase (HO) is an enzyme universally found in animals, plants and microbes. In plants, the role of heme oxygenase in the synthesis of the phytochrome chromophore is well recognized and has been extensively studied; however its role in regulating reactive oxygen species (ROS) in plants is just beginning to be explored, particularly in legumes. Legumes interact with *Rhizobium* bacteria to form symbiotic nitrogen fixing nodules. ROS plays an important role in the development of roots as well as symbiotic nodules. In the model legume *Medicago truncatula*, ROS in the root is regulated in part by the *LATD/NIP* gene. The *M. truncatula giraffe* mutant has a deletion that removes the entire HO coding sequence. We have found that the *M. truncatula GIRAFFE* HO regulates expression of some of the *LATD/NIP*-regulated ROS genes such as *RESPIRATORY BURST OXIDASE HOMOLOG C (RBOHC)* and a cell wall peroxidase (*cwPRX2*) in seedlings. This means that the wild-type function of *GIRAFFE* is to up-regulate expression of *RBOHC* and *cwPRX2* in roots, in contrast to *LATD/NIP*, which down-regulates them. We also found that *LATD/NIP* and *GIRAFFE* do not regulate expression of each other in seedlings. Given that the highest expression of *GIRAFFE* HO is in a senescing nodule, we tested the expression of ROS-regulatory enzymes in senescing nodules. We found that *GIRAFFE* up-regulates expression of *RBOHC* during nitrate-induced nodule senescence. At present, with changing climatic conditions and exposure to various environmental stresses that can alter ROS homeostasis, characterizing the role of *GIRAFFE* in the antioxidant machinery of legumes can be useful in improving crop productivity and for enhancing soil fertility.

Dedication

This thesis is dedicated in sweet memory of my mother *Indrani Ghosh* and father

Tapan Ghosh

Acknowledgement

I would like to express my deepest appreciation to my advisor, Dr. Jeanne Harris for being an incredible mentor during my graduate studies in every possible way. Undoubtedly her continual guidance, priceless training and faith on me, made it possible for me to complete my Master's degree.

I am deeply grateful to members of my Thesis Committee, Dr. Mary Tierney, Dr. David Barrington and Dr. Nicholas Heintz for their valuable comments, suggestions and encouragement that has been tremendously helpful in shaping my thesis the way it stands today.

I express my heartfelt thanks to Dr. Jill Preston, Dr. Terrance Delaney and Dr. Mary Tierney for the generous use of equipments in their laboratories and for their technical advice and suggestions all along. I thank every faculty in the Department of Plant Biology for thoughtful discussions and encouragement during my graduate work.

A big thanks to the Greenhouse facility at UVM, especially Colleen, Dave and Tom for helping me grow plants in the greenhouse for my experiments for extended time periods.

I am thankful to the Cell and Molecular Biology Program for giving me this opportunity to pursue my degree at UVM. I thank Erin and Kirstin for their kind support throughout my journey here.

I thank the Plant Biology Office staff Sarah, Karyn and Porky who have worked so hard to make my stay here pleasant and memorable. I thank all my friends in the Department Gabriela, Kattia, Lynn, Wes, Monique, Stacy, Cyntia, Meagan, Nikisha, Emily, Suryatapa and Prince for their generous help and cheerful company.

I am truly grateful to my laboratory colleagues, Yucan, Chang, Christine, Gianna, Sanhita, Beck, Amanda, Alex and Matt for their feedback, cooperation and kindness that has helped me learn the concepts and techniques that I have used in my work.

Last and very important I cherish the bonds of love and support that I share with my friends and family. Words fail to describe their selfless acts of staying by my side at some of the most challenging times while pursuing my thesis research. This thesis would have remained unwritten, had I not been blessed with the warmth and trust of such beautiful souls.

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Chapter 1: Introduction

Function of Heme Oxygenase in plants and animals

Heme Oxygenase (HO) catalyses the cleavage of heme to biliverdin with the release of equimolar amounts of iron and carbon monoxide (CO) (Tenhunen, Marver et al. 1968).

Role of heme oxygenase (HO) in plants and animals

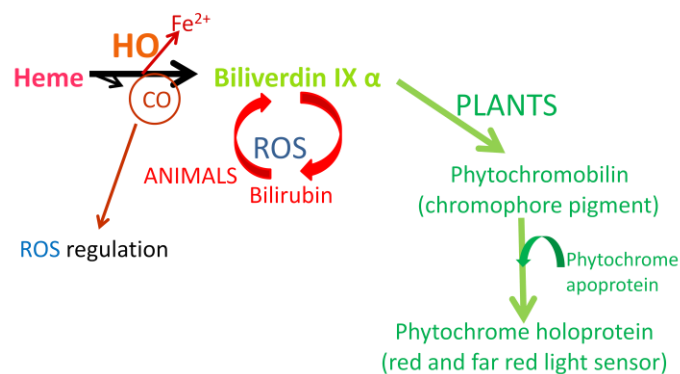


Figure 1: Heme Catabolism pathway in plants and animals. Heme is degraded to biliverdin by heme oxygenase. In plants biliverdin is a precursor in the synthesis of the phytochrome chromophore. In mammals, biliverdin is reduced to bilirubin, an antioxidant. HO, Heme Oxygenase; ROS, Reactive Oxygen Species; CO, Carbon Monoxide.

In mammals, biliverdin is reduced by biliverdin reductase (BVR) to bilirubin (BR) (Terry, Linley et al. 2002) which gets oxidized back into biliverdin (Baranano, Rao et al. 2002). An important role of the HO/BVR system has been established for neuronal disorders such as Alzheimer's disease (Barone, Di Domenico et al. 2013), cardiovascular diseases (Seki, Naruse et al. 1999) and diabetes (Abraham, Rezzani et al. 2004). In plants, HO is localized to the chloroplast, and the biliverdin it produces is a precursor for the synthesis of the phytochrome chromophore, phytochromobilin (Fig. 1) (Terry, Wahleithner et al. 1993). The phytochromobilin attaches to the phytochrome apoprotein, which is synthesised in the nucleus, to form the

phytochrome holoprotein, the red/far-red light sensor, which plays a significant role in photomorphogenesis (Terry 1997). In plants, recent literature suggests that CO regulates ROS levels in plant cells (Cui, Fu et al. 2011, Wu, Huang et al. 2011, Xie, Xu et al. 2011).

Today, the chloroplast is a permanent resident in a plant cell as a result of endosymbiosis of an ancestral cyanobacterium by a eukaryotic cell, about half a billion years ago (Lopez-Juez and Pyke 2005). The chloroplast still encodes for about a 100 proteins while the remaining 3000 proteins required for its biogenesis and function are encoded by the nucleus (Sato, Nakamura et al. 1999). This requires communicating signals from the chloroplast to the nucleus known as retrograde signaling (Nott, Jung et al. 2006). Heme oxygenase is one of the signaling molecules that influence transcription of the nuclear genome (Surpin, Larkin et al. 2002).

Heme Oxygenase gene in *Medicago truncatula*

Overview

Medicago truncatula has a single heme oxygenase gene, *GIRAFFE* (Medtr8g019320) (http://www.jcvi.org/medicago/ORF_infopage/23238/23238.m140766.html). The gene is 4 kb in size and is predicted to have four exons and three introns. The *giraffe* mutant was isolated in a fast neutron bombardment screen for plants with defects in both nodulation and development. The *giraffe* mutation is caused by a deletion of approximately 6.5 kb and is recessive (Zhang 2014).

Mutant phenotype in *Medicago truncatula*

The *giraffe* mutants have a photomorphogenic phenotype, with an elongated hypocotyl and petioles and yellowish-green leaves. Further, *giraffe* mutants fail to stimulate nodulation under red light or inhibit nodulation under far-red light (Zhang 2014). Co-segregation of the photomorphogenic and nodulation phenotypes and the deletion of the HO gene indicate that the *GIRAFFE HO* gene regulates both these traits (Zhang 2014).

Heme Oxygenase mutants in other species

In several plant species, heme oxygenase mutants have been identified that have a defect in the breakdown of heme to biliverdin and a characteristic photomorphogenic phenotype. In *Arabidopsis* photomorphogenic mutants with long hypocotyls that lack functional phytochrome chromophore have been characterised (Koornneef, Rolff et al. 1980, Chory, Peto et al. 1989). These mutants are deficient in a plastid-localised heme oxygenase that is encoded by the *HY1* gene (Davis, Kurepa et al. 1999, Muramoto, Kohchi et al. 1999). In pea the *phytochrome chromophore defective* mutant (*pcd1*), with etiolated seedlings and elongated hypocotyls, which has a defect in degrading heme to biliverdin (Weller, Terry et al. 1996), has a mutation in the pea heme oxygenase gene (*PsHO1*) (Linley, Landsberger et al. 2006). The phytochrome chromophore synthesis defective mutant in tomato, *yellow green-2* (*yg-2*) is also defective in heme degradation to biliverdin (Terry and Kendrick 1996).

How is ROS produced and scavenged?

A shift in the redox status of the earth's atmosphere to an oxygen-rich environment (Bekker, Holland et al. 2004), required the evolution of protective antioxidant defence mechanisms against damage from reactive oxygen species for survival (Scandalios 2005). The levels of reactive oxygen species (ROS) are regulated by a network of ROS-producing and ROS-scavenging enzymes (Fig. 2).

