MOLECULAR AND BIOLOGICAL MECHANISMS OF HOST PLANT RESPONSES TO AN INSECT VECTOR AND A BACTERIAL PATHOGEN

A Dissertation

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ABSTRACT

Zebra chip is an emerging plant disease of solanaceous crops that poses a threat to global food security. Understanding plant biological and molecular responses to *Bactericera cockerelli* and ‘*Candidatus* Liberibacter solanacearum’ (Lso) can provide knowledge to better understand and combat zebra chip. This dissertation aims to understand the effect of biotic factors (e.g. insect and pathogen) and abiotic factor (e.g. water stress) affecting plant responses. First, the effects of jasmonate and salicylate defenses were tested on plant induced resistance against *B. cockerelli*. The induction of jasmonate defenses did not reduce *B. cockerelli* eggs and nymphs on the plants. However, the induction of salicylate defenses reduced eggs, nymphs and insect survival on plants treated with 1 mM of acetylsalicylic acid. Second, the effect of dehydration stress on plant susceptibility to *B. cockerelli* with Lso was studied to evaluate the effect of drought on the outbreak of *B. cockerelli* and Lso. Results from this study indicated that dehydration stress enhanced *B. cockerelli* survival and rendered the host plant more susceptible to *B. cockerelli* infestation. Finally, plant transcriptomes were studied to evaluate significantly differentially expressed genes (DEGs) in plant responses to three stages of *B. cockerelli* colonization and Lso infection. The comparison between plants exposed to no insects and plants exposed to Lso-negative *B. cockerelli* resulted in 207 DEGs. The comparison between plants exposed to no insects and plants exposed to Lso-positive *B. cockerelli* resulted in 404 DEGs. The comparison between plants exposed to Lso-negative *B. cockerelli* and plants exposed to Lso-positive *B. cockerelli* resulted in

471 DEGs. Plants exposed to Lso-negative *B. cockerelli* up-regulated the expression of several defense genes after one, two and four weeks of exposure. Plants exposed to Lso-positive *B. cockerelli* resulted in a delay of up-regulating plant defense genes. Lso-positive plants down-regulated the expression of photosynthesis genes and up-regulated carbohydrate metabolic genes as early signs of disease development. Overall, this dissertation shows that plant induced responses to biotic and abiotic stress are temporally dynamic and that plant induced defenses could be effective against *B. cockerelli* but not necessarily effective against Lso infection.

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CHAPTER I

INTRODUCTION AND LITERATURE REVIEW

1.1 Bacterial pathogens and zebra chip

The emergence of vector-borne bacterial pathogens has recently become a major threat to food security. Bacterial pathogens in the genus of Liberibacter in particular cause devastating diseases in citrus and solanaceous plants (Haapalainen, 2014). Liberibacter species that infect citrus trees cause huanglongbing, the citrus greening disease. Between 2006 and 2011, huanglongbing caused a total estimated loss of $4.5 billion in Florida alone (Hodges & Spreen, 2012). Similarly, Liberibacter species that infects solanaceous plants can have a huge agricultural and economic impact by infecting solanaceous crops and causing zebra chip in potato plants. In potato, the phytopathogen can cause up 93% yield losses (Munyaneza, 2012) and results in millions of annual losses (CNAS, 2006). The potato industry in New Zealand lost over $96 million since the arrival of the vector insect harboring Liberibacter pathogen (Munyaneza, 2012). While Liberibacter species in citrus have been known to cause huanglongbing for more than a century (Bove, 2006), the Liberibacter species infecting solanaceous plants has only been described within the last decades (Munyaneza *et al.*, 2007). Zebra chip disease, caused by Liberibacter species of solanaceous plants, acquired its name from the striped brown coloration in potato tubers after frying for chip production. Aboveground symptoms of plant disease include leaf curling, chlorosis, aerial tubers, swollen nodes, and purple discoloration (Crosslin *et al.*, 2010; Secor *et al.*, 2009).

Zebra chip was first documented in Mexico in 1994, in Texas in 2000 (Munyaneza et al., 2007), and in New Zealand in 2008 (Liefting *et al.*, 2008; Teulon *et al.*, 2009). A gram-negative bacterium named '*Candidatus* Liberibacter solanacearum' (Lso), also known as '*Candidatus* Liberibacter psyllaurous', was identified as the causative agent of zebra chip (Hansen *et al.*, 2008; Liefting et al., 2008). Since its first documentation, Lso has been detected in several areas in North and Central America (Aguilar *et al.*, 2013; Crosslin *et al.*, 2012; Crosslin & Munyaneza, 2009; Munyaneza, 2012; Munyaneza et al., 2007; Munyaneza *et al.*, 2013; Munyaneza *et al.*, 2009b; Secor et al., 2009; Workneh *et al.*, 2013) and New Zealand (Liefting et al., 2008; Teulon et al., 2009). In Europe and Africa, Lso is associated with carrots and celery (Alfaro-Fernández *et al.*, 2012; Munyaneza *et al.*, 2010; Tahzima *et al.*, 2014; Teresani *et al.*, 2015; Teresani *et al.*, 2014) where it is vectored by carrot psyllids. However, in North and Central America and New Zealand, the primary vector is potato psyllid, *Bactericera cockerelli* (Munyaneza et al., 2007).

In attempts to reduce the detrimental effect of Lso, insecticides are used to control *B. cockerelli* populations and limit Lso transmission (Butler *et al.*, 2011; Nansen *et al.*, 2011; Prager *et al.*, 2013). However, insecticide treatment is not always effective since farmers had reported up to 75% of crop loss despite insecticide application (Munyaneza et al., 2007). Populations of *B. cockerelli* could be insecticide resistant (Chavez *et al.*, 2015; Prager et al., 2013). Currently, solanaceous crops are impacted by

B. cockerelli harboring Lso and yet there is no field-deployed resistant plant available commercially.

1.2 Vector biology and distribution

Commonly known as potato or tomato psyllid, *B. cockerelli* is a phloem-feeding hemipteran. The adult is approximately 1/12 inch to 1/10 inch long with long two pairs of clear wings, resembling a miniature cicada (Wallis, 1955). Male adults are characterized by six abdominal segments plus the genital segment and matting organ. Female adults are characterized by five abdominal segments plus a genital segment (Abdullah, 2008). The newly emerging adults are light green and become black after two to three days. The eggs are about 1/32 inch long with oval shape and bright yellow to orange color. The eggs are laid on a stalk attaching to the leaf. The eggs are usually found on the edge or under side of the leaves. Only 12% of the eggs are found on top of the leaf (Wallis, 1955). The nymphs are flat resembling scale insect, with short hairs around the margin of the body. They have five developmental instars from 1st to 5th. The developmental time, from eggs to adults, varies from 20 to 30 days depending on the host plants (Yang & Liu, 2009), rearing environment (Yang *et al.*, 2013; Yang *et al.*, 2010), rearing temperature (Tran *et al.*, 2012), and *B. cockerelli* biotype (Liu & Trumble, 2007; Swisher *et al.*, 2013a). Although *B. cockerelli* can be found on over 40 families of plants (Munyaneza, 2012; Pletsch, 1947; Torres *et al.*, 2015; Wallis, 1955), the primary host plants for *B. cockerelli* are plant species in the family of Solanaceae.

Bactericera cockerelli (Hemiptera: Triozidae) is an indigenous insect of North America (Munyaneza, 2012; Wallis, 1955). In 1955, *B. cockerelli* populations were endemic to Nebraska, Kansa, Oklahoma, Texas, North and South Dakota. Although *B. cockerelli* populations could be found in western states at the time, no populations were found in Washington and Oregon (Wallis, 1955). However, *B. cockerelli* populations were found overwintering on *Solanum dulcamara* in Washington and Oregon in 2012 (Swisher *et al.*, 2013b). Four haplotypes of *B. cockerelli* have been characterized according to their geographical regions in the United States: northwestern, western, central, and southwestern (Swisher *et al.*, 2014; Swisher *et al.*, 2012; 2013a). Biologically, central-haplotype *B. cockerelli* had faster development time, higher growth index and higher survivorship than western haplotype (Liu & Trumble, 2007; Swisher et al., 2013a). The interaction between different *B. cockerelli* haplotypes and host plants is still insufficiently studied.

Bactericera cockerelli is associated with psyllid yellows and zebra chip diseases of potato, both of which reduced tuber yield over 50% (Guenthner *et al.*, 2011; Pletsch, 1947). While the cause of psyllid yellows was believed to be *B. cockerelli* (List, 1935; Wallis, 1955), the cause of zebra chip was Lso, which is harbored by *B. cockerelli* (Munyaneza et al., 2007). Since both diseases share a number of closely resembling disease symptoms including leaf yellowing or purpling, leaf curing, and aerial tuber formation (Munyaneza, 2012; Munyaneza et al., 2007; Wallis, 1955), the distinction between psyllid yellow and zebra chip is not yet clear. Interestingly, potato tubers of Lso-positive plants showed striped pattern of necrosis when chipped and fried, but tubers of Lso-negative plants with psyllid yellows did not show such symptom (Sengoda *et al.*, 2010). Psyllid yellows has been reported in the US since late 1920s (Pletsch, 1947; Sengoda et al., 2010; Wallis, 1955) but zebra chip disease has only been reported since the early 2000s (Munyaneza et al., 2007).

1.3 Vector-pathogen interactions

'C*andidatus* Liberibacter solanacearum' circulates in *B. cockerelli*. This alphaproteobacterium can be horizontally transferred from *B. cockerelli* to plants and vertically transferred from mother to offspring (Hansen et al., 2008; Torres et al., 2015). In addition to transovarial transmission, Lso can remain within the vector from one life stage to the next through transtadial transmission. Evidence for sexual transmission of Lso from male to female *B. cockerelli* is not yet published but sexual transmission of their close relative, '*Candidatus* Liberibacter asiaticus', from male to female *Diaphorina citri*, was published (Mann *et al.*, 2011). In *Bactericera cockerelli*, Lso has high transmission efficiency. A *B. cockerelli* adult can inoculate Lso into plants within 6 hours. Even after vector was removed, infected plants still developed disease symptoms. With 20 *B. cockerelli* adults, transmission of Lso can occurs within one hour (Buchman *et al.*, 2011). The successful rate of inoculation increases with the increased number of vectors. Also, higher bacterial titer was found at the point of inoculation in plants with multiple vectors (Rashed *et al.*, 2012). In a three years field study, number of Lso-positive *B. cockerelli* was positively correlated with percentage potato tuber infection and crop lost (Goolsby *et al.*, 2012). Once acquired, Lso can persistently remain in *B.*

cockerelli. The vector can spread Lso from plant to plant through persistent transmission. An attempt to remove this phytopathogen from the vector by antiobiotic treatment was failed (Casteel *et al.*, 2012). The spread of Lso has been a major concern (Munyaneza, 2012).

Five haplotypes of Lso (A to E) has been described based on single-nucleotide polymorphisms and insertion-deletions in rRNA (Nelson *et al.*, 2013; Nelson *et al.*, 2011; Teresani et al., 2014). While haplotype A and B were found associated with solanaceous plants in North and Central America (A and B) and in New Zealand (A), haplotypes C, D, and E were found associated with apiaceous plants in Europe (Nelson et al., 2013; Teresani et al., 2015; Teresani et al., 2014). Based on these studies, *B. cockerelli* only vectors haplotype A and B. Based on field observation, haplotype B caused more destructive disease than haplotype A in potato (Wen *et al.*, 2013).

Lso has a negative effect on psyllid fecundity and nymphal survival (Nachappa 2011). In a later study, the effect of Lso on the survival of *B. cockerelli* nymphs was found dependent on Lso haplotype. Lso haplotype B reduced the survival of *B. cockerelli* nymphs but Lso haplotype A did not (Yao *et al.*, 2016). Thus, Lso effect on the plant or vector hosts may be dependent on the haplotype of the pathogen.

Recently, the genome of Lso was sequenced. The genome size of Lso (1,258,278 bp) is relatively smaller than most members of the *Rhizobiaceae* family but consistent with the genome size of its close relative *Candidatus* Liberibacter asiaticus (Lin *et al.*, 2011). The reduction of genome size could be the result of the co-evolution between the bacterial endosymbionts and host vector compensated by native host genes and/or lateral gene transfer from bacteria to the host (Sloan & Moran, 2012). Although Lso has relative small genome size, it has several prophages associating with the pathogenicity (Thompson *et al.*, 2015). Different prophages found in the genome could be associated with different haplotypes resulting in different severity of disease. Interestingly, only type I secretion system was found in the Lso genome. Although pathogenic bacteria transport toxins and other molecules through type I secretion system, the absence of type II, III, and IV secretion systems in the Lso genome is fascinating (Lin et al., 2011). Transcriptome analysis of Lso in *B. cockerelli* revealed that Lso expressed 92% of bacterial genes in the vector (Ibanez *et al.*, 2014). Transcriptome analysis of *B. cockerelli* in response to Lso revealed that Lso affected *B. cockerelli* biological, metabolic, development processes. Genes associated with Lso were also found expressed in *B. cockerelli* (Nachappa *et al.*, 2012a). The interaction between Lso and *B. cockerelli* is complex and is still not well-understood, but the pathogenicity of Lso could be in part involve in this complex interaction.

1.4 Plant-vector-pathogen interaction

Liberibacter of solanaceous plants, Lso, can affect *B. cockerelli* selection of host plants by manipulating and inducing plant volatile organic compounds (VOCs). The influence of a pathogen on a host plant and subsequently on an insect vector may vary depending on the relationship between host and the pathogen. Even within the same genus, different *Liberibacter* can differentially influence the production of plant VOCs. For example, Lso altered the volatile profile of potato (*Solanum tuberosum*) and tomato

(*Solanum lycopersicum*) plants, but the VOCs released by these solanaceous plants were species specific (Davis *et al.*, 2012; Mas *et al.*, 2014). The changes of VOCs following pathogen infection can affect vector behavior and preference. *Bactericera cockerelli* initially settled on infected potato plants but later moved to oviposit on plants that had been exposed to uninfected *B. cockerelli* (Davis et al., 2012). Lso-negative *B. cockerelli* settled preferentially on Lso-infected tomato plants while Lso-positive *B. cockerelli* preferred to settle on the Lso-negative tomato plants (Mas et al., 2014). The deterrence of *B. cockerelli* from Lso-positive solanaceous plants was linked to the induction of the plant defense compound β-caryophyllene (Davis et al., 2012). Interestingly, a common up-regulated VOC found in Liberibacter-infected plants was caryophyllene (Davis et al., 2012; Mann *et al.*, 2012b; Mayer *et al.*, 2008a). Thus, the plant volatile compounds elicited by the bacterial pathogens can be perceived by the insect vectors and may be influencing host plant selection. A blend of host plant VOCs has been recognized as the olfactory cues for an insect vector to select their quality host plant (Webster *et al.*, 2008).