Production and Removal of ROS species

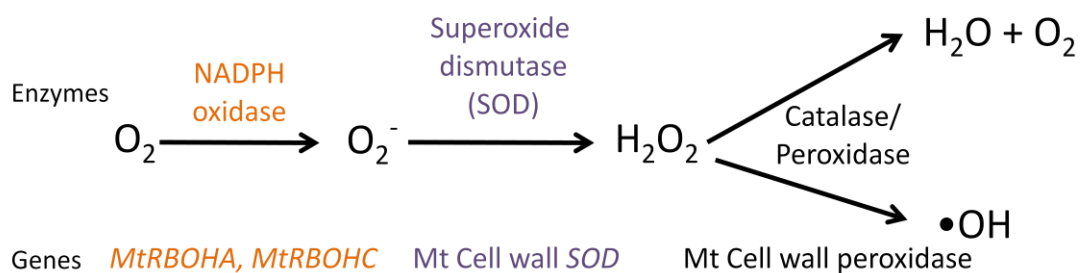


Figure 2: Cellular regulation of ROS intermediates via ROS-generating and scavenging enzymes.

Figure 2: Cellular regulation of ROS intermediates via ROS-generating and scavenging enzymes. Labels over the arrows indicate enzymes. Labels under the arrows are names of *Medicago truncatula* genes encoding those enzymes analyzed in this study.

Molecular oxygen is oxidized to superoxide anion (O_2^-), an ROS, by NADPH oxidases (Marino, Dunand et al. 2012). Subsequently, dismutation of the superoxide anion by superoxide dismutase (SOD) produces hydrogen peroxide (H_2O_2), another ROS (Fridovich 1995). Finally, catalases and peroxidases catalyse the decomposition of hydrogen peroxide to water and oxygen or to hydroxyl radical (Passardi, Penel et al. 2004, Zamocky, Gasselhuber et al. 2012).

Representatives of all these classes of enzymes are found in plants. The plant NADPH oxidases are known as *RESPIRATORY BURST OXIDASE HOMOLOGUES (RBOHS)* (Sagi and Fluhr 2001). These transmembrane proteins have an oxidase domain in their C-terminal region that oxidises molecular oxygen to superoxide anion. Similar to animal NADPH oxidases such as NOX5 and Duox, plant RBOHs have an N-terminal region containing EF hands, a motif that binds calcium (Grabarek 2006, Petry, Weitnauer et al. 2010, Suzuki, Miller et al. 2011). The EF hands and phosphorylation domain mark their importance in signal transduction pathways (Suzuki, Miller et al. 2011). Seven *RBOH* genes, *RBOHA-RBOHG*, have been identified in *Medicago truncatula* using protein sequence similarity with the Arabidopsis genome (Lohar, Haridas et al. 2007, Marino, Andrio et al. 2011).

The SODs are a large family of enzymes that can have mitochondrial, plastidial, cytosolic and apoplasmic localizations (Asensio, Gil-Monreal et al. 2012). There can be three types of SODs depending on the co-factor used by the enzyme SOD; Iron SOD (FeSOD), Manganese SOD (MnSOD) and Copper-Zinc (Cu-ZnSOD) (Alscher, Erturk et al. 2002). The SODs act as the first line of defence in protecting cells from oxidative damage (Gill and Tuteja 2010).

The toxicity of hydrogen peroxide in plants is ameliorated chiefly by two enzymes, catalases and peroxidases (Welinder, Mauro et al. 1992, Willekens, Inze et al. 1995, Morgenstern, Klopman et al. 2008, Zamocky, Furtmuller et al. 2010), which have characteristic affinities for hydrogen peroxide. Catalases convert hydrogen peroxide to water and oxygen and function in defense responses and development especially germination and senescence (Willekens, Inze et al. 1995). The thiol based peroxidases, found in compartments such as the mitochondrion, chloroplast and the

nucleus, reduce hydrogen peroxide by the exchange of thiol and disulphide groups in their redox active cysteine residue (Dietz, Jacob et al. 2006, Puerto-Galan, Perez-Ruiz et al. 2013) and contribute to processes such as plastid metabolism and nodule development (Frendo, Matamoros et al. 2013, Michelet, Zaffagnini et al. 2013). The heme-containing peroxidases reduce hydrogen peroxide by the transfer of oxygen atom and electron between ferric and ferrous enzymes (Berglund, Carlsson et al. 2002). These are secreted into the cell wall or into the vacuole and have diverse functions ranging from environmental responses to developmental processes (Cosio and Dunand 2009, O'Brien, Daudi et al. 2012, Zipor and Oren-Shamir 2013).

Abiotic stress, HO and plants

The expression of heme oxygenase responds to various environmental stresses in different plant species. Heme Oxygenase has been found to be induced by abiotic stress such as salinity in *Arabidopsis* (Xie, Xu et al. 2011). In wheat seedlings, heme oxygenase expression is up regulated by chemicals such as hydrogen peroxide and by salinity (Xu, Jin et al. 2011). In soybean, HO is induced in leaves, roots and nodules by UV-B radiation and cadmium (Noriega, Balestrasse et al. 2004, Yannarelli, Noriega et al. 2006, Balestrasse, Yannarelli et al. 2008). The increased expression of HO in soybean leaves in response to salinity has been implicated in protecting leaves from salt stress (Zilli, Santa-Cruz et al. 2009). In alfalfa the amelioration of cadmium induced oxidative stress is effected by salicylic acid via heme oxygenase induction (Cui, Li et al. 2012).

Nodule senescence as part of development

Overview of nodulation

Nodules are highly specialized symbiotic organs formed under nitrogen-limiting conditions, on roots and occasionally on shoots of legumes, following an interaction between the eukaryotic legume species and its specific prokaryotic rhizobial partner (Sprent 2007, Markmann and Parniske 2009). This symbiosis contributes enormously to biological nitrogen fixation, wherein atmospheric nitrogen is reduced to ammonia by the prokaryotic nitrogenase enzyme complex (Bulen and LeComte 1966, Raymond, Siefert et al. 2004), of the rhizobial partner housed within the legume nodules (Virtanen and Miettinen 1963, Vance 2001, Dupont 2012). Legume nodules can be of two types; elongated, indeterminate nodules, such as those of *Medicago truncatula*, with an apical meristem, and globular, determinate nodules with no active meristem such as those of *Lotus japonicus* (Hirsch 1992). The initiation of nodulation begins with an exchange and recognition of chemical signals in the form Nod factors (NF) secreted by bacteria and flavonoid molecules produced by plants (Long 1996). Thereafter rhizobia become entrapped within a deformed and curled root hair, the plant cell wall degrades and cell membrane invaginates resulting in a growing apoplastic incipient tubule called infection thread (IT), populated by bacteria that grow and divide while in the IT (Gage and Margolin 2000, Gage 2004, Fournier, Timmers et al. 2008). Subsequent nodule organogenesis involves plant cortical cell division and differentiation, under tight genetic and hormonal regulation (Ding, Kalo et al. 2008, Den Herder and Parniske 2009, Popp and Ott 2011, Mortier, Holsters et

al. 2012). The developing IT ramifies, and spreads throughout the nodule primordium. The bacteria are eventually released from the tip of the IT into a young nodule cell as an infection droplet, with the surrounding plasma membrane becoming the peribacteroid membrane to form a compartment called the symbiosome. Within the symbiosome, the rhizobia terminally differentiate into bacteroids (Kereszt, Mergaert et al. 2011).

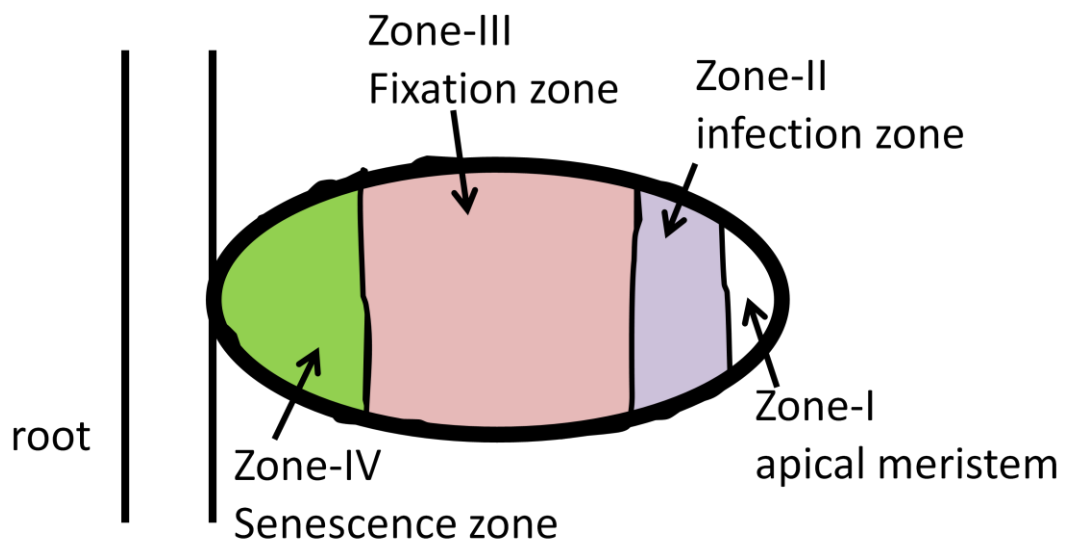


Figure 3: Schematic representation of developmental stages inside an indeterminate nodule

A symphony of intricate and coordinated cellular mechanisms in the nodule provides a microaerobic environmental niche to the nitrogenase enzyme complex of these bacteroids allowing them to fix atmospheric nitrogen to ammonia (Boyd and Peters 2013). The nitrogenase activity in the nodules begins to decline toward the end of flowering when pod filling begins (Klucas 1974). As part of the developmental biology of nodules, the process of nodule senescence sets in (Fig. 3), wherein a complex network of signaling pathways orchestrate the transition of the nodule from a carbon sink to a carbon source (Van de Velde, Guerra et al. 2006).