Host plants of Lso were confirmed by studying the host plants of *B. cockerelli*. Several solanaceous crops including potato, tomato, eggplants, and pepper were confirmed infected and killed by Lso (Liefting et al., 2008; Liefting *et al.*, 2009). The disease symptoms in these plants vary in degrees of stunting, leaf yellowing, and necrosis (Crosslin et al., 2010; Secor et al., 2009). Several pest management practices including biological and chemical controls were implemented in attempt to reduce crop loss. The current and primary control strategy for Lso is controlling *B. cockerelli* through chemical treatment. However, this strategy is not always effective as previously discussed (Munyaneza, 2012). Insecticide resistant populations of *B. cockerelli* were discovered and were verified by both lab and field tests (Chavez et al., 2015; Prager et al., 2013). Even with the use of traditional chemical and cultural practices for pest and disease management, farmers still encountered crop losses causing by *B. cockerelli* and/or Lso (Munyaneza, 2012). One of the challenges was reducing reservoir host plants to prevent recurrence of *B. cockerelli* infestation and Lso infection. Naturally, *B. cockerelli* and Lso depend on reservoir host plants when crop plants are not available. In the wild, several species of wild solanaceous plants could reservoir hosts of *B. cockerelli* and Lso. Currently, bitter-sweet nightshade, *Solanum dulcamara*) (Swisher et al., 2013b) and silver-leaf Nightshade, *Solanum elaeagnifolium* (Thinakaran *et al.*, 2015a) were confirmed as reservoir hosts. Eliminating these plants is not economically feasible and not environmental sustainable because *B. cockerelli* can also migrate (Goolsby et al., 2012; Nelson *et al.*, 2014). In spite of having several documented host plants, *B. cockerelli* adults prefer cultivated crop plants over wild plants (Thinakaran *et al.*, 2015b) which explains the seasonal outbreak of *B. cockerelli* during the potato season (Munyaneza, 2012; Nelson et al., 2014).

Different host plants affect the developmental time of *B. cockerelli*. For example, the estimated developmental time from egg to adult was 24.1 days on eggplant, 26.2 days on bell pepper, and 19.6 days on potato (Yang & Liu, 2009; Yang et al., 2010). Variation developmental time of *B. cockerelli* on different host plants could be due to plant nutritional quality or defense compounds. Plants have been known to defend against insects as part of their innate immune response to damage (Karban & Baldwin, 1997; Walling, 2000).

Plants activate induced defenses when under an attack by insects or pathogens. Plants can produce anti-nutritive factors (e.g. proteinase inhibitor) and/or anti-microbial compounds (e.g. phytoalexins) as induced defense. The phytohormones such as jasmonic acid (JA), salicylic acid (SA) and ethylene (ET) signal and modulate the production of these defense compounds. The activation of each of these signinaling pathways can lead to a myriad of responses including the production of defensive compounds aimed at protecting the plant and fighting off attackers (Karban & Baldwin, 1997; Thaler *et al.*, 2001; Walling, 2000). Plant defenses against leaf-chewing herbivores and wounding are generally associated with the JA signaling pathway. Plant defenses against phloem feeding herbivores and biotrophic pathogen are generally associated with the SA signaling pathway (Glazebrook, 2005; Howe & Jander, 2008; Karban & Baldwin, 1997; Kessler & Baldwin, 2002; Thaler et al., 2001; Walling, 2000). These signaling pathways can interact or crosstalk to fine-tune plant responses to different attackers (Reymond & Farmer, 1998; Rojo *et al.*, 2003). For instance, ET and JA signaling pathway can interact to enhance plant resistance against pathogens. Similarly, the negative crosstalk between SA and JA can be found in in different systems (Baldwin *et al.*, 1996; Doherty *et al.*, 1988; Harms *et al.*, 1998; Penacortes *et al.*, 1993). Interestingly, a positive interaction between the SA and JA signaling pathway can be found in the case of aphid infestations (De Vos *et al.*, 2005; Ellis *et al.*, 2002; Moran & Thompson, 2001; Zhu-Salzman *et al.*, 2004) or pathogen infection (van Wees *et al.*, 2000). The types of defense pathway and their interaction (antagonist or positive) depends on phytohormone concentration

(Devadas *et al.*, 2002).

Understanding how plants respond to pathogens is one of the first crucial steps to enhance plant resistant against Lso. The mechanism of plant defense against pathogens has been well documented in the study of SA signaling pathway. In this pathway, one quick strategy of defense against pathogen infection is hypersensitive response (HR). During HR plants activate programmed cell death (PCD) at local leaves isolating infected cells from the main system thus preventing systemic proliferation of the pathogen (Mur *et al.*, 2008). Plants exposed to avirulent pathogen strains, rapidly produce an oxidative burst resulting in reactive oxygen species (ROS) production such as hydrogen peroxide (H_2O_2) which triggers PCD, and activates HR (Levine *et al.*, 1994). ROS and HR have been associated with SA signaling transduction pathway (Chen *et al.*, 1993). In plants, SA functions as a phytohormone and is involved with not only the signaling of ROS for HR but also with the activation of pathogenesis related (PR) genes. PR genes encode proteins that elicits plant systemic acquire resistance (SAR). SAR is a plant innate immune response that enhances the resistance against infection to subsequent attacks by the same or related pathogens (Chester, 1933; Enkerli *et al.*, 1993). While the activation of HR is quick, the induction of SAR is relatively slow. Hence, HR serves as the primary wall of defense whereas SAR serves as the secondary wall of defense. In plants, SAR and HR are also associated with protection against phloem-feeding vectors (Karban & Baldwin, 1997).

Other phytohormone pathways also play a role in plant defense against vectors and pathogens. JA defense pathway has been known to elicit compounds that have antimicrobial properties helping plant defense against pathogen (Creelman & Mullet, 1997). Furthermore, mutant Arabidopsis plants that cannot synthesize JA are more susceptible to infection by fungus *Pythium mastophorum* (Vijayan *et al.*, 1998). This indicates that JA can also play a role in plant defense against pathogen infection. JA also interacts with other phytohormones in the defense against pathogen. For instance, treatment with abscisic acid (ABA) can elicit lipoxygenase gene expression that controls the biosynthesis of JA (Melan *et al.*, 1993), and ABA was shown to cooperate or precede JA in the activation of *A. thaliana* defense genes against *Pythium irregulare and other necrotrophic pathogens* (Adie *et al.*, 2007). ABA is a phytohormone that regulates plant response to abiotic and biotic stresses. ABA is usually associated with cold and drought stress, but also commonly associated with leaf abscission. Upon pathogen infection, ABA production might be induced to regulate leaf abscission, which may reduce the spread of the pathogen or delay the development of the disease since by abscising the infected leaf, plants can stop the infection progression. ABA might also be involved in priming callose biosynthesis after pathogen recognition (Ton & Mauch-Mani, 2004), a plant response to fungal pathogens. Therefore, ABA cannot only play a direct role but also an indirect role in plant defense against pathogen. As shown, various phytohormones have been documented to play a vital role in plant defense against pathogens and insects. Thus, phytohormones affect plant and may mediate pathogen transmission by vectors.

Tomato plants exposed to Lso-positive *B. cockerelli* up-regulated the expression of genes that regulate the synthesis of JA and SA and up-regulated the expression of genes that modulated by JA and SA (Casteel et al., 2012). Furthermore, Lso infection significantly affected the level of phenolic compounds in plant leaf and stem. For example, Lso-positive plants also had greater level of dichlorogenic acid, epicatechin gallate, procyanidin A and procynidin digalloy dimer in leaf than Lso-negative plants. However, the trend of up-regulating defense compound in Lso-positive plants is not yet clear. Plants testing positive for Lso also had lower level of betuloside, diflavone, ferulic acid derivative, quercetin diglycoside 2, and quinic acid in leaf than Lso-negative plants (Wallis *et al.*, 2015). In the tuber, however, total phenolics were higher in Lso-positive plants than in Lso-negative plants. Interestingly, salicylic acid concentration was also higher in Lso-positive tuber than in Lso-negative tuber (Navarre *et al.*, 2009). Thus, these results provide some evidences that plants could be defending against *B. cockerelli* and Lso infection but the effect of *B. cockerelli* and Lso on plant induced defenses is not yet clear. Furthermore, the effect of these induced defenses on *B. cockerelli* and Lso is not yet known. The induction of plant innate defenses may be reducing *B. cockerelli* colonization and delaying Lso infection. More studies in this area are in much needed.

1.5 Environment-plant-vector-pathogen interaction

Environmental factors may affect *B. cockerelli* population and Lso epidemiology. For example, the number of Lso-positive *B. cockerelli* was negatively correlated with latitudinal location and maximum temperature (Workneh et al., 2013). Furthermore, temperature was reported to significantly affect *B. cockerelli* reproduction (Workneh *et al.*, 2011). The increase in temperature can promote the outbreak of *B. cockerelli* and

Lso. Another major factor that contributes to the outbreak of insect is water stress. Scarcity of water has been known to change plant physiological response. In some cases, water stress increase plant susceptibility to insects and promote insect outbreaks (Mattson & Haack, 1987; Showler, 2014; White, 1969). Incidences of droughts have been increase annually as incidences of insect and disease outbreaks. Thus, studying plant response to *B. cockerelli* and Lso under water stress conditions is crucial for the management of insect and disease, especially in the context of global climate change.

CHAPTER II

THE ROLE OF JASMONIC ACID IN PLANT INDUCED DEFENSES AND RESISTANCE AGAINST *BACTERICERA COCKERELLI*

2.1 Introduction

Understanding plant molecular defense mechanisms associated with plant resistance against insect herbivory and pathogen infection is essential in combating crop loss (Smith & Clement, 2012). Plants have refined mechanisms of response to insect herbivory and pathogen infection. When plants detect damage caused by insects or pathogens, they can respond by producing toxic chemicals and/or anti-nutritive enzymes to reduce the growth and proliferation of the attacker (Huot *et al.*, 2013; Karban & Baldwin, 1997; Schaller, 2008). This type of plant response is referred to as induced defenses. Induced defenses are mediated by a network of phytohormones that regulates plant growth and defense. The main phytohormones involved in plant induced defenses are JA and SA. While JA is usually associated with leaf-chewing herbivores, SA is frequently associated with phloem-feeding herbivores (Huot et al., 2013; Karban & Baldwin, 1997). Although the induction of one pathway may inhibit the induction of the other, at any given time point plants can elicit both pathways simultaneously (Anand *et al.*, 2008; De Vos et al., 2005; Schaller, 2008; Thaler et al., 2001).

Plant induced defenses can be chemically manipulated to induce plant resistance and protect crops prior to insect infestation and pathogen transmission (Sessa, 2012). However, plant induced defenses vary across plant-insect and plant-pathogen combinations (Agrawal, 2000; Huot et al., 2013; Karban & Baldwin, 1997). Due to reciprocal adaptations between the exploiters (e.g. insect and pathogens) and defenders (e.g. plants), plant induced defenses can be specific to certain groups of exploiters (Ehrlich & Raven, 1964; Janz, 2011). For example, plants defend against certain lepidopterans by synthesizing specific proteinase inhibitors (Bode *et al.*, 2013). Thus, knowledge regarding the effectiveness of a specific pathway of plant induced defenses and resistance against certain insect pests can provide essential information for crop protection programs.

Induced resistance is an enhancement of resistance in susceptible plants in response to a biotic or abiotic elicitor (Karban & Baldwin, 1997; Schonbeck, 1997). Exogenous application of JA has been documented to have a role in induced plant defenses against insects (Farmer *et al.*, 1992; Thaler, 1999b). Jasmonic acid and its derivatives can induce the expression of plant proteinase inhibitors (PIs) in induced systemic resistance (Farmer et al., 1992; Hare & Walling, 2006; Walling, 2000). The primary interest of this study focused on understanding the effectiveness of plant induced defenses and resistance against an insect vector, the potato psyllid.

Potato psyllids, *Bactericera cockerelli* Sulc (Hemiptera: Triozidae), also known as tomato psyllids, have received much attention in recent years due to the discovery of their ability to harbor and transmit '*Candidatus* Liberibacter solanacearum' (Lso) (Munyaneza et al., 2007; Secor et al., 2009), a Gram-negative bacterium that can infect and kill several members in the Solanaceae family (Liefting et al., 2009). In potato, Lso causes zebra chip resulting in millions of dollars in crop loss (Munyaneza, 2012;

Munyaneza et al., 2007). The effectiveness of chemical and biological controls against Potato psyllidis still under investigation (Munyaneza, 2012). Presently, only one study focused on plant induced defenses against *B. cockerelli* and Lso (Casteel et al., 2012). This study showed that immature psyllids harboring Lso induce defenses in *S. lycopersicum* by up-regulating the expression of *AOS* and *Pin2* genes in the jasmonic acid (JA) defense pathway and the expression of *PAL5* and *PR1* genes in the salicylic acid (SA) defense pathways (Casteel et al., 2012). However, the effect of the induction of these defense pathways against *B. cockerelli* is yet to be tested. For instance, the up-regulation of genes involved in the production of defense proteins may not result in effective reduction of insect performance and fitness, while in the case of plant-induced resistance, induced defenses result in negative insect performance and/or fitness (Agrawal, 1999; Karban & Baldwin, 1997; Underwood, 2012). Furthermore, it has been described that the association of microorganisms with insects might affect plant induced defenses and plant induced resistance (Casteel et al., 2012; Huot et al., 2013; Mann *et al.*, 2012a; Rodrigues *et al.*, 2013; Wallis & Chen, 2012). No study has addressed yet the defense mechanisms induced by *B. cockerelli* in the absence of Lso. This study focuses on the effect of JA-mediated defenses and resistance on the infestation of Lso-positive and Lso-negative *B. cockerelli* (psyllids harboring Lso or not harboring Lso, respectively). *S. lycopersicum* were exogenously applied with JA solution to induce the expression defense genes and tested the effectiveness of JA-mediated induced defenses against the Lso-negative or Lso-positive *B. cockerelli*. Although Casteel and colleagues showed that Lso-positive *B. cockerelli* up-regulated the expression of genes in the JA defense pathway, the induction of these genes could be not effective against Lso-positive *B. cockerelli*. Thus, determining whether the plant induced defenses regulated by JA is effective in enhancing plant resistance against *B. cockerelli* is crucial for future study in plant immunity against vectors with or with bacterial pathogens.

2.2 Materials and methods

2.2.1 Effect of JA-mediated plant defenses on proteinase inhibitor gene expression

Twelve *Solanum lycopersicum* cv. Money Maker (tomato) were grown from seeds (Victory Seeds) in 3.5-inch square pots with soil (Sun Gro® Metro-Mix 900) in the laboratory under the room temperature and 16:8 light:dark cycle. Plants were watered and fertilized weekly according to the label rate of the Miracle-Gro® Water Soluble Tomato Plant Food (18-18-21 NPK). At six weeks old, six plants were treated with JA solution and six plants were treated with the control solution (~2.4 mL per plant) to evaluate the expression of a marker gene for the JA defense response. A JA solution was made by dissolving jasmonic acid ((±)-1α,2β-3-Oxo-2-(cis-2-pentenyl) cyclopentaneacetic acid) (Sigma Aldrich) in HPLC graded methanol at 100 g/L, and by mixing this solution with water to make a 0.5 mM of JA solution. The 0.5 mM JA concentration is well below the toxic level for *S. lycopersicum* and known to induce plant resistance against leaf-chewing herbivores (Thaler *et al.*, 1996; 2001). A control solution was similarly made but without the (±) jasmonic acid to control for the placebo effect. Six-week-old *S. lycopersicum* were sprayed on the leaves with three sprays of either JA or control solutions (~2.4 mL per plant) using hand-sprayer. Three days after the application, plant tissues were collected from the top most-fully-expanded leaf and were quickly flash-frozen in liquid nitrogen. Tissues were finely homogenized in a 1.5 mL tube with TRIzol Reagent (Life Technologies) using sterile plastic pestles (Fisher Scientific Co.) and RNA was purified according to the manufacturer's protocol. RNA concentrations were quantified using Infinite® 200 PRO NanoQuant (Tecan, San Jose, CA, USA). Potential DNA contamination was removed using TURBO DNA-free™ Kit (Life Technologies, Carlsbad, CA, USA). Quantitative RT-PCR was performed in CFX96 Real-Time PCR Detection System (Bio-Rad Inc.) using SensiFast SYBR Hi-ROX One-Step Kit. Briefly, each RT-qPCR was performed in a 10 µL reaction using 5 µL of 2x SensiFast SYBR HI-ROX One-Step mix, 0.4 µL of each primer, 0.1 µL of reverse transcriptase, 0.2 µL of RiboSafe RNAse Inhibitor, 2.9 µL of DEPC-H_2O, and 1 µL of 100ng RNA. The RT-qPCR was done as suggested by the manufacturer: 45 °C for 10 mins for reverse transcription, 95 °C for 2 mins for polymerase activation, and 40 cycles of 95 °C for 5s, 60 °C for 10s, and 72 °C for 5s. Amplification and melting curve were verified to validate the results. Primer efficiency was estimated according to the published method using LinRegPCR 11.1 (Ruijter *et al.*, 2009). The relative gene expression was calculated according to the published Delta Delta CT method (Fleige *et al.*, 2006). *S. lycopersicum* 18s ribosomal RNA gene (GQ280796.1) with primer pair of 5'-AGAAACGGCTACCACATCCA-3' and 5'-GCCCTCCAATGGATCCTC-3' was used as normalizer gene for its stability (Casteel et al., 2012). *S. lycopersicum* proteinase inhibitor II gene (AY129402.1) with primer pair of 5'-TATCCATCATGGCTGTCCACA-3' and 5'-AACACACAACTTGATCCCCACA-3' was used as target gene and as a marker for the JA defense pathway (Casteel et al., 2012). The product sizes of the normalizer and target genes are 157 bp and 302 bp respectively.

2.2.2 Insect source

Bactericera cockerelli colonies (central haplotype) were maintained in the laboratory at Texas A&M University, College Station on *S. lycopersicum*. Lso-positive and Lso-negative colonies were kept in separate 14” X 14” X 24” insect cages (BioQuip) at room temperature of 23 ± 1°C and photoperiod of 16:8 (L:D) hours. Lso-positive *B. cockerelli* were obtained by allowing *B. cockerelli* to acquire Lso from *S. lycopersicum* infected with Lso haplotype A and haplotype B. The Lso-positve and Lso-negative colonies were routinely tested for Lso infection using diagnostic polymerase chain reaction (PCR) as previously published (Nachappa *et al.*, 2012b).

2.2.3 Effect of JA-mediated plant induced-resistance against Lso-positive and Lso-negative B. cockerelli

S. lycopersicum were grown from seeds (Victory Seeds) in the greenhouse for four weeks (four leaves stage). The seeds were planted in soil (Sun Gro® Metro-Mix 900) in 4-inch round pots, watered and fertilized weekly with a 20-20-20 NPK fertilizer. Plants were monitored regularly to prevent exposure to insects prior to the experiment. Plants were moved to the laboratory and allowed to acclimate for two weeks (room temperature, 12:12 light:dark cycle). At six weeks old, *S. lycopersicum* were sprayed with three simultaneous sprays of either JA or control solutions (~2.4 mL per plant) as previously described. Each plant was sprayed on the top and on the sides while having one top most-fully-expanded leaf covered by a wooden block to prevent any residual effect on the insects later. One day after the spray, paired *B. cockerelli* adults (a male and a female) were placed in 1” BioQuip clip cages (catalog number #1458) on the previously covered leaf of the *S. lycopersicum*. To prevent stress or damage on the leaf, a bamboo stick was used to support the clip cage. After one week, *B. cockerelli* eggs and nymphs on each plant were counted. The number of adults was also measured to estimate if *B. cockerelli* mortality affected egg laying. Progeny counts were used as a proxy to measure plant resistance: the number of progeny on plants is inversely correlated with plant resistance. The resistance assays were independently conducted using either Lso-positive (N = 17: JA=9, control =8) or Lso–negative *B. cockerelli* (N = 22: JA=11, control =11 plants each treatment). Each biological assay was limited to one week to avoid the crowding that potentially force the nymphs to move to other parts of the plant. The focus of this study was on plant induced systemic resistance; therefore it was important that the measured insect responses were from their interaction with the plant’s own defense compounds, rather than with the sprayed JA.

2.2.4 Validating JA-mediated plant defenses in plants grown parallel to the insect experiment

To verify that application of JA resulted in induction of JA defense during the insect bioassay, plant tissues were collected from two plants treated with JA solution and two plants treated with control solution three days after the initial application. RNA samples were extracted as described above. RNA integrity was analyzed by gel electrophoresis, and RNA concentration and purity were evaluated using a NanoVue Plus Spectrophotometer (GE Healthcare). DNA contamination was removed using TURBO DNA-free kit (Life Technologies) and retested for purity and concentration as previously described. Two biological replicates were analyzed for each treatment. Complementary DNA was prepared from 825 ng of purified RNA (A260/A280: ~1.94) using the Verso cDNA Synthesis kit (Thermo Scientific) following the manufacturer's instructions. PCR reactions were performed using GoTaq Flexi DNA Polymerase (Promega) according to manufacturer's instructions. Each reaction contained 2.5 μL of 5X Green GoTaq® Reaction Buffer, 0.0625 μL of 5 units/μL GoTaq Flexi DNA polymerase, 1 μL of 25 mM $MgCl_2$, 0.25 μL of 10 mM of each dNTP (Promega), 0.25 μL of 10 μM of each primer, and 1.5 μL of cDNA. The PCR conditions were: 2 min at 94°C followed by 22, 25, 30, or 35 cycles of 30 sec at 94°C, 30 sec at 60°C, 90 sec at 72°C, and a final extension of 72°C for 10 min. In addition to the tested PI2 gene (AY129402.1) tested by RT-qPCR, the expression of two other proteinase inhibitor II genes (PI2: K03291.1 and PINII: AB110700.1) was tested to verify if JA induce more than one PI genes. *S. lycopersicum* elongation factor 1-alpha (EF1: NM_001247106), a known stable endogenous gene was used as reference (Wieczorek *et al.*, 2013). The EF1 primers (F: 5'- AGATGGTCAGACCCGTGAAC-3' and R: 5'-GTCAAACCAGTAGGGCCAAA -3') were predicted to produce a 435 bp amplicon. PI2 primers (F: 5'- TGTTGATGCCAAGGCTTGTA-3' and R: 5'-

AGCAACCCTTGTACCCTGTG-3’) and PINII primers (F: 5’-TGTTGATGCCAAGGCTTGTA -3’ and R: 5’- AGCAACCCTTGTACCCTGTG -3’) were predicted to amplify a 302 bp amplicon each. The PCR products were run on 1% agarose gel stained with ethidium bromide and digitally documented using the Foto/Analyst® Investigator photographic system (Fotodyne, Hartland, WI, USA) with ImageJ 1.34s software.

2.2.5 Statistical analyses

Statistical analyses were performed using JMP® Pro v.10. The number of eggs and nymphs observed after seven days were compared between the control and JA groups using Wilcoxon tests. The nymph to egg ratio was calculated by dividing the number of nymphs by the number of eggs. Samples with 0 eggs were excluded from the ratio calculation. The ratios were then subjected to the same nonparametric statistical test indicated above. The mean effect size between the treatment groups were calculated using the Cohen’s equations (Cohen, 1988). The relative gene expression of proteinase inhibitor from the RT-qPCR result was log-transformed and tested for normality with Shapiro-Wilk test. Data that passed the normality test were used for the two-sided t-test.

2.3 Results

2.3.1 Effect of JA-mediated plant defenses on proteinase inhibitor gene expression

Quantitative RT-PCR suggested that jasmonic acid induced the expression of proteinase inhibitor gene to enhance plant immune defense. *S. lycopersicum* that were treated with 0.5 mM JA solution had significantly higher expression of proteinase inhibitor II gene (t (12) = 4.15, *P* = 0.0052) than the control plants. On average, expression of the proteinase inhibitor II gene was approximately 1459 folds higher in the JA-treated plants than in the control plants (Fig. 2.1) suggesting an up-regulation of JA-mediated defense.

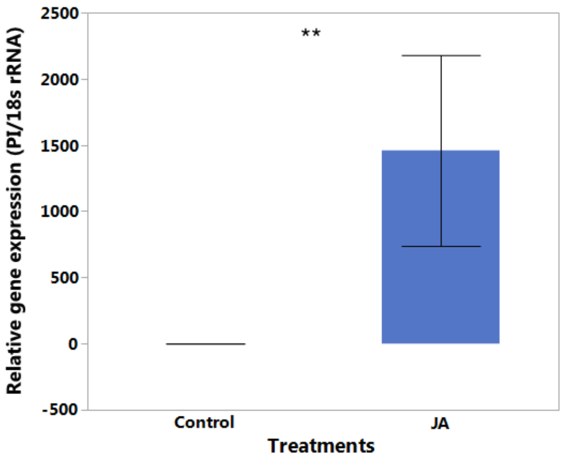

Figure 2.1 Jasmonic acid significantly up-regulated the expression of proteinase inhibitor gene in *Solanum lycopersicum*. The mean (±SE) of the expression of proteinase inhibitor II (PI) gene in *S. lycopersicum* leave three days after applied with either jasmonic acid solution or control solution tomato plant. The relative abundance transcript of PI gene was normalized with the transcript of 18s rRNA reference gene. Symbol ** denotes significant level with p-value less than 0.01.

2.3.2 Effect of JA-mediated plant induced-resistance against Lso-positive and Lso-negative B. cockerelli

After verifying that the JA spray induced plant defenses, the effect of JA-mediated plant induced defenses against Lso-negative *B. cockerelli* was assessed by measuring *B. cockerelli* eggs and nymphs on treated and control plants. The results indicated that the JA treatment had no significant effect on the number of *B. cockerelli* eggs (*Z* = -0.763, *P* = 0.445, Fig. 2.2A) and the number of *B. cockerelli* nymphs (*Z* = -0.370, *P* = 0.711, Fig. 2.2B) on *S. lycopersicum*. The nymph to egg ratio (*Z* = -0.168, *P* = 0.866, Fig. 2.2C) and the total number of offspring (*Z* = -0.564, *P* = 0.573, Fig. 2.2D) were also not different. This indicated that application of 0.5 mM JA solution did not affect *S. lycopersicum* resistance against *B. cockerelli* without Lso. If JA-induced defenses resulted in induced resistance, the number of eggs and/or nymphs would have been significantly lower on JA-treated plants relative to the control.