Nodule senescence

Physiologically, during nodule senescence, bacteroids get degraded, symbiosomes get resorbed, plant cells die and undifferentiated rhizobia in the infection thread get released into the soil (Paau, Bloch et al. 1980, Timmers, Soupene et al. 2000, Van de Velde, Guerra et al. 2006). The process of nodule senescence can be visually identified with a change in color from pink, nitrogen-fixing nodules to green, senescing nodules due to an irreversible oxidative degradation of pink-colored leghemoglobin into green-colored biliverdin (Virtanen and Miettinen 1963, Lehtovaara and Perttila 1978, Pfeiffer, Torres et al. 1983). Functionally, nodule senescence is characterized by a decrease in nitrogenase activity and an increase in proteolytic activity (Vance, Heichel et al. 1979, Malik, Pfeiffer et al. 1981). Proteolytic enzymes such as cysteine and papain proteases are implicated to play a role during nodule senescence (Florence., Mathis. Rene et al. 2003, Perez Guerra, Coussens et al. 2010, Pierre, Hopkins et al. 2014).

Environmental stresses such as salinity, drought, prolonged darkness and nitrate have a detrimental effect on nodule functioning and induce premature nodule senescence (Vauclare, Bligny et al. 2010, Mhadhbi, Dje'wali et al. 2011). It is long known that nitrate treatment is inversely related to the growth and the nitrogenase activity in nodules (Streeter 1981, Carroll and Gresshoff 1983, Streeter 1985, Streeter 1985). On nitrate exposure there is a decrease in the antioxidant milieu in the nodule that results in oxidative damage to proteins such as nitrogenase and leghemoglobin (Escuredo, Minchin et al. 1996).

ROS in the initiation and development of nodule formation

During the process of nodulation the levels of ROS in plant root cells in the nodulation zone is tightly regulated. In *M. sativa*, during infection there is accumulation of superoxide and hydrogen peroxide in the ITs and in the infected cells (Santos, Herouart et al. 2001). In *M. truncatula*, the perception of Nod factor and its function in regulating early nodulation gene expression requires signaling via ROS within 12 hours of inoculation (Ramu, Peng et al. 2002). Interestingly, root hair cells of *Phaseolus vulgaris* show a transient increase in ROS levels when treated with NFs (Cardenas, Martinez et al. 2008), and ROS production is required for the *M. truncatula* root hair cell curling, during initiation of the legume-rhizobia symbiosis (Peleg-Grossman, Volpin et al. 2007).

When *M. truncatula* roots are treated with NFs from its bacterial symbiont, *Sinorhizobium meliloti*, within 1 hour, the levels of *RBOH2* (*MtRBOHB*) and *RBOH3* (*MtRBOHE*) transcripts decrease transiently with a concomitant decrease in ROS, indicating a correlation between ROS levels and *RBOH* levels during infection (Shaw and Long 2003, Lohar, Haridas et al. 2007). In *Phaseolus vulgaris*, *PvRBOHB* expression correlates with ROS levels in roots that affects the initial stages of nodulation including structural deformities in ITs and anomalies in symbiosome structure, resulting in low nodule numbers and a drastic decrease in nitrogen fixation (Montiel, Nava et al. 2012, Arthikala, Sanchez-Lopez et al. 2014). The efficacy of nitrogen fixation in *M. truncatula* nodules correlates with the up-regulation of

MtRBOHA and is reduced in roots in which *MtRBOHA* expression is reduced by RNAi (Marino, Andrio et al. 2011).

The *LATERAL ROOT ORGAN DEFECTIVE/NUMEROUS INFECTIONS* and *POLYPHENOLICS (LATD/NIP)* gene in *M. truncatula* regulates superoxide levels in *M. truncatula* roots by regulating levels of *MtRBOHA*, *MtRBOHC* and *MtRBOHD* genes (Chang Zhang and Jeanne Harris, unpublished data). The *LATD/NIP* gene encodes a transmembrane nitrate transporter (Bagchi, Salehin et al. 2012). The *latd/nip* mutants have defects in root growth and in the development and functioning of nodules (Veereshlingam, Haynes et al. 2004, Bright, Liang et al. 2005).

ROS in nodule senescence

Overall, nodule senescence is characterized by significant shifts in the redox balance in the senescing nodule tissue (Dupont 2012). The auto-oxidation of leghemoglobin is correlated with levels of the ROS superoxide anion in nodules (Puppo, Rigaud et al. 1981) and lower leghemoglobin levels correlates with lower levels of hydrogen peroxide, another ROS (Gunther, Schlereth et al. 2007).

Beyond these observations, relatively little is known about the role of ROS during the process of nodule senescence, making this a fruitful area for investigation.

Interestingly, the highest expression of GIRAFFE HO is in a senescing nodule (*Medicago truncatula* Gene Expression Atlas; <http://bioinfo.noble.org/gene-atlas/>), and thus provides an entry point for studying ROS regulation in nodule senescence.

Summary

This thesis examines the role of *GIRAFFE* heme oxygenase of *Medicago truncatula* in modulating expression levels of ROS-regulatory enzymes in seedlings and in nitrate-induced senescing nodules. In this study, the expression of several genes that regulate levels of ROS and are modulated by the *LATD/NIP* gene has been assessed. Interestingly, the *LATD/NIP*-regulated *RBOHC* gene was found to also be regulated by the *GIRAFFE HO* in both seedlings and nitrate-induced senescing nodules and the *LATD/NIP*-regulated gene, *cwPRX2* was also found to be regulated by *GIRAFFE HO* in seedlings.

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Chapter 2: Results

Introduction

The ubiquitous heme oxygenase (HO) enzyme catalyzes the breakdown of heme to biliverdin in bacteria, animals and plants (Tenhunen, Marver et al. 1968, Brown and Holroyd 1984, Frankenberg-Dinkel 2004). The oxidation of heme by bacterial HO releases iron that facilitates iron acquisition from heme by bacteria (Schmitt 1997). In animals, following the degradation of heme to biliverdin by heme oxygenase, biliverdin is converted by biliverdin reductase (BVR) to bilirubin, a powerful physiological antioxidant involved in regulating levels of reactive oxygen species (ROS) (Stocker, Yamamoto et al. 1987). In plants too, HO catalyzes the first and rate-limiting step of heme catabolism to biliverdin. Unlike animals, plants do not have a BVR enzyme and thus no bilirubin is produced; instead biliverdin serves as the precursor for the biosynthesis of the phytochrome chromophore (Terry, Wahleithner et al. 1993).

Reactive Oxygen Species (ROS) play important roles as signaling molecules during stress and in various developmental processes (Puppo, Groten et al. 2005, Mittler, Vanderauwera et al. 2011). Environmental stresses such as drought and salinity alter the cellular redox balance that trigger ROS-regulated pathways, which in turn facilitate adaptation of plants to the abiotic stress (Golldack, Li et al. 2014). ROS molecules such as superoxide anion (O_2^-), hydrogen peroxide (H_2O_2) and hydroxyl radical (OH^\cdot) play crucial roles in regulating developmental and growth processes throughout the plant (Foreman, Demidchik et al. 2003, Cardenas, Martinez et al. 2008). Superoxide anion produced in aerobic biological systems is efficiently reduced

to hydrogen peroxide by superoxide dismutase (Fridovich 1995). The toxicity and the signaling potential of hydrogen peroxide is regulated by robust enzymatic mechanisms that degrade hydrogen peroxide to either to hydroxyl radical or to water and oxygen by peroxidases and catalases, respectively (Passardi, Penel et al. 2004, Zamocky, Furtmuller et al. 2008, Puerto-Galan, Perez-Ruiz et al. 2013).

The *RESPIRATORY BURST HEME OXYGENASE (RBOH)* genes encode plasma-membrane localized NADPH oxidases, related to animal NADPH oxidases such as NOX5 and Duox (Grabarek 2006, Petry, Weitnauer et al. 2010, Suzuki, Miller et al. 2011) that catalyze the reduction of oxygen to extracellular superoxide (Babior, Lambeth et al. 2002, Sagi and Fluhr 2006, Marino, Dunand et al. 2012). The *RBOH* genes play important roles in ROS signaling and development processes, promoting the length and density of lateral roots in *Phaseolus vulgaris* (Montiel, Arthikala et al. 2013), mediating the wound healing response in *Lycopersicon esculentum* (Sagi, Davydov et al. 2004) and cell wall growth in *Arabidopsis* (Monshausen, Bibikova et al. 2007).

In plants, altered levels of ROS in response to abiotic stresses such as ultraviolet radiation, salinity, and heavy metals are correlated with the induction of expression and activity of heme oxygenase (Noriega, Balestrasse et al. 2004, Yannarelli, Noriega et al. 2006, Han, Zhang et al. 2008, Wu, Huang et al. 2011). One of the *Arabidopsis* heme oxygenase enzymes, *LONG HYPOCOTYL 1 (HY1)*, functions to regulate expression of *RBOHD* to mediate the plant's response to salt acclimation by regulating levels of ROS (Xie, Xu et al. 2011). The induction of HO expression and activity ameliorates the cadmium-induced oxidative stress in *M. sativa* roots by up-regulating NADPH levels (Cui, Li et al. 2012). Increased expression of HO in the

aleurone layer of the wheat seed correlates with decreased amounts of the ROS molecule, hydrogen peroxide, resulting in a delay in programmed cell death during germination (Wu, Huang et al. 2011).

In *Medicago truncatula* the *GIRAFFE* (*GIR*) gene encodes the only HO in its genome (Zhang 2014), unlike *Arabidopsis* where three heme oxygenase genes (*HY1*, *AtHO3*, *AtHO4*) have been identified (Davis, Bhoo et al. 2001). The deletion of the entire coding region of the *GIR* HO in *giraffe* mutants results in a classic photomorphogenic phenotype, presumably due to a lack of phytochrome synthesis, and plants are thus insensitive to Red/Far-red light for both seedling growth and regulation of nodulation (Zhang 2014). The photomorphogenic phenotype of *giraffe* is very similar to that of the *hyl* mutant in *Arabidopsis* as well as that of the *phytochrome chromophore deficient 1* (*pcd1*) mutant in pea (Weller, Terry et al. 1996, Davis, Kurepa et al. 1999, Muramoto, Kohchi et al. 1999).

The roots of legumes are unique in that they form symbiotic associations with specific *Rhizobium* bacterial partners that result in the development of root nodules, highly specialized organs that function as a factory for biological nitrogen fixation by intracellular rhizobium by reducing atmospheric nitrogen to ammonia (Virtanen and Miettinen 1963, Hirsch 1992). At the molecular level, the recognition between the legume host and its rhizobial partner is effected via a chemical dialog between Nod factors secreted by the rhizobia and flavonoid signals secreted by legume roots (Oldroyd and Downie 2008). The levels of ROS are tightly regulated by a network of players during initiation, development, functioning and senescence of nodules in a manner not completely understood (Puppo, Groten et al. 2005).

At least seven *RBOH* genes have been identified in *Medicago truncatula* (Lohar, Haridas et al. 2007, Marino, Andrio et al. 2011). All seven genes are expressed in either roots or nodules or both. Due to independent gene duplication in different plant families and independent discoveries in different labs, similar gene names in different species do not correspond to orthologous genes. In *M. truncatula*, *MtRBOHA* is expressed in the nitrogen-fixing zone of mature nodules and is required for nitrogen-fixation activity and the requirement of *PyRBOHB* in rhizobial infection in *Phaseolus vulgaris* has been established (Marino, Andrio et al. 2011, Arthikala, Montiel et al. 2013). The expression of *MtRBOH2* and *MtRBOH3* (which correspond to *MtRBOHB* and *MtRBOHE* (Marino, Andrio et al. 2011)) and levels of ROS is down-regulated in the first hour after treatment with Nod factors (Lohar, Haridas et al. 2007). The *LATERAL ROOT ORGAN DEFECTIVE/NUMEROUS INFECTIONS* and *POLYPHENOLICS (LATD/NIP)* gene, encodes a nitrate transporter, which is required for root and nodule development (Veereshlingam, Haynes et al. 2004, Bright, Liang et al. 2005, Yendrek, Lee et al. 2010, Bagchi, Salehin et al. 2012) as well as regulating the expression of *MtRBOHA*, *MtRBOHC* and *MtRBOHD* (Zhang, Bousquet et al. 2014). *MtRBOHC* expression, which is very low in *M. truncatula* roots (Marino, Andrio et al. 2011), is inversely correlated with root length (Zhang, Bousquet et al. 2014). High levels of *MtRBOHC* expression in *latd/nip* mutants are associated with decreased root elongation. A reduced level of *MtRBOHC* expression, either due to RNAi knockdown or down-regulation stimulated by the hormone Abscisic acid, causes increased root elongation (Zhang, Bousquet et al. 2014). *LATD/NIP* also regulates the expression of other ROS-related enzymes, Cu/Zn superoxide dismutase (*Cu/ZnSOD*) and cell wall peroxidase (*cwPRX2*).

The *giraffe* mutant gives us an opportunity to determine whether the GIRAFFE HO in *M. truncatula* is a component in the ROS-regulatory network both in seedlings and during nodule senescence. Our findings indicate that *GIRAFFE HO* regulates expression of *RBOHC* and a cell wall peroxidase that are involved in scavenging and regulating ROS levels during development and senescence.

Results

***GIRAFFE* regulates expression of *RBOHC* in seedling**

In *Arabidopsis*, acclimation to salt stress is mediated by ROS levels that require the combined functions of *HY1 HO* and *AtRBOHD* (Xie, Xu et al. 2011). We wondered whether the *Medicago HO*, *GIRAFFE*, might function similarly to regulate *RBOH* expression in *M. truncatula* during root growth. To test this, we compared expression of all seven *MtRBOH* genes in wild-type and *giraffe* seedlings in both root and shoot using qRT-PCR. We found that *RBOHC* expression is strongly down-regulated in *giraffe* mutant roots and significantly up-regulated in shoots (Fig. 4). In contrast, expression of the other *RBOH* genes was unaffected by the *giraffe* mutation (Fig. 4). Our results indicate that *GIRAFFE* function is required for normal *RBOHC* expression in roots and shoots, but not that of other *RBOH* genes.

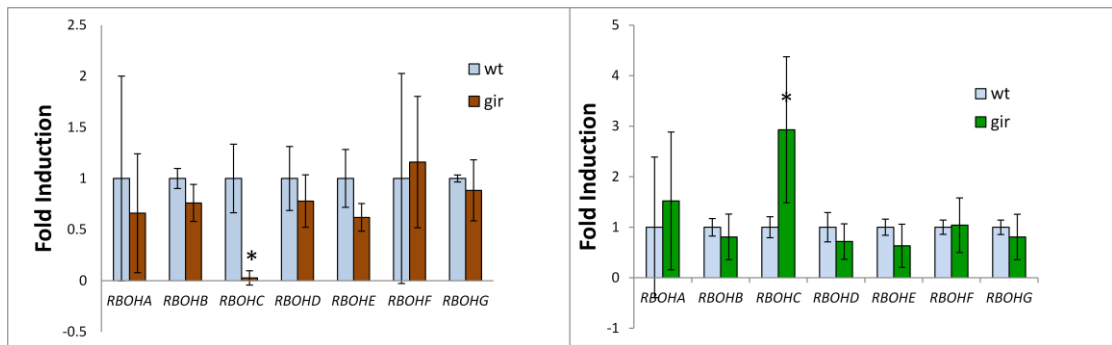


Figure 4: *GIRAFFE* regulates *RBOHC* expression in seedling roots and shoots

Roots and shoots were harvested at 6 days and *RBOH* gene expression analyzed by quantitative real-time RT-PCR. Values were normalized to *UBC* and *UBC9*. Error bars represent SEM between three biological replicates. n=10 plants per genotype for each replicate. Asterisks (*) represent a significant difference between *giraffe* and *wild-type* for $p < 0.05$ according to a student's t-test of the relative expression.

***GIRAFFE* regulates expression of *cwPRX2* but not *cwCu/Zn SOD* in seedlings**

The *LATD/NIP* gene up-regulates expression of *cwPRX2* and down-regulates that of *Cu/Zn SOD* (Zhang, Bousquet et al. 2014). We wondered whether *GIR* might also regulate the expression of these ROS-regulatory genes in seedlings, since both *LATD* and *GIRAFFE* regulate expression of the *MtRBOHC* gene. We compared the expression of these two genes in 6-day old roots and shoots in wild-type and *giraffe* mutants. Our results show that *cwPRX2* expression is down-regulated in *giraffe* roots and up-regulated in *giraffe* shoots, but expression of the *Cu/Zn SOD* is not significantly different from wild-type (Fig. 5). Thus, our results indicate that in seedling roots, *GIR* HO up-regulates the expression of *cwPRX2* but not that of *Cu/Zn SOD*.

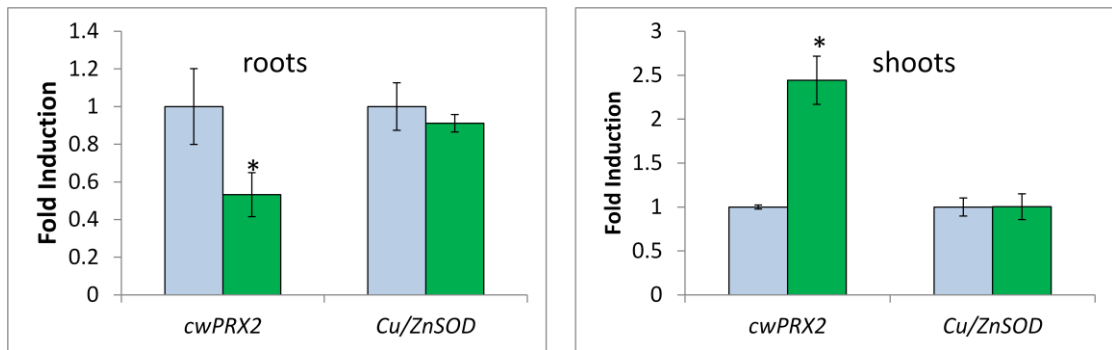


Figure 5: Regulation of ROS-regulatory genes by *GIRAFFE* in 6-day old roots and shoots

Plant tissue was harvested as described and gene expression analyzed by quantitative real-time RT-PCR and averaged from three biological replicates. Values are normalized to *UBC* and *UBC9*. Error bars indicate the SEM between three biological replicates. $n = 10$ for each genotype per replicate. Asterisks (*) represent a significant difference between *giraffe* and *wild-type* for $p < 0.05$ according to a student's t-test of the relative expression).