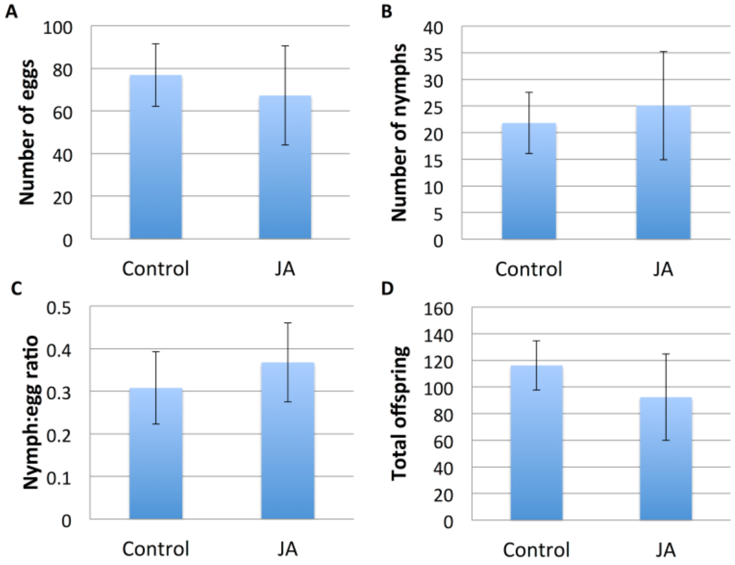

Figure 2.2 The effect JA-treated *Solanum lycopersicum* on number of Lso-negative *B. cockerelli* progeny. JA-mediated plant defense did not affect (A) mean (±SE) number of eggs, (B) mean (±SE) number of nymph, (C) mean (±SE) ratio of nymph to egg, and (D) mean (±SE) of total offspring (a combination of eggs and nymphs) of Lso-negative *B. cockerelli*. Symbol * indicates significant at p<0.05 and symbol ** indicates significant at p<0.01.

A similar study was conducted using Lso-positive *B. cockerelli*. The results indicated that there was a significant effect of JA spray on plants on the number of eggs seven days post infestation. There were significantly fewer eggs on plants sprayed with JA (*Z* = 2.069, *P* = 0.0386, Fig. 2.3A). The mean numbers of eggs on the control and JA sprayed plants were 71.38 (±14.12 SE) and 40.22 (±14.85 SE), respectively. On average, the control plants had 1.77 times more eggs than the JA plants. The Cohen's effect size value (d = 0.74) between the control and JA sprayed groups suggested a moderate to high significance on the number of eggs, based on the consideration that a 0.5 effect size is moderate while a 0.8 effect size is large (Cohen, 1988). Similarly, a significant effect of JA-spray on the nymph to egg ratio (*Z* = 2.678, *P* = 0.0074, Fig. 2.3C) was observed for Lso-positive *B. cockerelli*. A very large Cohen's effect size value (d = 4.12) was estimated when comparing the mean and standard deviation of the nymph to egg ratio. However, there was no significant effect of the treatment on the number of nymphs (*Z* = -0.963, *P* = 0.335, Fig. 2.3B) nor on the combined number of eggs and nymphs (*Z* = 1.203, *P* = 0.229, Fig. 2.3D) of Lso-positive *B. cockerelli*. Since there was a significant decrease in the number of eggs at seven days post-infestation on JA sprayed plants, the induction of *S. lycopersicum* defenses can resulted in a reduction of *B. cockerelli* oviposition. Therefore, induction of JA-induced defenses might have an effect on induced plant resistance against *B. cockerelli* infestation when *B. cockerelli* harbor Lso.

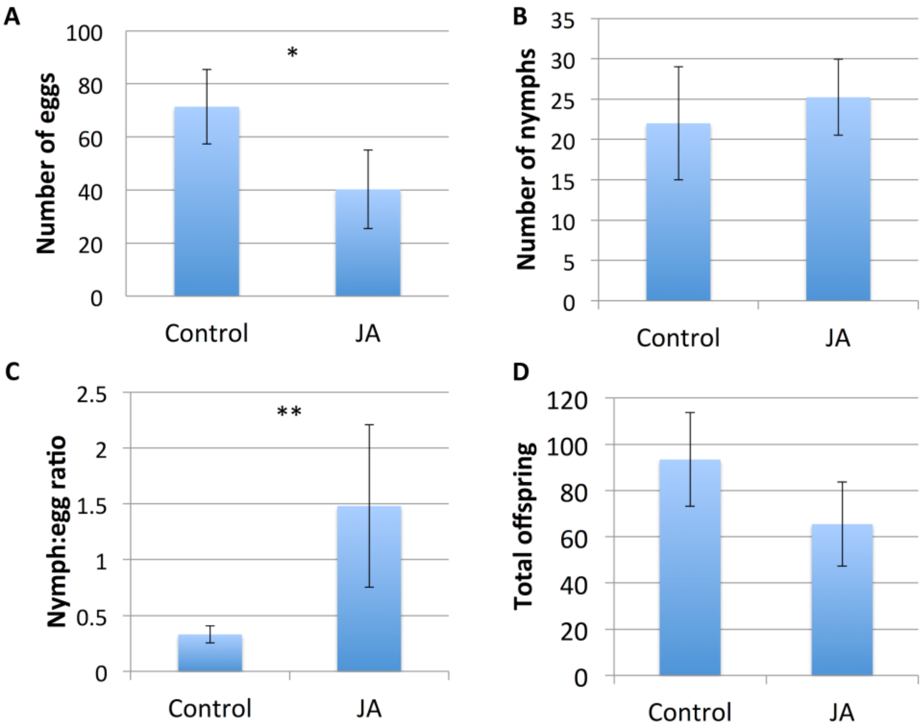

Figure 2.3 The effect JA-treated *Solanum lycopersicum* on number of Lso-positive *B. cockerelli* progeny. JA-mediated plant defense significantly reduced (A) mean (±SE) number of eggs and increased (C) mean (±SE) ratio of nymph to egg, but had no effect on (B) mean (±SE) number of nymphs and (D) mean (±SE) total offspring (a combination of eggs and nymphs) of Lso-positive *B. cockerelli* Lso. Symbol * indicates significant at $p<0.05$ and symbol ** indicates significant at $p<0.01$.

There was no significant difference in the adult mortality among the treatments, implicating that oviposition and infestation responses were not confounded by adult mortality. Mortality measured in control and JA treatments were not significantly different from each other in the study using Lso-negative *B. cockerelli* ($Z = 1.446$, $p = 0.148$) and the study using Lso-positive *B. cockerelli* ($Z = 0.519$, $P = 0.604$).

2.3.3 Validating JA-mediated plant defenses in plants grown parallel to the insect experiment

Results from gene expression by RT-PCR indicated that plants grown in parallel to the plants used in insect assays had an up-regulation of proteinase inhibitor genes in response to the treatment. This showed that genes encoding two proteinase inhibitors II, PI2 and PINII, were induced in response to JA application (Fig. 2.4). After 35 PCR cycles, expression of both genes was detected in JA sprayed plants, whereas no PCR products could be detected in the control plants (plants sprayed with water). Reference gene EF1 signal was visible at 22 cycles in both JA and control plants. The EF1 signal (amplicon intensity) from each treatment was similar in brightness (Fig. 2.4) and this signal reached saturation at 25 PCR cycles (data not shown). Expression of PI2 and PIN2 genes encoding PIs was only detected after 35 PCR cycles in JA sprayed plants, but not the control plants. This indicated that JA treated plants expressed plant defense genes in the JA defense pathway in response to the JA treatment. This result was similar to that found earlier in the RT-qPCR. Thus, different genes encoding proteinase inhibitor showed similar pattern of up-regulation of gene expression in response to the JA application.

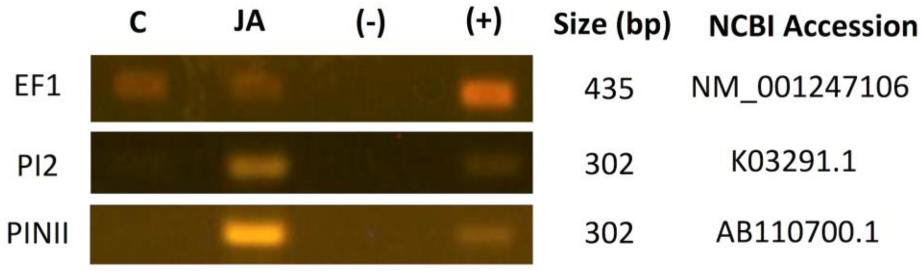

Figure 2.4 Jasmonic acid induced the expression of proteinase inhibitor genes in *Solanum lycopersicum*. RT-PCRs show that the *Solanum lycopersicum* treated with 0.5 mM of jasmonic acid solution (JA) had induced the expression of proteinase inhibitor II genes (PI2 & PINII) whereas plants treated with 0 mM solution (C) did not. cDNA samples from plant tissues were processed for 22 PCR cycles for the reference gene (EF1) and 35 PCR cycles for the target genes (PI2 and PINII). Water was used as negative control (-) to verify that the PCRs were not contaminated. Plant DNA was used as positive control (+).

2.4 Discussion

Since induced defenses might not translate into an enhancement of resistance against insects, the effect of the induction of defenses on insect fitness needs to be investigated (Zarate *et al.*, 2007). *B. cockerelli* carrying Lso were shown to induce the expression of proteinase inhibitor II gene, a marker gene for the JA defense pathway, in *S. lycopersicum* (Casteel et al., 2012). The effect of the induction of this defense pathway against *B. cockerelli* has yet to be evaluated. Therefore, it is still unknown whether JA-mediated induced defenses against *B. cockerelli* result in induced resistance.

Results from this study suggested that application of JA solution on *S. lycopersicum* leaf significantly up-regulated the gene expression of proteinase inhibitor II. Both quantitative RT-PCR from an independent experiment and RT-PCR from a parallel experiment showed that 0.5 mM elicited an expression of proteinase inhibitor II gene suggesting enhanced plant defenses. Furthermore, the three genes showed an up-regulation of expression in response to the JA spray. These results are in agreement with a number of studies showing the role of PIs in the JA defense pathway (Walling, 2000, Thaler et al., 1996, Casteel et al., 2012). Therefore, the application of JA treatments was used to test the effect of JA-mediated induced defenses on plant induced systemic resistance. Since proteinase inhibitor II gene was activated in response to *B. cockerelli*feeding (Casteel et al., 2012), up-regulation of this gene was thought to confer plant induced defense against *B. cockerelli*. This hypothesis was tested in this study to determine the effectiveness of an enhanced JA defense against *B. cockerelli*.

Result from the study suggested that induction of plant JA defense gene does not necessarily confer an enhanced resistance against insects. Although JA-mediated defense was induced in *S. lycopersicum*, this defense pathway showed no effects on the number of *B. cockerelli* colonizing the host plant. There were no significant differences in the total number of *B. cockerelli* offspring after 7 days, on Lso-positive or –negative *B. cockerelli*. In this case, JA-mediated induced defenses did not appear to enhance plant resistance against *B. cockerelli*. Nevertheless, plant defenses are complex. Several studies have shown that plant induced defenses are spatially and temporally dynamic (Chen *et al.*, 2009; Datta & Lal, 2012; Raghava *et al.*, 2010; Vulic *et al.*, 2013). Moreover, the effect of induced defenses on insect fitness, the indicator of induced resistance, might be delayed with respect to the experimental observations. Therefore it is important to evaluate the composition of *B. cockerelli* life stages after infestation and oviposition to reveal subtle effects otherwise not perceived.

To uncover subtle effects of JA-mediated defenses on *B. cockerelli* fitness, the numbers of eggs, nymphs, and the ratio nymphs to eggs were also evaluated. In the case of Lso-negative *B. cockerelli*, JA-treatment had no effect on any of these parameters. However for Lso-positive *B. cockerelli*, JA spraying resulted in a reduction on the number of eggs but not on the number of nymphs and an increase on the nymph to egg ratio seven days after infestation. Life-history studies of *B. cockerelli* on *S. lycopersicum* indicated that on average eggs hatch after 6.5 days (Nachappa et al., 2012b). *B. cockerelli* can lay a proportion of nonviable eggs (Yang et al., 2010) and egg hatching time depends on host plant quality (Yang & Liu, 2009).

The nymphs present on the plants on day seven corresponded to the first batch of eggs that were laid and hatched after plant infestation. The absence of significant differences on the counts of eggs, nymphs, total offspring, or on the nymph to egg ratio of Lso-negative *B. cockerelli* implies that egg laying and hatching was not affected by the induced systemic defenses in these experiments. Therefore, the JA treatment did not affect the temporal dynamic of oviposition by Lso-negative *B. cockerelli*. On the contrary, JA treatment affected the temporal dynamic of oviposition on Lso-positive *B. cockerelli*; as no differences were observed between nymphs (proxy for early oviposition) but number of eggs was affected (later oviposition) at day seven. Since no differences were observed for total offspring nor for total nymphs while the nymph to egg ratio was higher in JA treated plants, egg hatching could be affected in the experiments using Lso-positive *B. cockerelli*.

The number of eggs of Lso-positive *B. cockerelli* at seven days was significantly reduced by the JA treatment. This suggests that the JA treatment may enhance plant resistance against Lso-positive *B. cockerelli*. A study on another psyllid species had reported exogenous application of methyl jasmonate enhance *Pistacia vera* L. cv. Fandoughi resistance against *Agonoscena pistaciae* by reducing nymph density by 73% and increasing the activity of antioxidant enzymes (Shahabinejad *et al.*, 2014). Interestingly, the number of nymphs was not significantly affected by the treatment in this study, which suggesting that the JA treatment might not affect early egg oviposition. However, the nymph to egg ratio on plants treated with the JA solution was significantly higher than plant treated with the control solution. This suggests that *B. cockerelli* adults on the JA treated plants laid a larger proportion of eggs early and laid a smaller proportion of eggs later whereas the *B. cockerelli* adults on the control plants laid similar proportion of early and later eggs. The effect of plant induced resistance against egg oviposition by *B. cockerelli* adults could be temporally dynamic.

The effects observed in our study could result from the interactions among pathogen, insect, and plant. Different pathogen-mediated effects could be envisioned resulting in decreased *B. cockerelli* fitness (Nachappa *et al.*, 2014), encouraging vector movement to seek better hosts and therefore enhancing pathogen dispersion (Fig. 2.5):

1. Pathogen-induced vector susceptibility to plant defense hypothesis (Fig. 2.5 blue arrow): presence of microorganisms (in this study Lso) could affect the susceptibility of the insect host to plant defenses. This is a direct effect of microorganisms on insect vector fitness. For example, Lso-positive *B. cockerelli*

could be more susceptible to plant defenses than Lso-negative *B. cockerelli*, in particular JA-mediated defenses.

2. Pathogen-induced plant defense against vector hypothesis (Fig. 2.5 red arrow): plant quality (nutritious value and defenses) could be modified upon vector-borne pathogen infection. A number of studies have indicated that vector-borne microorganisms can modify the quality of the host plant (Casteel et al., 2012; Wallis & Chen, 2012), which in turn affects the vector fitness (Stout *et al.*, 2006). This is an indirect effect of microorganisms on insect fitness mediated by changes in plant defenses. Under this hypothesis, plant infection by Lso upon *B. cockerelli* feeding modifies plant defenses which on JA elicited plants result in lower *B. cockerelli* fitness.
3. Pathogen-manipulated vector interaction with plant hypothesis (Fig. 2.5 yellow arrow): insect saliva could be modified by the associated microorganism resulting in induction of plant defenses. For example, presence of *Buchnera* GroEL in aphid saliva has been shown to negatively affect aphid fitness by triggering plant defenses (Chaudhary *et al.*, 2014). Under this hypothesis, the presence of Lso associated with *B. cockerelli* may modify the insect saliva, which in JA primed plants would result in enhanced induced defenses affecting *B. cockerelli* fitness.

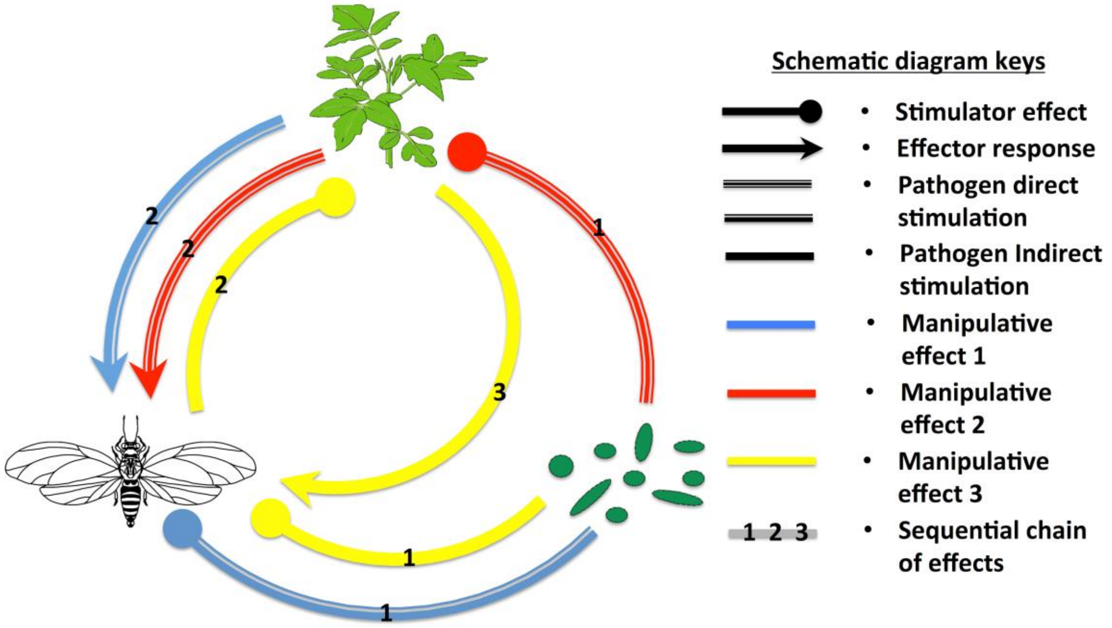

Figure 2.5 Potential mechanisms of plant response mediated by bacterial pathogens that reduce the vector fitness and encourage pathogen dispersion. The schematic diagram shows possible scenarios explaining pathogen (direct and indirect) manipulative effects on the vector: (1) pathogen-induced vector susceptibility to plant defense (blue arrows), (2) pathogen-induced plant defense against vector (red arrows), and (3) pathogen-manipulated vector interaction with plant (yellow arrows). The stimulator effect (dashed line) is initiated by the pathogen manipulating the plant or insect target. As a result of this manipulation, the pathogen affects the interaction between plant and insect (solid line); ● represents the initiation of the stimulus; ♦ indicates the target of the stimulus; and ➤ represents the plant response. Numbers represent the sequence of effects.

These hypotheses are not mutually exclusive. The effect of JA primed plants on Lso-positive *B. cockerelli* fitness could be mediated by several of the mentioned effects above. Therefore plant induced defenses and induced resistance against insects vectoring pathogens have a multitude of complex layers that need to be dissected to unravel the mechanisms of plant response to herbivory and infection.

This is the first study to distinguish the effect of plant-induced defenses from plant-induced resistance against Lso-positive and Lso-negative *B. cockerelli*. Other similar studies shown that plant-induced resistance against insects could be impacted by the presence of microorganisms (Davis et al., 2012; De Vos et al., 2005; Mayer *et al.*, 2008b; Wallis *et al.*, 2012). The microorganisms could mediate the effect of plant defenses on insect fitness directly and/or indirectly (Mayer et al., 2008a; Wielkopolan & Obrepalska-Steplowska, 2016). This study showed that JA-mediated plant induced defenses affected the temporal dynamic of oviposition by Lso-positive *B. cockerelli*. Therefore, teasing apart the mechanisms leading to plant induced resistance against *B. cockerelli* is an important first step for enhancing crop protection. Plant induced defenses is complex involving the interaction among different phytohormones and genes (Glombitza *et al.*, 2004; Robert-Seilaniantz *et al.*, 2011; Sendon *et al.*, 2011). Plant induced defenses can be elicited in response to specific target insect or elicited to protect against damages (Agrawal, 1998; Rosli & Martin, 2015; Stout *et al.*, 1998).

CHAPTER III

THE ROLE OF ACETYLSALICYLIC ACID IN PLANT INDUCED DEFENSES AND RESISTANCE AGAINST *BACTERICERA COCKERELLI* AND ‘*CANDIDATUS* LIBERIBACTER SOLANACEARUM’

3.1 Introduction

Within the last decade, potato psyllids *Bactericera cockerelli* (Hemiptera: Triozidae) have become a major agricultural pest (Crosslin et al., 2010). These insects were found associated with a newly emerging disease of potato called Zebra Chip in 2007 (Munyaneza et al., 2007). Zebra Chip was first documented in Mexico in 1994, in Texas in 2000 (Munyaneza et al., 2007), and in New Zealand in 2008 (Liefting et al., 2008; Teulon et al., 2009). However, it was not until 2008 that the causative agent of Zebra Chip was found. A Gram-negative bacterium named ‘*Candidatus* Liberibacter solanacearum’ (Lso), vectored by potato *B. cockerelli*, was identified to be the cause of the disease (Hansen et al., 2008; Liefting et al., 2008). In addition to infecting potato, this pathogen can infect and kill numerous solanaceous plants including tomato, pepper, eggplant, tamarillo, and Cape gooseberry (Liefting et al., 2008; Liefting et al., 2009). Since its first documentation, Lso has been detected in several new areas in North and Central America (Aguilar et al., 2013; Crosslin et al., 2012; Crosslin & Munyaneza, 2009; Munyaneza, 2012; Munyaneza et al., 2007; Munyaneza et al., 2013; Munyaneza et al., 2009b; Secor et al., 2009; Workneh et al., 2013) and New Zealand (Liefting et al., 2008; Teulon et al., 2009). In Europe, Lso is associated with carrots and celery (Alfaro-

Fernández et al., 2012; Munyaneza et al., 2010; Teresani et al., 2015; Teresani et al., 2014) where it is vectored by carrot psyllids.

The current and primary control strategy for Lso is to control the vector populations by pesticide applications. However, chemical control is not always effective. Farmers have reported up to 75% of crop losses despite insecticide application (Munyaneza, 2012). The effectiveness of the non-systemic pesticide application is limited to its coverage and capability to reach places where *B. cockerelli* are protected, such as the underside of the leaves. Moreover, the insect's rapid life cycle, three to four weeks from the egg to emerging adult (Yang et al., 2010), makes them prone to develop pesticide resistance. *B. cockerelli* populations in parts of Texas have already developed resistance against neonicotinoid insecticide. Imidacloprid, a systemic insecticide, was reported to be ineffective against *B. cockerelli* in both greenhouse and the field (Prager et al., 2013).

One potential solution to reduce crop losses is to enhance plant resistance against the insect vector or the pathogen. Plants can be manipulated to increase defenses against insects and pathogens by enhancing their immune system. With an enhanced immune system, plants can quickly respond to the pathogen infection and/or insect herbivory. For example, plants can induce apoptosis as hypersensitive response to reduce insect feeding and prevent pathogen infection (Jaouannet *et al.*, 2014; Levine et al., 1994; Morel & Dangl, 1997). Various chemical elicitors similar to plant defense hormones can be used to enhance plant defenses and induce resistance against insects (Heil & Bostock, 2002;

Thaler, 1999a; Thaler et al., 1996) and pathogens (Bokshi *et al.*, 2003; Karatolos & Hatcher, 2009; White, 1979). Induced resistance is an enhancement of the plant capacity to defend and withstand insect and/or pathogen attacks under a susceptible condition (Agrawal, 1999; Enkerli et al., 1993; Huot et al., 2013; Karban & Baldwin, 1997; Thaler, 1999a). The inducing agent can be abiotic or biotic (Karban & Baldwin, 1997; Ouchi, 1983; Thaler, 1999a). For example, aspirin (acetylsalicylic acid, ASA) is an abiotic agent that can induce plant resistance against phloem-feeding hemipterans (Karatolos & Hatcher, 2009) and against pathogens (White, 1979). ASA is a derivative of the defense phytohormone salicylic acid (SA). Salicylic acid induces the expression of plant *pathogenesis-related* (PR) genes for the activation of plant systemic acquired resistance (SAR) (Kessmann *et al.*, 1994) conferring higher resistance quality than in their prior susceptible state. SA plays a crucial role in plant induced defenses and induced resistance against herbivores and pathogens (An & Mou, 2011; Huot et al., 2013; Mandal *et al.*, 2009; Vlot *et al.*, 2009; Walling, 2000). However, the role of ASA on plant induced resistance remains poorly understood (Bokshi et al., 2003; Christ & Mosinger, 1989; Karatolos & Hatcher, 2009; Lopez *et al.*, 2001; White, 1979). Although ASA can induce PR proteins (Carr *et al.*, 1985; Jung *et al.*, 1993) and programmed cell death (Garcia-Heredia *et al.*, 2008), its link to plant induced resistance against insects and pathogens is poorly understood especially in the study of plant defense against bacterial pathogens.

The main objectives of this study were to assess the effect of ASA on tomato plants, *B. cockerelli* and Lso infection. The effect of ASA on plant induced resistance against *B. cockerelli* was measured using choice, non-choice, and survival bioassays. Lso infection was assessed following the bioassays. The role of ASA in the induction plant *PR* gene was subsequently tested to validate the induced of plant defense and to link to plant induced resistance. Although *B. cockerelli* herbivory and Lso infection are known to induce plant defensive genes and compounds (Casteel et al., 2012; Wallis et al., 2015), this is the first attempt to evaluate the effect of ASA on tomato induced resistance, on *B. cockerelli* and on Lso. This study can provide new insights into plant innate defenses against *B. cockerelli* using a stimulation approach to enhance plant immunity.

3.2 Materials and methods

3.2.1 Plant source

Tomato plants, *Solanum lycopersicum* cv. Moneymaker (Thompson & Morgan), were grown from seed in Sun Gro® Metro-Mix 900 soil and transplanted into 3.5-inch square pots four weeks later. Plants were watered and fertilized weekly according to the label rate of the Miracle-Gro® Water Soluble Tomato Plant Food (18-18-21 NPK). Six-week-old plants of similar size were used in all experiments described here.

3.2.2 Insect source

Bactericera cockerelli colonies (Central haplotype) were maintained in the laboratory at Texas A&M University, College Station on tomato plants. Colonies with Lso haplotypes A and B, and without Lso were kept in separate 14” x 14” x 24” insect cages (BioQuip Products Inc.) at room temperature and a photoperiod of 16:8 (Light: Dark) hours. These colonies were routinely tested for Lso infection using diagnostic PCR as regularly performed in our laboratory (Nachappa et al., 2012a). On average, 90% of the tested *B. cockerelli* from the colonies with Lso were Lso-positive, whereas none of the *B. cockerelli* from the colonies without Lso tested positive for Lso infection. The female to male ratio in each of these colonies was approximately 50:50.

3.2.3 ASA hydrolysis and plant priming

ASA was hydrolyzed in water to form salicylic acid (Kelly, 1970) by dissolving aspirin powder in double distilled water overnight. Six-week-old tomato plants were primed by three sprays (approximately 2 mL) with 0 mM, 0.35 mM, 1 mM, 5 mM, 10 mM, 25 mM, or 50 mM of ASA solution using small spray bottles. Plants were used the following day after priming. Sprays were repeated weekly for the duration of the bioassays to maintain the effect of plant induced defenses.

3.2.4 Choice study 1

Plants of similar size and node counts were randomly assigned to each of the seven ASA treatments (Fig. A.1). Plants were sprayed with one of the following ASA concentrations 0 mM, 0.35 mM, 1 mM, 5 mM, 10 mM, 25 mM, or 50 mM of ASA solution prepared as previously described, and caged together in a 61 x 61 x 61 cm with 54.6 cm per arch insect rearing tent (BugDorm). One day after spraying, 15 *B. cockerelli* adults from the Lso-positive colony and 15 *B. cockerelli* adults from the Lso-negative colony were introduced into each cage. For this experiment I used a mix of Lso-positive and Lso-negative insects to mimic the natural population with lower Lso frequency than the laboratory colonies. Nymphs and eggs of *B. cockerelli* on each plant were counted weekly for three weeks; counts represented the *B. cockerelli* colonization index on the host plants. The lower the average colonization index the more resistant the plant. Each plant received a re-application of the treatment solution after the number of *B. cockerelli* adults was recorded. Three replicates of experiments were conducted each time and the experiment was repeated twice to monitor the average *B. cockerelli* progeny on each plant.

3.2.5 Choice study 2

A second choice study was conducted using only plants treated with 0 mM and 1 mM of ASA solution. The two plants were caged with ten male and ten female *B. cockerelli* adults from the Lso-positive colony for one day. The number of adults and eggs on each plant were subsequently counted. Four trials of experiment were conducted using a total of 30 cages and 60 plants.