***LATD/NIP* and *GIRAFFE* do not regulate expression of each other**

Our results show that in seedlings, *GIR* regulates the expression of *RBOHC* and *cwPRX2*. The regulation of these two genes by both *LATD/NIP* (Zhang, Bousquet et al. 2014) and *GIR* in roots could be due to their independent regulation by *GIR* and *LATD/NIP* (i.e. parallel pathways) or because *GIR* and *LATD/NIP* function in the same pathway. There are two possible linear pathways connecting *GIR* and *LATD/NIP*: a) *GIR* down-regulates *LATD/NIP*, which in turn down-regulates expression of the *MtRBOHC* and *cwPRX2* genes in roots or b) *LATD/NIP* could down-regulate *GIR*, which is required to up-regulate the target genes. We tested the expression of *LATD/NIP* in *giraffe* mutants and that of *GIR* in *latd/nip* mutants and compared them with their expression in wild-type roots and shoots of 6-day old plants. We found no change either in the expression of the *LATD/NIP* gene in *giraffe*

mutants or in the expression of the *GIR* gene in *latd* mutants (Fig. 6), indicating that *GIR* and *LATD/NIP* do not regulate expression of each other in seedlings.

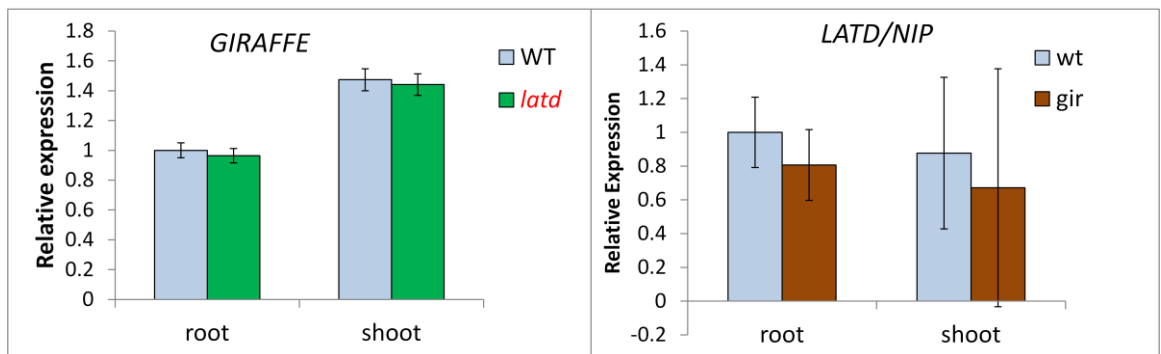


Figure 6: *GIRAFFE* and *LATD/NIP* do not regulate each other's expression

Seedling roots and shoots were pooled from 10 seedlings per genotype per replicate and gene expression analyzed by quantitative real-time RT-PCR. Values are normalized to *UBC* and *UBC9*. Error bars represent SEM between three biological replicates. Differences between genotypes are not significant, according to a t-test of the relative expression.

***GIRAFFE* regulates expression of *RBOHC* and *RBOHE* in senescing nodules**

In functional symbiotic nodules of *M. truncatula*, the expression and upregulation of *MtRBOHA* is required for efficient nitrogen fixation (Marino, Andrio et al. 2011).

Interestingly, the highest expression of *GIR*, which encodes a heme degrading enzyme, is in senescing nodules (Medicago truncatula Gene Expression Atlas (MtGEA); <http://bioinfo.noble.org/gene-atlas/>). We have found that *GIR* regulates expression of *RBOHC* in seedlings. Might *GIR* regulate *RBOH* expression in a senescing nodule, thereby playing a role in regulating ROS levels during the process of nodule senescence? We compared expression of all seven *RBOH* genes in both *giraffe* and wild-type mature, nitrogen-fixing nodules and in senescing nodules.

Nodule senescence was induced by treating once with 10 mM KNO₃ and senescing nodules were harvested from the top 10 cm of the root at 72 hours and gene expression was compared with that of a control group treated in parallel with 10 mM KCl. We found that *RBOHC* is induced during nitrate-induced senescence in wild-type but not *giraffe* nodules (Fig. 7). Instead, expression of *RBOHC* was significantly down-regulated in *giraffe* senescing nodules. In addition, we found that levels of *RBOHE* transcripts were also significantly lower in *giraffe* senescent nodules, although they were not significantly induced by nitrate treatment in wild-type nodules (Fig. 7). The expression of the other RBOH genes, *RBOHA*, *RBOHB*, *RBOHD*, *RBOHF* and *RBOHG*, were not altered significantly either by nitrate treatment in wild-type or in the mutants. In summary, our findings indicate that *GIR* functions to induce *RBOHC* and *RBOHE* expression in senescing nodules.

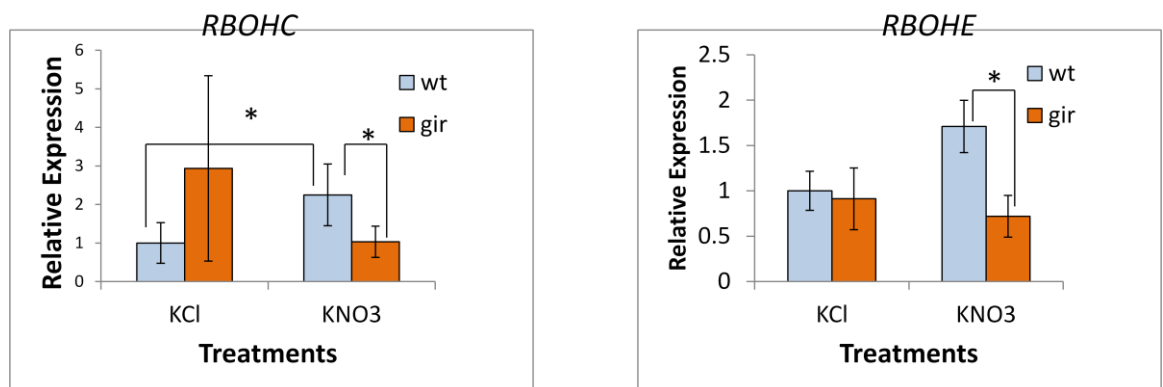
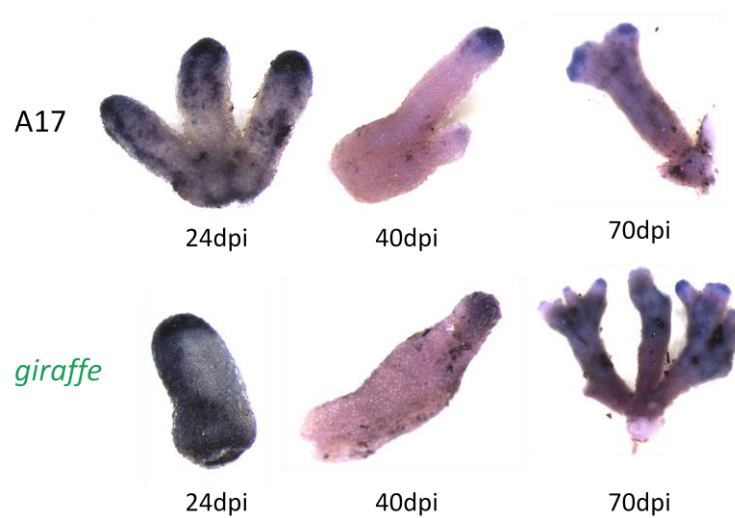


Figure 7: *GIRAFFE* regulates *RBOHC* and *RBOHE* expression in senescing nodules

Nodules were harvested 72 hours after treatment with either 10mM KCl (control) or 10mM KNO₃ (senescent) and gene expression analyzed by quantitative real-time RT-PCR. The average of three biological replicates is represented. Values are normalized to *UBC* and *UBC9*. Error bars represent the SEM between three biological replicates. Asterisks (*) represent a significant difference between genotypes or treatments, as indicated, for $p < 0.05$ according to the student's t-test of relative expression).

In the meristems of pea nodules, the levels of superoxide decrease as the nodules age (Puppo, Groten et al. 2005). Our results show that *GIR HO* regulates *RBOHC* and *RBOHE* expression in senescing nodules. We wondered if mutation in the *GIRAFFE HO* gene would show an altered superoxide distribution pattern in *Medicago* nodules at the time of senescence. We used Nitro Blue Tetrazolium (NBT) to stain for superoxide in whole and longitudinal sections of nodules at different stages of development in both wild-type and *giraffe* mutants (Fig. 8). We noted a gradual decrease in staining intensity, especially of the meristem of mature nodules as they progress toward senescence. The amount of staining varied from plant to plant and we were unable to determine a clear difference in the pattern of staining between wild-type and *giraffe* nodules.