3.2.6 No-choice study

Tomato plants were sprayed with one of the following ASA concentrations: 0 mM, 0.35 mM, or 1 mM prepared as previously described, and were caged individually in 12” cube observation cages (BioQuip Products Inc.). Twenty-four hours after the spray, 10 *B. cockerelli* adults from a Lso-positive colony were released into each cage.

The numbers of *B. cockerelli* progeny (nymphs and eggs) on each plant were recorded weekly for four weeks. The infestation rate was calculated using the one, two, and three weeks post-infestation counts. Infestation rate (IR) was defined as the change in total number of *B. cockerelli* eggs and nymphs on plants over an interval of time, and it was calculated as follows: $IR = (Ln(P_{T2}) - Ln(P_{T1}))/(T2-T1)$, where P_{T2} describes the *B. cockerelli* population on plants at time 2 (T2) and P_{T1} describes the *B. cockerelli* population on plants at time 1 (T1) (Newbold, 2010). Short-term infestation rate was calculated based on the difference between second and first week data whereas long-term infestation rate was calculated based on the difference between third and first week data. Each experimental trial consisted of three replicates per treatment. Four trials of the experiment were conducted. The infestation rate was used to evaluate the change in *B. cockerelli* population over time after the initial colonization. While a positive rate indicates population proliferation, a negative rate indicates population decay. The lower the rate the more resistant the plants.

3.2.7 Nymphal survival study

To evaluate the effect of ASA on nymphal survival, ten third-instar *B. cockerelli* nymphs from the Lso-infected colony were placed on the middle leaflet of the top most-fully expanded leaf of tomato plants previously sprayed with 0 mM or 1 mM of ASA. The nymphs of *B. cockerelli* were observed for two minutes for movement to verify their survival after the transfer or replaced otherwise. The nymphs of *B. cockerelli* were then caged in a clip cage (BioQuip Products Inc.) propped up by a bamboo stick. After seven days, the clip cages were removed and the numbers of adults and of each developmental instar on the plants were recorded. There were seven plants in each ASA treatment.

3.2.8 DNA extraction and Lso detection by PCR

Presence of Lso in *B. cockerelli* was assessed by PCR as previously published (Nachappa *et al.*, 2011). To assay Lso infection in plants, approximately 0.1 g of petiole and mid-vein tissues of the top-most fully-expanded leaf from each plant in the *Choice study 1* and *No-choice study* were collected three weeks after the plants were exposed to Lso-positive *B. cockerelli*. DNA extraction and diagnostic PCR to detect Lso were performed as previously published (Levy *et al.*, 2011), using primers targeting Lso *16S ribosomal RNA* gene (Nachappa et al., 2011) and *S. lycopersicum elongation factor 1* (*EF1*) (Nachappa et al., 2014) (Table 3.1).

Table 3.1 ***Solanum lycopersicum*** **primer sets used for diagnostic PCR and quantitative RT-PCR.**

Target gene, NCBI accession number	**Primer Name**	**Primer Sequence**	**Amplicon size (bp)**	**Efficiency (%)**
Lso PRR1 16S ribosomal RNA, EU812559	CLs16S_F	5'-ATGCAAGTCGAGCGCTTATT-3'	1100	NA
	CLs16S_R	5'-CGAGCGCTTATTTTTAATAGGAGC-3'		
S. lycopersicum elongation factor 1-alpha, NM_001247106	TomEF1_F	5'-AGATGGTCAGACCCGTGAAC-3'	435	NA
	TomEF1_R	5'-GTCAAACCAGTAGGGCCAAA-3'		
S. lycopersicum 18S ribosomal RNA, GQ280796.1	Tom18s_F	5'-AGAAACGGCTACCACATCCA-3'	157	100%
	Tom18s_R	5'-GCCCTCCAATGGATCCTC-3'		
S. lycopersicum pathogenesis-related protein 1 (PR1b1), NM_001247385	TomPR1 F	5'-TCTTGCGGTTCATAACGATG-3'	289	100%
	TomPR1 R	5'-GACTGAGTTGCGCCAGACTA-3'		

NA: not applicable.

3.2.9 Expression of pathogenesis-related 1 gene by qRT-PCR

Six-week-old *S. lycopersicum* plants were individually sprayed with 0 mM or 1 mM of ASA and re-treated weekly as described previously, when applicable. After one day, plant tissue from the top most-fully expanded leaf was excised, flash-frozen, and stored at -80 ^{o}C. The experiment was repeated on another set of plants, but tissues were collected 10 days after the initial treatment. Six plants per treatment were assayed within each time point to evaluate the short (1 day)- and long (10 days)-term effects of the ASA treatments on the expression of *pathogenesis-related 1* gene (*PR1*). Each biological sample was assayed in duplicate by qRT-PCR.

Plant tissues were finely homogenized in a 1.5 mL tube with TRIzol® Reagent (Life Technologies, Carlsbad, CA, USA) using sterile plastic pestles (Thermo Fisher Scientific Inc., Waltham, MA, USA) powered by the handheld motor. Total RNA was purified according to the manufacturer's protocol. RNA concentrations were quantified using Infinite® 200 PRO NanoQuant (Tecan, San Jose, CA, USA). RNA integrity was evaluated by gel electrophoresis. Potential DNA contamination was removed using TURBO DNA-free^{TM} Kit (Life Technologies, Carlsbad, CA, USA).

Quantitative RT-PCR (RT-qPCR) was performed in a CFX96 Real-Time PCR Detection System (Bio-Rad Inc.) using SensiFast SYBR Hi-ROX One-Step Kit following the manufacturer's protocol. Briefly, each RT-qPCR was performed in a 10 μL reaction using 5 μL of 2x SensiFast SYBR HI-ROX One-Step mix, 0.4 μL of each primer (10 μM each), 0.1 μL of reverse transcriptase, 0.2 μL of RiboSafe RNAse Inhibitor, 2.9 μL of DEPC-H_2O, and 1 μL of 100 ng/μL RNA. The RT-qPCR was done as suggested by the manufacturer: 45 °C for 10 mins for reverse transcription, 95 °C for 2 mins for polymerase activation, and 40 cycles of 95 °C for 5s, 60 °C for 10s, and 72 °C for 5s. Amplification and melting curve were verified to validate the results. Primer efficiency was estimated according to the published method using LinRegPCR 11.1 (Ruijter et al., 2009). The relative gene expression was calculated according to the published Delta Delta CT method (Livak & Schmittgen, 2001). *S. lycopersicum 18S ribosomal RNA* gene (GQ280796.1) was used as normalizer gene (Casteel et al., 2012) and *pathogenesis-related 1* gene (PR1) was used as a marker gene for SA-mediated plant defense (Maleck *et al.*, 2000; Molinari *et al.*, 2014; Wildermuth *et al.*, 2001) (Table 1).

3.2.10 Plant biomass assay

To evaluate the effect of ASA treatment on plants, *S. lycopersicum* roots and shoots were collected three and half weeks and four weeks after the start of the *Choice study 1* and the *No-choice study*, respectively. The roots were gently cleaned to remove soil. Shoots and roots were placed at 60 ºC in a drying oven for two days before measuring the plant dried biomass.

3.2.11 Statistical analyses

All data analyses were conducted using JMP$^{®}$ Pro v.10. Shapiro-Wilk W test was used to test for normality prior to conducting parametric tests. Non-parametric analyses (Wilcoxon or Kruskal-Wallis) were used for non-normal data while parametric analyses (ANOVA or t-test) were used for normal data. When a significant difference was detected ($p<0.05$) in a statistical test, a post-hoc analysis was conducted to determine the difference between or among the treatments. Percent differences between the treatments were calculated using the means of the control group and the treatment group. Ratio associated data were transformed using arcsine transformation prior to conducting statistical analyses. To determine if infection frequency was dependent on the treatments, a contingency analysis using Chi-Square test of independence was performed.

3.3 Results

3.3.1 Choice study 1: identification of ASA does affecting B. cockerelli

In order to identify ASA doses that might affect tomato induced resistance against *B. cockerelli* without affecting tomato bioamass, a choice bioassay testing seven ASA concentrations was performed. In the seven-choice experiment, a significant effect of ASA treatment was found on the total number of *B. cockerelli* eggs and nymphs (colonization index) on plants at each time point: 1 week (H = 14.5, 6 d.f., $P = 0.0249$), 2 weeks (H = 29.8, 6 d.f., $P < 0.001$) and 3 weeks (H = 29.3, 6 d.f., $P < 0.001$) (Table 3.2). Plants treated with ASA on average had 35-93%, 49-100%, and 62-100% fewer eggs and nymphs than the control plants after one, two and three weeks, respectively. At any given infestation interval within the measured three weeks, the number of *B. cockerelli* offspring (eggs and nymphs) on the 0 mM treated (control) plants was on average two- to three-fold higher than those on plants treated with 0.35 mM of ASA, and three- to four-fold higher than on plants treated with 1 mM of ASA. The effect was greater when control plants were compared to plants treated with higher ASA concentrations suggesting that plants primed with ASA solution were significantly more resistant against *B. cockerelli* colonization than plants primed with water solution.

Table 3.2 The effect of acetylsalicylic acid (ASA) on plant resistance against *B. cockerelli* colonization.

ASA treatments	1 week	2 weeks	3 weeks
0 mM	102 ± 29.0	161.3 ± 59.3	150.2 ± 66.0
0.35 mM	66.5 ± 39.7	82.5 ± 38.6	57.7 ± 27.5
1.00 mM	28.3 ± 18.5	58.8 ± 22.2	37.2 ± 7.3
5.00 mM	12.7 ± 5.5	12.2 ± 6.6*	10.3 ± 6.9
10.00 mM	9.0 ± 3.2	3.2 ± 3.2*	0.0 ± 0.0*
25.00 mM	2.7 ± 1.2*	0.0 ± 0.0*	0.0 ± 0.0*
50.00 mM	7.5 ± 2.3	0.0 ± 0.0*	0.0 ± 0.0*

Mean (±SE) *B. cockerelli* infestation index on plants one, two, and three weeks after colonization was used to evaluate host plant resistance. Symbols * indicate significant differences at $P < 0.05$ following a post-hoc test comparison of control (0 mM) to ASA (0.35mM, 1 mM, 5 mM, 10 mM, 25 mM, or 50 mM).

When the treatment effect was analyzed separately on the number of eggs and on the number of nymphs, the significant effect across times remained. The ASA treatments had a significant effect on the number of eggs on each plant after one week (H =14.42, 6 d.f., $P = 0.0252$, Fig. 3.1A), two weeks (H =23.04, 6 d.f., $P < 0.0008$, Fig. 3.1B), and three weeks (H = 14.44, 6 d.f., $P = 0.025$, Fig. 3.1C). The ASA treatments also had a significant effect on the number of nymphs on each plant after one week (H = 13.47, 6 d.f., $P = 0.036$, Fig. 3.1D), two weeks H = 28.25, 6 d.f., $P < 0.0001$, Fig. 3.1E), and three weeks (H = 31.044, 6 d.f., $P < 0.0001$, Fig. 3.1F). There was a significant effect of the treatment across times (Fig. 3.1A-C and 3.1D-F), suggesting that ASA treated plants were more resistant than the control (0 mM) plants.

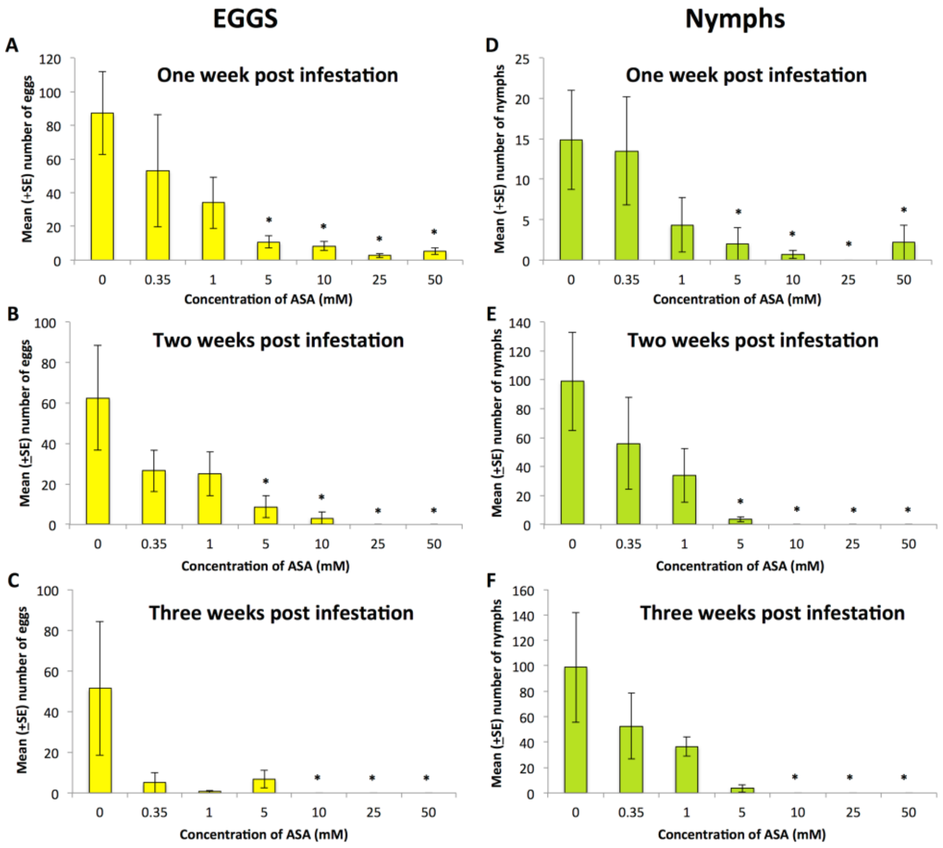

Figure 3.1 Role of ASA-mediated plant induced resistance against *B. cockerelli*. (A) Mean number (±SE) of *B. cockerelli* eggs on *S. lycopersicum* plants after one week ($P = 0.025$). (B) Mean number (±SE) of *B. cockerelli* eggs on *S. lycopersicum* plants after two weeks ($P < 0.0008$). (C) Mean number (±SE) of *B. cockerelli* eggs on *S. lycopersicum* plants after three weeks ($P = 0.025$). (D) Mean number (±SE) of *B. cockerelli* nymphs on *S. lycopersicum* plants after one week ($P = 0.036$). (E) Mean number (±SE) of *B. cockerelli* nymphs on *S. lycopersicum* plants after two weeks ($P < 0.0001$). (F) Mean number (±SE) of *B. cockerelli* nymphs on *S. lycopersicum* plants after three weeks ($P < 0.0001$). Symbols * indicate significant differences at $P < 0.05$ following a post-hoc test comparison of control (0 mM) to ASA (0.35mM, 1 mM, 5 mM, 10 mM, 25 mM, or 50 mM).

The ASA solution that enhances plant resistance against insects can also affect plant growth, development and performance due to auto-toxicity and/or resource cost. To evaluate plant performance under different dosages of ASA, dried shoot and root biomass were compared at the end of the choice experiment (three weeks after the first ASA spray). There was no significant effect of the treatment on plant shoot dried biomass (H =10.47, 6 d.f., *P* = 0.106, Fig. A.2A). However, there was a significant effect of the treatment on plant root dried biomass (H = 16.16, 6 d.f., *P* = 0.0129, Fig. A.2B). The reduction in belowground growth could be visualized as shown in Fig. A.2D. Plants exposed to high ASA concentrations (25 mM and 50 mM) on average had 76-78% lower dried root biomass than plants in the control treatment (0mM). ASA had no effect on plant roots in the low concentration treatments (0.35 and 1 mM ASA) when compared to the control (0 mM) (Fig. A.2B). Also, the effect of the treatment on root to shoot dry biomass ratio showed a similar response as the root dried biomass (H =18.29, 6 d.f., *P* = 0.005, Fig. A.2C). Furthermore, high ASA concentrations appeared to affect plant mortality during the experiment (Table A.1).

3.3.2 No-choice study

The infestation of *B. cockerelli* on a host plant can change in a temporal manner depending on the infestation rate of *B. cockerelli*. Thus, the no-choice study was conducted to evaluate *B. cockerelli* infestation rate in response to the ASA-mediated plant induced resistance. No significant change in short-term infestation rate (Z = 1.07, *P* = 0.285) or in long-term infestation rate (Z = 1.13, *P* = 0.260) of *B. cockerelli* was found between plants treated with 0 mM (control) and plants treated with 0.35 mM of ASA (Fig. 3.2). However, significant changes in short-term (Z = 2.05, *P* = 0.040) and in long-term infestation rates (Z = 1.99, *P* = 0.046) of *B. cockerelli* were found between 0 mM and 1 mM ASA treated plants (Fig. 3.2). These results indicate that plants treated with 1 mM of ASA displayed significantly lower infestation rates of *B. cockerelli* in both the short- and the long-term than plants treated with 0 mM of ASA. While plants treated with 0 mM and 0.35 mM of ASA showed mean positive rates representing an increase in *B. cockerelli* population, plants treated with 1 mM of ASA showed mean negative rates representing a decrease in *B. cockerelli* population within both short- and long-terms. Plants treated with 1 mM of ASA had lower average number of *B. cockerelli* and were more resistant than plants treated with 0 mM of ASA.

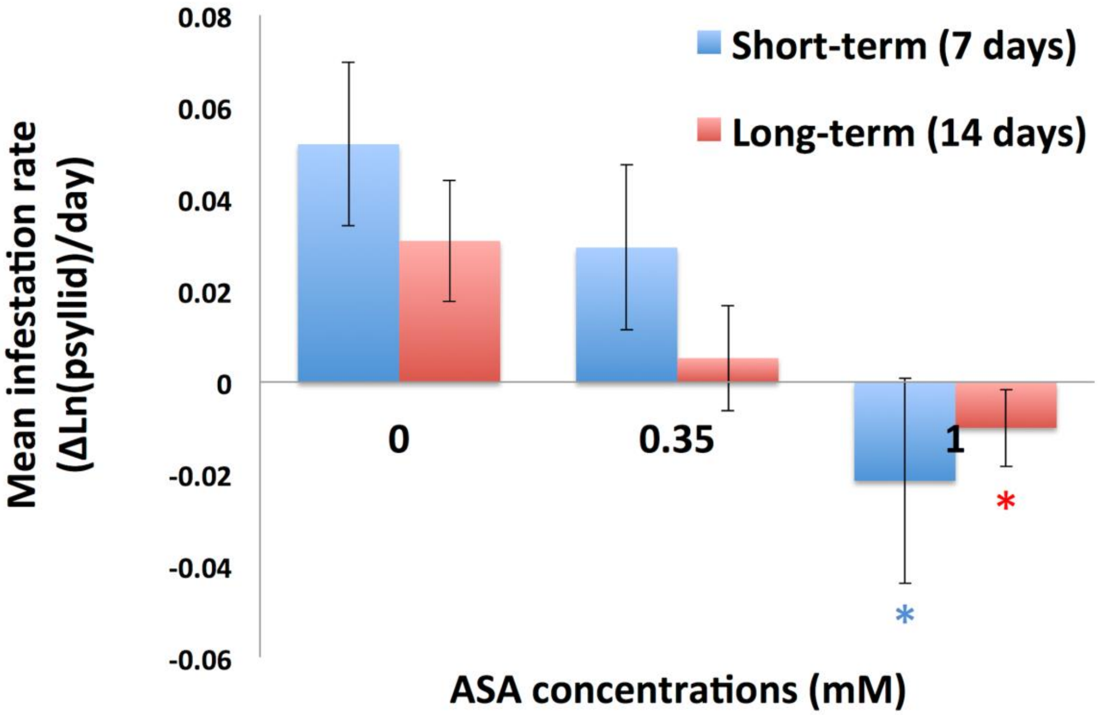

Figure 3.2 The effect of 0.35 mM and 1 mM ASA treatment on short- (7 days) and long-term (14 days) infestation rate of *B. cockerelli*. Mean (±SE) infestation rates (ΔLn (*B. cockerelli*)/day) within 7 days interval and within 14 days interval. ASA treatment of 0.35 mM had no significant effect on the short-term (P = 0.285) and long-term (P = 0.260) infestation rates of *B. cockerelli*. ASA treatment of 1 mM significantly affected short- (P = 0.040) and long-term infestation rates of *B. cockerelli* (P = 0.046). A positive rate value represents an increase in *B. cockerelli* population over time while a negative rate value represents a decrease in *B. cockerelli* population over time. Symbols * indicate significant differences at $P < 0.05$ compared to the 0 mM treatment.

Similar to the choice study 1, plant-dried biomass was measured at the end of the experiment to validate the absence of ASA effect on plant performance (four weeks after the initial treatment). No significant differences were found between the control group (0 mM ASA) and the ASA groups (0.35 and 1 mM ASA) for shoot dry biomass (0 mM vs 0.35 mM ASA: Z = 0.18, P = 0.860; 0 mM vs 1 mM ASA: Z = 0.353, P = 0.724, Fig.

3.3A) nor for the root dry biomass (0 mM vs 0.35 mM ASA: Z = 0.795, *P* = 0.427; 0 mM vs 1 mM ASA: Z = 1.37, *P* = 0.171, Fig. 3.3B). Similarly, the root to shoot dry biomass ratio was not significantly affected by 0.35 mM ASA (Z = 0.618, *P* = 0.537, *P* = 0.508, Fig. 3.3C) nor by 1 mM ASA (Z = 0.618, *P* = 0.537, Fig. 3.3C). Hence, plant performance (function of biomass) was not affected by low concentrations of ASA spray.

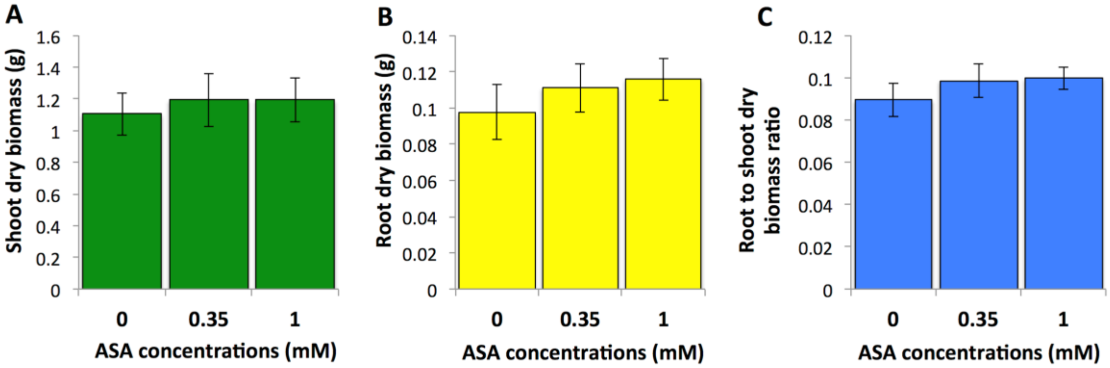

Figure 3.3 Effect of ASA on *S. lycopersicum* shoot and root biomass in the no-choice study. (A) Mean (±SE) shoot dry biomass, (B) Mean (±SE) root dry biomass, and (C) Mean (±SE) root to shoot dry biomass ratio. No significant effects of the treatments were measured.

3.3.3 Nymphal survival study

In an effort to understand the effect of ASA treated plants on the survival of *B. cockerelli* nymphs, ten third-instar *B. cockerelli* nymphs were transferred onto each plant previously primed with either 0 mM or 1 mM of ASA (control), and they were allowed to feed on the host plant for a week. The development and mortality of 120 *B. cockerelli* nymphs were monitored after seven days. At the end of the experiment, *B. cockerelli* mortality was significantly higher on plants treated with 1 mM of ASA (58.57%) than on plants treated with 0 mM of ASA (38.57%) (t (12) = 1.46, *P* = 0.043, Fig. 3.4A). This suggests that plants primed with 1 mM of ASA were more resistant to *B. cockerelli* than plant primed with 0 mM of ASA. The number of nymphs on plants after one week was not significantly different (t (12) = 0.59, *P* = 0.141, Fig. 3.6B) but the mean number of adults per plant was significantly higher on the 0 mM treated plants than 1 mM treated plants (Z = 2.09, *P* = 0.036, Fig. 3.4C). Thus, the ASA treatment can affect *B. cockerelli* life stage composition within the populations (e.g. ratio of immature to mature insects). On average, 0 mM treated plants had five times more adults than the 1 mM treated plants. Out of the surviving *B. cockerelli*, there were more adults than immature *B. cockerelli* on the 0 mM treated plants whereas there were more nymphs than adults on the 1 mM treated plants. The percentage of surviving *B. cockerelli* nymphs that became adults was also significantly higher (t (12) = 2.24, *P* = 0.011, Fig. 3.4D) on the 0 mM plants (57.62%) than the 1 mM plants (16%). This suggests that ASA treatment affected *B. cockerelli* development since there were more third instar *B. cockerelli* that developed to adult on the 0 mM treated plants than on the 1 mM treated plants. As a result, ASA not only enhanced plant resistance by reducing overall *B. cockerelli* survival but also reduced the percentage of *B. cockerelli* that developed into adults.

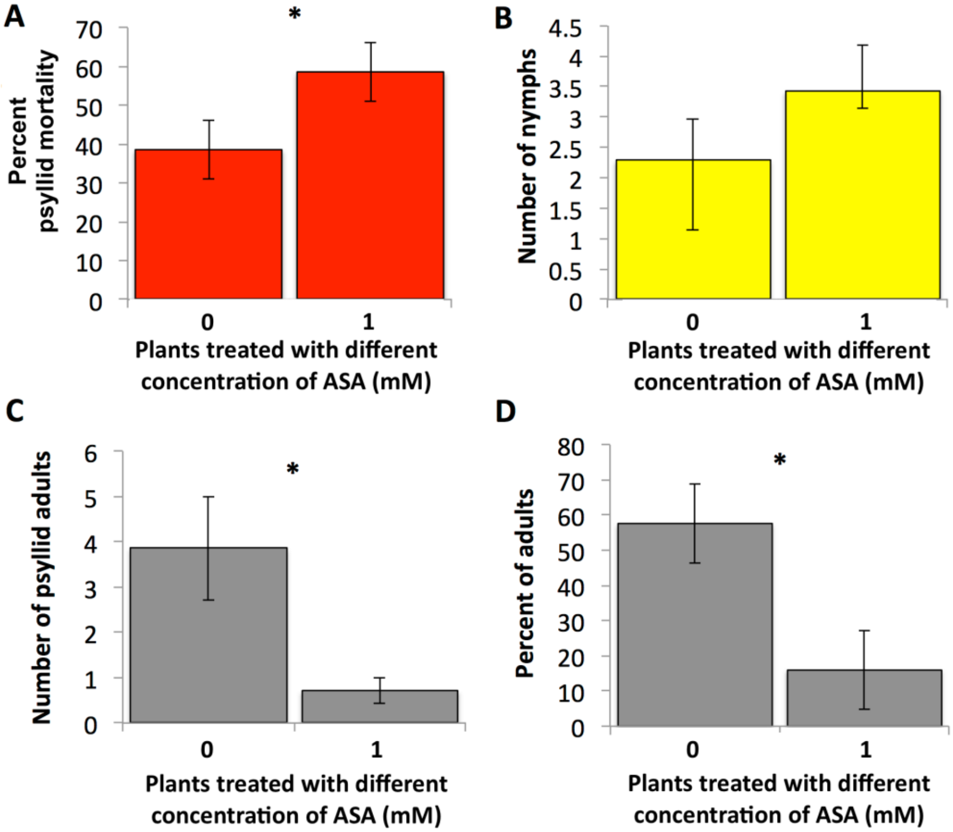

Figure 3.4 Effect of ASA-mediated plant resistance on *B. cockerelli* survival and development. (A) Mean (±SE) *B. cockerelli* mortality (one-side t-test: $P = 0.043$). (B) Mean (±SE) number of *B. cockerelli* nymphs after one week on ASA or water treated plants (one-side t-test: $P = 0.141$). (C) Mean (±SE) number of *B. cockerelli* adults on ASA or water treated plants after seven days (Wilcoxon: $P = 0.036$). (D) Mean (±SE) percentage of surviving *B. cockerelli* that reached adulthood on each plant (one-side t-test: $P = 0.011$). Symbols * indicate significant differences at $P < 0.05$.