Whole mounts of NBT stained nodules



Longitudinal sections of nodules

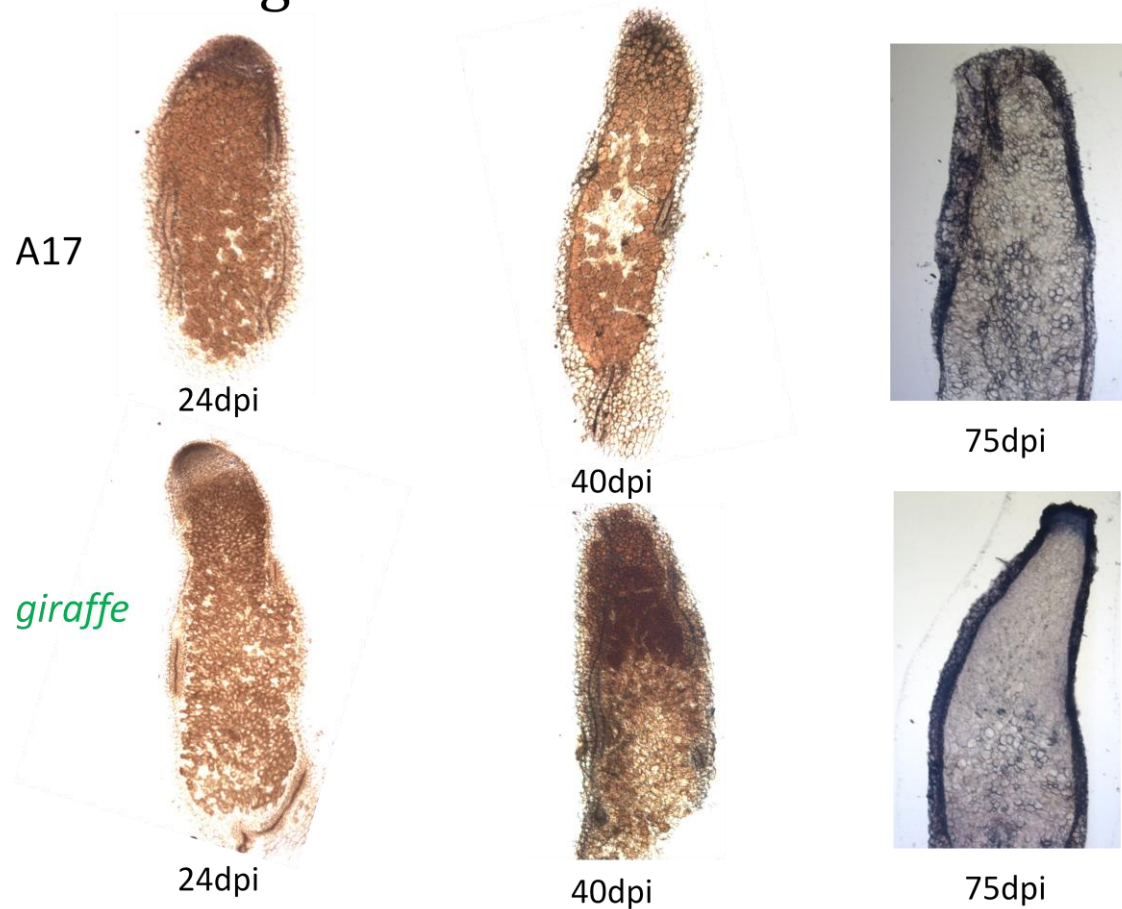


Figure 8: Whole mounts and longitudinal sections of nodules

Nodules were harvested from wild-type and giraffe mutants at 24dpi, 40dpi and 70 or 75dpi and they were stained with NBT for superoxide distribution in whole mounts and longitudinal section

***GIRAFFE* does not regulate leghemoglobin expression in the senescing nodule**

The transcript levels of leghemoglobin (LB, a heme containing protein), is down-regulated in senescing nodules (Moreau, Verdenaud et al. 2011). We know that the expression of *GIR*, a heme degrading enzyme, is highest in a senescing nodule

(MtGEA; <http://bioinfo.noble.org/gene-atlas/>). Therefore we asked if *GIR* regulates expression of *LB* in a senescing nodule. Our results show that there is no significant change in *LB* expression between wild-type and *giraffe* mutants in mature or senescing nodules (Fig. 9). These observations suggest that *GIR* does not regulate *LB* expression in mature or senescing nodules.

***GIRAFFE* does not regulate *LATD/NIP* expression in senescing nodules**

We have shown that *GIRAFFE HO* regulates expression of *RBOHC* and *RBOHE* in senescing nodules. Given that *GIRAFFE* expression is highest in a senescing nodule (MtGEA; <http://bioinfo.noble.org/gene-atlas/>) and the expression of *LATD/NIP*, which regulates expression of several *RBOH* genes in seedling roots (Zhang, Bousquet et al. 2014), is up-regulated in nodules four hours after nitrate treatment (Cabeza, Koester et al. 2014), we asked whether *GIRAFFE* regulates *RBOHC* expression in senescing nodules by controlling *LATD/NIP* expression. We examined the expression of *LATD/NIP* in senescing nodules of wild-type and *giraffe* mutants and found that the expression of *LATD/NIP* remains unaltered between wild-type and *giraffe* nodules whether or not they are induced to senesce (Fig. 9). Thus we conclude that *GIRAFFE* does not regulate *RBOH* gene expression by regulating *LATD/NIP* expression during nodule senescence.

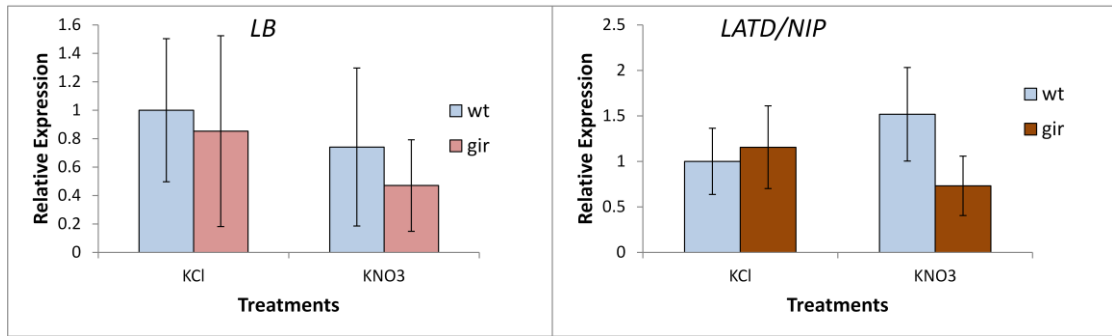


Figure 9: GIRAFFE does not regulate LB or LATD/NIP expression during nodule senescence

Nodules were harvested 72 hours after treatment with either 10 mM KCl (control) or 10 mM KNO₃ (senescent) and gene expression was determined by quantitative real-time RT-PCR. The average gene expression values of three biological experiments is represented and normalized to *UBC* and *UBC9*. Error bars are SEM between three biological replicates.

Discussion

Our results show that the *GIR HO* of *M. truncatula* is involved in transcriptional regulation of *MtRBOHC* and *cwPRX2* in both roots and shoots. The other members of the superoxide-generating *RBOH* gene family and a *LATD/NIP*-regulated *Cu/ZnSOD* enzyme tested in this study were not found to be regulated by *GIR*. In nitrate-induced senescing nodules, *GIR* was found to again regulate the expression of *RBOHC* and in addition regulate expression of one other family member, *MtRBOHC*, but not that of any of the other *RBOH* genes or of *LB*.

Different RBOH genes have evolved unique functions in different developmental processes and stress responses.

The multigenic *RBOH* family is comprised of members with different spatio-temporal functions and regulations during plant development and stress responses, both biotic and abiotic. *RBOH* genes were first discovered in *Oryza sativa* (rice) (Groom, Torres

et al. 1996), where there are at least nine homologues (Wong, Pinontoan et al. 2007). Analysis of RBOH gene expression and function in several species demonstrate specific roles of specific RBOH genes in different species. In *Arabidopsis*, out of the ten paralogues (Keller, Damude et al. 1998, Torres, Onouchi et al. 1998, Kwak, Mori et al. 2003), *AtRBOHC* functions in the expansion of cell wall and root growth (Foreman, Demidchik et al. 2003) while *AtRBOHD* and *AtRBOHF* functions in stomatal closure induced by the plant hormone abscisic acid via nitric oxide signaling (Bright, Desikan et al. 2006). The *RBOH* homologs in *Lycopersicon esculentum* (tomato), *LeRBOHI* and *whitefly-induced (Wfi1)*, are involved in regulating wound response genes and growth transcription factors (Sagi, Davydov et al. 2004) and *LeRBOHI* has the highest expressed in cold-stressed seedlings (Amicucci, Gaschler et al. 1999). At least four *RBOHs* have been identified in *Solanum tuberosum* (potato) and *StRBOHB* is induced by fungal cell wall elicitor while *StRBOHC* and *StRBOHD* are highly induced during late blight disease of potato (Yoshioka, Sugie et al. 2001, Yamamizo, Kuchimura et al. 2006). In *Nicotiana benthamiana* (tobacco), *NtRBOHA* and *NtRBOHB* are required in defense responses during fungal infection (Yoshioka, Numata et al. 2003).

A unique role for *MtRBOHC* in seedlings and nodules

Out of the seven RBOH homologues in *M. truncatula*, *RBOHC* is expressed at very low levels in roots and nodules compared to other RBOH family members (Marino, Andrio et al. 2011). We find that *RBOHC* is up-regulated by *GIR HO* in seedling roots and down-regulated in seedling shoots (Fig. 4). Interestingly, *RBOHC* expression is also regulated by *LATD/NIP* in the root but in the opposite way from *GIR*; the wild-type function of *LATD/NIP* is to reduce *RBOHC* expression (Zhang,

Bousquet et al. 2014). However, we found that *GIR* and *LATD/NIP* do not regulate the expression of each other in seedlings. The regulation of an otherwise less expressed *RBOHC* by *GIR HO* and *LATD/NIP* could indicate an important role of *RBOHC* in regulating ROS during cell wall synthesis (Monshausen, Bibikova et al. 2007). It is possible that *GIR* and *LATD* regulate cell wall synthesis by regulating ROS-regulatory enzymes such as *RBOHC* and *cwPRX2* in roots. This is consistent with the observation that the cell length and primary root length is altered in both *gir* (Beck Powers and Jeanne Harris unpublished data) and *latd* (Bright, Liang et al. 2005, Zhang, Bousquet et al. 2014) mutants oppositely.

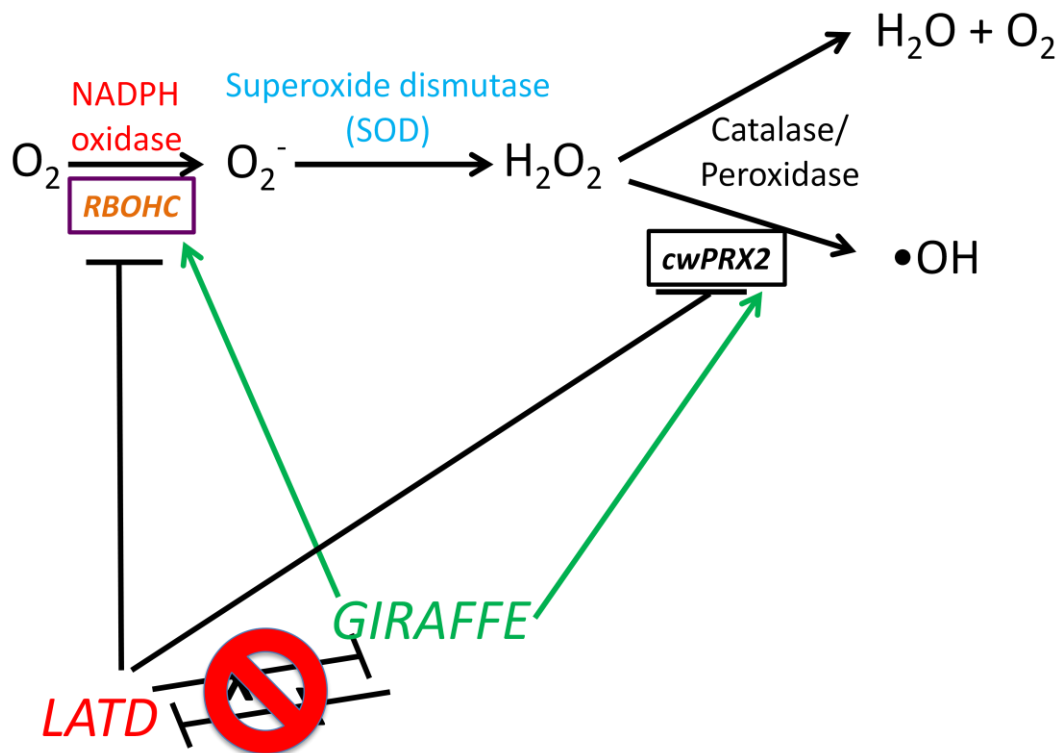


Figure 10: Summary of modulatory effects of *GIRAFFE* and *LATD/NIP*

GIRAFFE and *LATD/NIP* regulate expression of *RBOHC* and *cwPRX2* in opposite ways in *M. truncatula* seedlings

The development and functioning of legume nodules requires optimum levels of ROS and hence antioxidants and ROS levels are tightly regulated in nodules to maintain a

balance between N-fixation and damage by oxidative stress (Puppo, Groten et al. 2005, Chang, Damiani et al. 2009). When nodules senesce, leghemoglobin (pink) levels decrease (Pfeiffer, Torres et al. 1983) and the pink N-fixing nodule tissue turns into green senescent tissue as a result of an irreversible oxidation reaction (Virtanen and Miettinen 1963) due to breakdown of leghemoglobin (LB) into biliverdin (Lehtovaara and Perttila 1978). The auto-oxidation of LB is linked to the levels of superoxide anion in nodules (Puppo, Rigaud et al. 1981) and lower LB levels correlate with lower levels hydrogen peroxide (Gunther, Schlereth et al. 2007). Interestingly, the levels of nitric oxide-LB complex formed especially when nodules are treated with oxidant stress is comparable to those found in senescing nodules (Mathieu, Moreau et al. 1998). It would be interesting to investigate the oxidative modifications of leghemoglobin in the absence of *GIRAFFE* activity.

Role of GIRAFFE Heme Oxygenase in retrograde signaling

Chloroplasts have evolved from an ancestral free-living, photoautotrophic cyanobacterium that was endosymbiosed into a eukaryotic cell more than 450 million years ago (Lopez-Juez and Pyke 2005). The modern day eukaryotic plant cell has several functional nuclear genes of chloroplast origin (Martin, Stoebe et al. 1998, Timmis, Ayliffe et al. 2004, Kleine, Maier et al. 2009). Today, the highly reduced chloroplast genome barely encodes about a 100 proteins, the remaining 3000 proteins required for chloroplast biogenesis and function is encoded by the nuclear genome (Sato, Nakamura et al. 1999). This situation, requires chloroplast to nucleus signaling, known as retrograde signaling, to coordinate chloroplast development and function with nuclear gene expression (Surpin, Larkin et al. 2002, Mochizuki, Tanaka et al. 2008, Moulin, McCormac et al. 2008). Retrograde signaling can be triggered by ROS

molecules such as hydrogen peroxide (Maruta, Noshi et al. 2012). In animals under oxidative stress, the endoplasmic reticulum localized heme oxygenase translocates to the mitochondria or the nucleus to activate transcription factors (Lin, Weis et al. 2007, Bansal, Biswas et al. 2014). Our results show that in plants, the chloroplast-localized heme oxygenase regulates expression of cell wall localized ROS-regulatory enzymes. This implies that the chloroplast genome not only regulates expression of nuclear genes pertaining to its own biogenesis and function, but also of those involved in other cellular processes such as regulating ROS-regulating enzymes in the cell wall. It would be interesting to study the localization of heme oxygenase in plants under oxidative stress to study its signaling mechanism to the nucleus.

Materials and Methods

Plant Material and Growth Conditions

Seeds were scarified with 98% sulphuric acid, washed twice with distilled water and surface sterilized with 30% bleach (Clorox) followed by six washes in sterile water. Washed seeds were imbibed for 4-6 hours at room temperature, while shaking, then stored at 4° C overnight in sterile water and subsequently germinated overnight in an inverted petri plate sealed with parafilm in the dark at room temperature.

Harvesting seedlings: Seedlings were grown on filter paper (3M, cat no. 1530-0) laid over Nitrogen-free Buffered Nodulation Medium (BNM; (Ehrhardt, Atkinson et al. 1992)) solidified with 1.15 % agar in round 150mm X 15mm (Fisher Scientific Cat no. 08-757-14) petri plates with 20 plants per plate. Plates were sealed with surgical tape (Micropore 3M Cat. No. 1530-0) and the lower part of each plate was wrapped

with tin foil. Three biological replicates of plants were grown for six days in MTR30 Conviron growth chambers with 16 hr light period and 50% humidity at 20° C. Roots and shoots were harvested separately from a pooled sample of 10 plants in each replicate. The harvested tissue was frozen immediately in liquid nitrogen.

Harvesting nodules: Seeds were started and germinated for three biological replicates as described above, potted in 3 ⁵/₈ -inch pots, in a mix of calcined clay (Profield Calcined Clay Soil Modifier): sand (all purpose)-1: 1 and grown in the greenhouse with temperature 64-66° C during day and 68-72° C at night. Supplemental lighting was provided to maintain 16 hour daylight period conditions at above 700µmol m⁻² s⁻¹. Plants were fertilized 3 times a week with 20 ml of 1/2X BNM and watered with tap water as required. At 3 days, plants were inoculated with 5 ml of a 1:100 dilution of an overnight culture of *Sinorhizobium meliloti* 1021, grown in LB supplemented with 500µg/ml of Streptomycin and washed and diluted in 10 mM MgSO₄. After inoculation, plants were not watered until the following day. At 21 days post inoculation (dpi), plants were treated with 20 ml of either 10 mM KCl or 10 mM KNO₃. At 24dpi, nodules were harvested from the top 10 cm of the primary root, to yield approximately 0.5g fresh weight of nodule, and frozen immediately in liquid nitrogen.

Quantitative Real Time-PCR

Frozen tissue was ground over liquid nitrogen and total RNA extracted using the RNeasy Plant Mini kit (Qiagen Cat. No. 74904), DNase treated (Ambion Turbo DNA-free AM 1907) and cleaned using the Plant MinElute Clean-up kit (Qiagen Catalog no.74204). For first strand cDNA synthesis, 1µg RNA was reverse

transcribed using SuperScriptIII (Invitrogen), following the manufacturer's instructions. Quantitative Real Time-PCR was done on an ABI Step One qPCR machine with conditions for 20µl reactions set as 0.5µl cDNA, 0.1µM primers and 10µl PerfeCTA SYBR Green FastMix (Quanta Perfecta <http://www.quantabio.com/>). Gene expression was analysed using the $\Delta\Delta$ CT method, as in (Sun, Cardoza et al. 2006).

ROS staining, sectioning and microscopy

A modified protocol to stain nodules for superoxide with Nitroblue Tetrazolim (NBT) was developed from a protocol outlined by Ramu *et. al.* (Ramu, Peng et al. 2002). Nodules were incubated in a staining solution prepared with 10 mM sodium phosphate, 10 mM NaN₃ and 1mg/ml NBT (Sigma-Aldrich) for 15 minutes at 37°C. Two washes with 80% alcohol followed, to stop the staining reaction. Whole mounts were observed under Leica dissecting microscope. Nodules were longitudinally sectioned at 90µm thickness in a Lancer Vibratome Series 1000 and observed under Olympus microscope.

Statistical Analysis

Statistics were done using GraphPad Prism version 6.00 for windows. Expression data was analysed using Student's t-test on the logarithmic values of relative expression from three biological replicates.

Primers used in qRT-PCR

Gene	Accession in Mt4.0	Forward Primer Sequence (5'-3')	Reverse Primer Sequence (5'-3')	Reference
<i>RbohA</i>	Medtr1g083290	GCGCAACTCC TTTGATTAGC	GAAATAGGCT CGCTTGGTTG	(Marino, Andrio et al. 2011)
<i>RbohB</i>	Medtr3g098380	GCTCGCTCTGC TCTTATTGC	TGCGCTTGTA GACACTACGC	

<i>RbohC</i>	Medtr3g098350	GGGAGACCTG ATGCTATTCA AG	TGTCTTCAACA ATAATGTCCA TCTG	
<i>RbohD</i>	Medtr3g098320	ACATGGCTCA GGAGCAAGAC	TGAAGAAGGC GTGGAAAGTC	
<i>RbohE</i>	Medtr8g095520	CCAAATTCTC ACAGGCTTGC	CTCCATACGG ACCATCAATC	
<i>RbohF</i>	Medtr7g060540	GAAGAGCCTT TGTCAAGAGT TTAG	GGATTGATGC TTTAGCTGTGT G	
<i>RbohG</i>	Medtr7g113130	GTGATGGATG AAATCGCAGA	TGGCATGATG AAGTGATTGA	
<i>ApoCu/ ZnSOD</i>	Medtr6g029200	GGGCCTGCAA GAATGTTACC	CCTGAGGATG AGACTCGACA	(Zhang, Bousquet et al. 2014)
<i>cwPRX 2</i>	Medtr2g084000	GGAAGAAGGG ATAGTCTAGA GGCA	GGAGCTGGGA CCTGGAAGAT	
<i>LATD</i>	Medtr1g009200	CCATAGCCTTT GGAGCAGAG	CTATCCCGAT GCGGACTTTA	(Yendrek, Lee et al. 2010)
<i>GIRAF FE</i>	Medtr8g019320	TGGGAAGAAG ATTGCTGGTC	TGTCCCTCACA TTCTGCAAC	(Zhang 2014)
<i>MtLBI 1</i>	Medtr5g081000. 1	TTGGGTGCTAT CCACATTCA	TTCAGTTGCCA GTGCATCAT	
<i>UBC 1</i>	Medtr3g110110. 1	CTGACAGCCC ACTGAATTGT GA	TTTTGGCATTG CTGCAAGC	(Kakar, Wandrey et al. 2008)
<i>UBC9 1</i>	Medtr7g116940. 1	GGTTGATTGCT CTTCTCTCCCC	AAGTGATTGC TCGTCCAACC C	

Acknowledgements

The authors would like to thank Jill Preston for the generous use of her qPCR machine, the Greenhouse facility, especially Colleen, Dave and Tom, at UVM for their immense help in growing plants, Terry Delaney for his training and the liberal use of his microscopes, Mary Tierney for the kind use of her shaker, scales and centrifuge, the Vermont Genetics Network at UVM for Bioanalyzer assessment of RNA quality; supported by IDeA P20GM103449 from NIH and every member of the Harris lab for valuable suggestions and enthusiastic support during this study,

especially to Yucan for her technical advice and consistent efforts in helping with data analysis.

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Chapter 3: Future Directions

In this thesis I have shown that the GIRAFFE HO functions to regulate expression of ROS-regulatory genes in both seedlings and senescing nodules of *Medicago truncatula*. Such findings open up several avenues for future investigations.

Does carbon monoxide play a role in regulating ROS gene expression?

Heme Oxygenase catalyzes the degradation of heme to biliverdin with the release of carbon monoxide. Carbon monoxide acts as an important cellular signaling molecule (Xuan, Xu et al. 2008). To test if the carbon monoxide produced during heme degradation by heme oxygenase is responsible for the altered expression of ROS regulatory enzymes, *giraffe* mutants need to be exposed to carbon monoxide and their target gene expression can be compared to those of untreated *giraffe* mutants and wild-type +/- carbon monoxide. If the expression of target genes in carbon monoxide-exposed *giraffe* mutants shows a similar level as in wild-type, it can be concluded that carbon monoxide is the signaling molecule that regulates the expression of these target genes.

Does GIRAFFE HO regulate translational expression of RBOHC and PRX2?

In this study, I have shown that *GIRAFFE HO* regulates the expression of target genes transcriptionally. It would be interesting to test whether the protein expression of *RBOHC* and *cwPRX2* is also altered in the *giraffe* mutant. This would help us to understand if the regulation at the level of gene transcription is translated to protein expression as well.

What is the expression of the *RBOHC* and *PRX2* in a *gir latd* double mutant?

In this thesis I have shown that *GIRAFFE* and *LATD/NIP* oppositely regulate the expression of *RBOHC* and *PRX2* in six-day old seedling roots. I have also shown that *GIRAFFE* and *LATD/NIP* do not regulate expression of each other at the transcriptional level. To confirm if *GIRAFFE HO* and *LATD/NIP* act in the same pathway, we need to test the expression of their common targets in a *gir latd* double mutant. In such a double mutant, the expression of the common targets could be like that of the a) *latd* mutants b) *giraffe* mutants or c) in between. If *GIRAFFE* inhibits the function of *LATD/NIP*, i.e. *GIRAFFE* is upstream of *LATD/NIP*; the expression of the target genes in the *gir latd* double mutant would resemble that of *latd* mutant. If *LATD/NIP* inhibits the function of *GIRAFFE*, i.e. *LATD/NIP* is upstream of *GIRAFFE*; the expression of their common targets would be the same as in a *giraffe* mutant. If the expression of the common target genes matches neither with the single mutants' *giraffe* or *latd/nip*, we can confirm that the *GIRAFFE* and *LATD/NIP* regulate their common targets independent of each other and thus their effects are additive.

Do the superoxide levels or distribution pattern alter as nodules senesce? Does the *giraffe* mutation disrupt this pattern?

In this study, I have carried out ROS staining with NBT for superoxide at three time points: 25 dpi, 40 dpi and at around 70 dpi. Overall the sample size was small with as few as one nodule per genotype at some of the time points. In all samples, I found that superoxide staining was more intense in the nodule meristem. In my limited sample

size, I also noticed a decrease in the intensity of NBT stain as the nodules age. I did not notice any significant difference in superoxide staining pattern between wild-type and *giraffe* mutants. Experiments to quantify NBT stain would give conclusive evidence if there is a difference in the distribution profile of superoxide between wild-type and giraffe nodules (Ramel, Sulmon et al. 2009). The experiments will have to be designed with a greater sample size. Additionally, incorporating more time points in the experimental design and studying superoxide pattern in nitrate-induced senescence model can provide a comprehensive understanding of the distribution of superoxide during nodule senescence and whether *GIRAFFE HO* plays a role in altering the pattern. Such experiments would help find out if there are differences in superoxide distribution between a) wild-type and *giraffe* mutant nodules and b) between developmental and nitrate-induced senescence.

In which cells or tissues in the nodule is GIRAFFE HO expressed?

The regions in the nodule where GIRAFFE HO is expressed can be informative in elucidating the function and mechanism of its function. To understand which cells in the nodule express GIRAFFE HO a promoter-GUS fusion can be expressed in the nodule. Such spatio-temporal expression pattern of GIRAFFE HO will help characterize the function of GIRAFFE HO.

Does *GIRAFFE HO* regulate expression of genes involved in nitrogen fixation and proteases that function in proteolytic degradation?

The efficiency of the legume-rhizobium symbiosis requires interaction between the plant and bacterial genomes. The GIRAFFE HO is expressed at high levels in a

mature nodule (*Medicago truncatula* Gene Expression Atlas (MtGEA); <http://bioinfo.noble.org/gene-atlas/>). It would be interesting to test whether GIRAFFE HO alters the expression of genes required for nitrogen fixation in both in the legume and the rhizobial partners. The highest expression of GIRAFFE HO is in senescing nodules (MtGEA). During nodule senescence, several proteolytic enzymes are upregulated due to various degradation pathways that are activated to bring about a programmed cell death and ensure re-mobilization of the resources in the nodule to the rest of the plant. A comparative study of the expression of these proteases between wild-type and *giraffe* mutants could give insights into the role of *GIRAFFE* HO in nodule senescence.

Does the plastid-localized HO move out of the plastid to signal the nuclear genome?

The GIRAFFE HO is a plastid-localized enzyme that serves as a molecule of communication in the process of chloroplast-nucleus signaling (Surpin, Larkin et al. 2002). Such a signaling mechanism ensures the proper development and functioning of the chloroplast and possibly regulates other cellular functions (Nott, Jung et al. 2006). The question arises, as part of the signaling mechanism; does the HO itself leave the chloroplast and move to the nucleus to regulate transcription of the nuclear genome? Although this seems unlikely, in fact this is the fate of the animal HO1 which has been shown to move from the endoplasmic reticulum to the mitochondria and the nucleus (Lin, Weis et al. 2007, Bansal, Biswas et al. 2014). The movement of the MtHO within the cell can be monitored by expressing a HO-GFP fusion protein and observing it on a confocal microscope. The answer to the mobility of the HO can

give clues to the mechanism by which GIRAFFE HO regulates nuclear gene expression.

Is HO plastid-localized in the root?

Heme Oxygenase is localized to the chloroplast, a differentiated plastid present in the leaves and stems of plants (Muramoto, Kohchi et al. 1999). We do not know whether plastids that are present in roots contain heme oxygenase. To test this, the localization of the GIRAFFE HO-GFP fusion protein inside a root cell should be investigated. If the fusion protein is detected in the plastid, it means that HO is localized in the plastids of root.

The experiments described here would help further characterize the expression and the regulation of *GIRAFFE* HO. This would also help to understand the functions of the only known heme oxygenase gene in the *Medicago truncatula* genome.

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