3.3.4 The effect of ASA on Lso infection

In the *choice study I*, lower Lso infection frequency was found in plants treated with 0.35 mM ASA (4 of 6 plants were infected, 66.7%) and 1 mM ASA (5 of 6 plants were infected, 83.3%) than plants treated with 0 mM (6 of 6 plants were infected, 100%) of ASA (Table A.2).

In the *no-choice study* in which the starting number of *B. cockerelli* in the cages was controlled, the infection frequency was depended on the ASA concentration. Although no difference between the 0.35 mM of ASA and the 0 mM treatments (X^2 (1, N = 24) = 0.254, *P* = 0.615), a significant difference was found between 1 mM of ASA and the 0 mM treatments (X^2 (1, N = 24) = 0.254, *P* = 0.041, Fig. 3.5) in the contingency analyses. Lso was detected in 75% of the 0 mM of ASA treated plants, in 83.3% of the 0.35 mM of ASA treated plants and in 33.3% of the 1 mM of ASA treated plants (Table A.3). The lower percentage of plants testing positive for Lso in the 1 mM of ASA treatment may not be due to the reduced number of *B. cockerelli* but may be due to the enhancement of plant defenses since there was no significant difference in the average number of *B. cockerelli* found between the Lso-positive and Lso-negative plants (Fig. 3.6). While only 12 plants per treatment were evaluated, plants treated with 1 mM of ASA had a lower percentage of plants tested positive for Lso, in each of the four experimental trail, compared to plants in other treatment (Table A.4). This suggests a consistency in lower Lso infection found in plants treated with 1 mM of ASA.

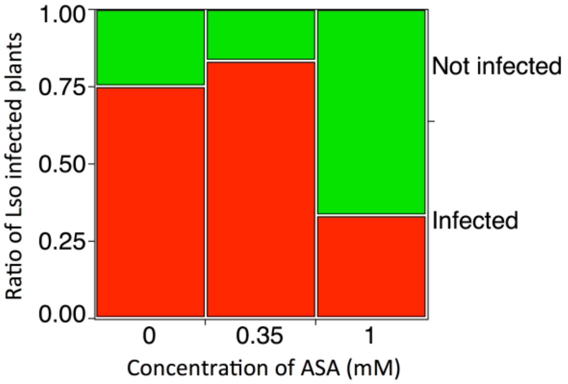

Figure 3.5 The impact of ASA spray on plant resistance to Lso infection. Mosaic plots containing the ratio of plants in which Lso was detected by PCR (red corresponds to plants in which Lso was detected and green are plants in which Lso was not detected). Contingency analyses of plant infection showed no significant effect of 0.35 mM of ASA (Chi-Square test of independence: *P* = 0.615), but showed a significant effect of 1 mM of ASA when compared to the control (Chi-Square test of independence: *P* = 0.041).

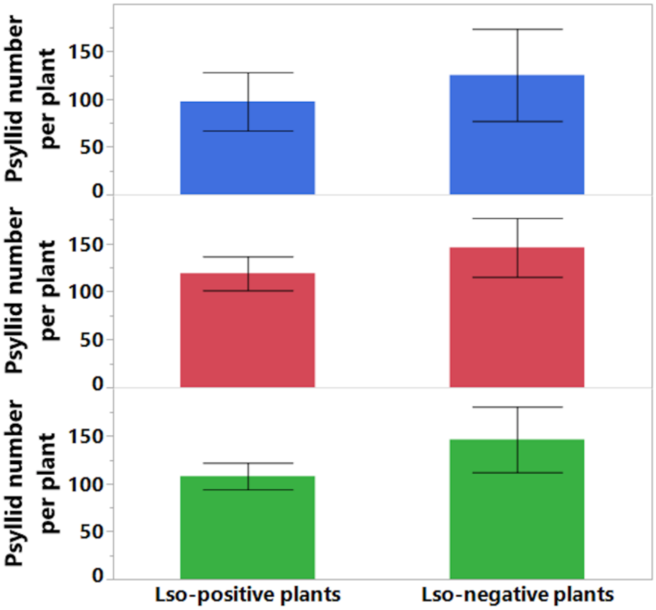

Figure 3.6 Pathogen infection in plant was independent on the number of *B. cockerelli*. Lso-positive and Lso-negative plants did not have significant different number of *B. cockerelli* at week 1 (Z = 0.87, *P* = 0.383, blue), week 2 (Z = 0.66, *P* = 0.510, red), or week 3 (Z = 0.725, *P* = 0.469, green).

3.3.5 Expression of pathogenesis-related gene study

To potentially link the effects of ASA on plant induced defenses to plant induced resistance against *B. cockerelli* and Lso, the expression of *PR1*, a marker gene for SAR and SA defense pathway was tested in plants treated with 0 mM and 1 mM of ASA. Short- (1 day) and long- (10 days) term expression of *PR1* gene was analyzed to evaluate plant induced defenses over time. The results showed that the expression *PR1* gene was significantly higher in plants treated with 1 mM of ASA than in plants treated with 0 mM of ASA in both short- (Z = 2.65, *P* = 0.0081, Fig. 3.7A) and long-term (Z = 2.80, *P* = 0.0051, Fig. 3.7B) evaluation. Thus, plants primed with 1 mM of ASA solution had enhanced defenses by mean of up-regulating the expression of *PR1* gene for SAR as predicted previously. This enhanced systemic defense was significant at day one and remained significant at day ten but at a lower effect size. The ASA solution up-regulated the expression of *PR1* gene by 128 folds at day one (Fig. 3.7A) and by 6 folds at day ten (Fig. 3.7B). This result showed that the induction of *PR1* as a marker for salicylate defenses was temporally dynamic.

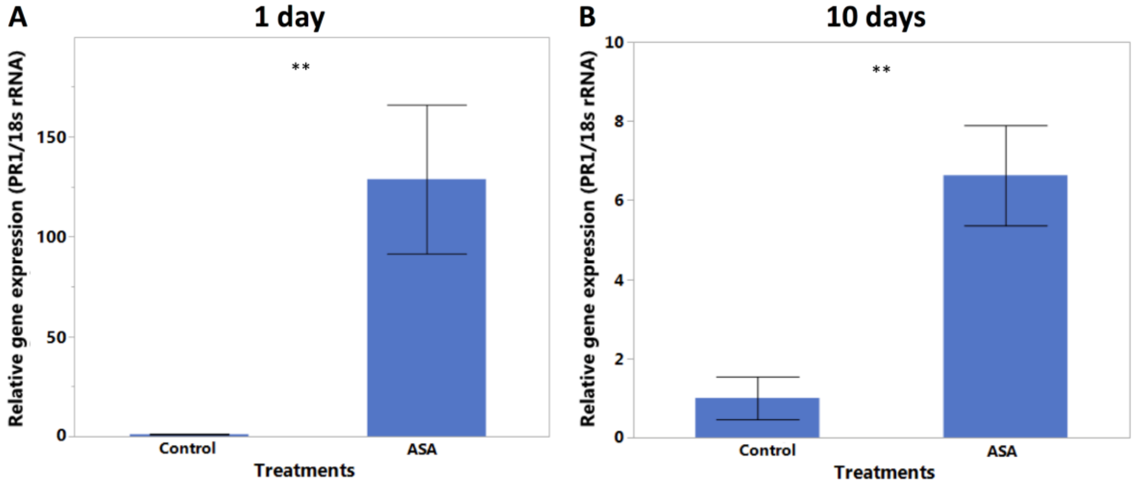

Figure 3.7 Effect of ASA on the expression of *pathogenesis-related 1* (*PR1*) gene, a marker gene for systemic acquired resistance. (A) Relative expression of *PR1* gene in *S. lycopersicum* one day after the ASA treatment. (B) Relative expression of *PR1* gene in *S. lycopersicum* at day 10. Symbol ** represents significant level at *P* <0.01.

3.3.6 Choice study 2: validating the effect of 1 mM ASA on psyllid preference

Since 1 mM of ASA up-regulated the expression of *PR1*, reduced the survival and infestation rate of *B. cockerelli*, the effect of 1 mM of ASA on plant induced resistance was further verified using *B. cockerelli* populations of five males and five female to control for sex ratio. In this two-choice experiment, I assessed if 1 mM of ASA could affect *B. cockerelli* preference. Plants treated with 1 mM of ASA had significantly lower number of adults (t (60) = 2.97, *P* = 0.004, Fig. 8A) and eggs (t (60) = 3.38, *P* = 0.001, Fig. 8B) than plants treated with 0 mM of ASA. On average, plants treated with 0 mM of ASA had 33.7% more adults and 60.6% more eggs per plant than plants treated with 1 mM of ASA. Thus, plants treated with 1 mM of ASA were more resistant against *B. cockerelli* than plants treated with 0 mM of ASA.

3.4 Discussion

The results from the choice assay indicated that plants treated with 1 mM of ASA or higher had the lower the number of *B. cockerelli* eggs and nymphs than plants treated with 0 mM of ASA. This implies that ASA could enhance plant resistance against *B. cockerelli* by reducing *B. cockerelli* colonization preference. However, population of *B. cockerelli* on the plant can change over time depending on the rate of oviposition and/or nymphal survival (infestation rate). Thus, no-choice study was conducted to evaluate the infestation rate of *B. cockerelli*. Results from this study also suggested that ASA also enhanced plant resistance but only in a concentration-dependent manner. Only plants treated with 1 mM of ASA were more resistant than plants treated with 0 mM of ASA. Similar to ASA, other chemical elicitors induced plant defenses and resistance against insects in a concentration-dependent manner (Thaler, 1999b; Thaler et al., 1996). The effectiveness of a particular dosage (concentration) may also be predicated by the temporal dynamic of plant immune defenses and/or level of defense phytohormones in the plants (Erb *et al.*, 2012).

Since ASA is a derivative of SA and ASA induced *PR1* gene similar to SA, ASA potentially induced salicylate defense resulting in enhanced plant resistance. Thus, the expression of *PR1*, a marker gene for SAR and SA defense pathway (De Vos et al., 2005; Garcion & Métraux, 2007; Maleck et al., 2000; Molinari et al., 2014; Wildermuth et al., 2001; Zhu *et al.*, 2012), was tested in plants treated with 0 mM and 1 mM of ASA to evaluate the temporal dynamic of plant induced defenses. The expression of *PR1* in plants one day and ten days after treated with ASA solution was evaluated. The gene expression result indicated that treatment of 1 mM of ASA significantly up-regulated *PR1* for salicylate defense. The effect size of *PR1* expression in plants after one day was at least ten folds higher than that in plants after ten days. This result verified that (1) ASA induced plant defenses by up-regulating the expression of *PR1*, (2) the induction of plant defenses by ASA is temporally dynamic, and (3) the induction of plant defenses by ASA is associated with the reduction of *B. cockerelli* number on plants. Previous studies also showed that solution of ASA can induce the expression of *PR1* in the salicylate defense pathway (Carr et al., 1985; Jung et al., 1993) and enhanced plant resistance against phloem-feeding hemipterans (Karatolos & Hatcher, 2009). The high mortality of *B. cockerelli* nymphs on plants treated with 1 mM of ASA could be associated with the induction of plant defenses by ASA. Salicylate defense pathway, as it was shown induced by the ASA treatment, plays an important role in plant immunity (An & Mou, 2011) and plant induced defenses against insects and pathogens (Cueto-Ginzo *et al.*, 2016; Karban & Baldwin, 1997; Schaller, 2008). Several publications indicate that the increase of salicylic acid by a chemical elicitor like ASA can trigger the production of plant secondary compounds involved in plant immunity (Karban & Baldwin, 1997; Kessmann et al., 1994; Schaller, 2008; Walling, 2000). Interestingly, salicylate defense also play important role in insect deterrence. For example, methyl salicylate has been known to deter insects and inhibit the oviposition response (Ulland *et al.*, 2008), which may be explained the lower average number of *B. cockerelli* on plants treated with 1 mM of ASA in the choice studies.

The reduction of *B. cockerelli* number can decrease incidence of infection but may not necessarily protect plants from bacterial infection (Levy & Tamborindeguy, 2014). For example, pathogens transmitted by insects can infect and cause diseases if plant specific defenses are not induced to prevent the infection and limit the spread of the pathogen in plant system. For this reason, plants exposed to Lso-positive *B. cockerelli* were tested to verify the enhancement of plant resistance against Lso in response to the ASA treatment. When compared to plants treated with 0 mM of ASA, plants treated with 1 mM of ASA had lower frequency of Lso infection. This lower frequency of infection was not attributed to the reduction of *B. cockerelli* number on the tested plants since there was no significant difference in the number of *B. cockerelli* on Lso-negative and Lso-positive plants. This suggests that *PR1* induced by ASA could also enhance plant resistance against bacterial pathogen in addition to the insect vectors. *Pathogenesis related gene 1* not only plays an important role in systemic acquire resistance against insects but also plays an important role in plant defenses against bacterial pathogens (An & Mou, 2011; Molinari et al., 2014).

Interestingly, there is a cost of inducing plant defenses (Karban & Baldwin, 1997). The elicitors of plant defense hormones like ASA are acidic by nature and tend to elicit acidic defensive compounds in plants. At high concentration, these elicitors of plant defense can have an adverse effect on plant growth and development (Thaler, 1999a; Thaler et al., 1996). This tradeoff effect between plant growth and defense was extensively reviewed (Karban & Baldwin, 1997; Schaller, 2008; Zavala *et al.*, 2004). Briefly, the resource availability and plant optimal defense hypotheses indicate that allocation of resources for defense is done at the detriment of growth and development since plants have finite resources (Coley *et al.*, 1985; Karban & Baldwin, 1997). Furthermore, the antagonism between the SA and auxin signaling pathways (Wang *et al.*, 2007) may explain the observed reduction of root biomass in the ASA-treated plants since auxin is a phytohormone that promotes root growth (Fu & Harberd, 2003).

Plants treated with 1 mM of ASA had higher *B. cockerelli* mortality than plants treated with 0 mM of ASA. Mortality of *B. cockerelli* was associated with the reduction in *B. cockerelli* infestation rate in plants treated with 1 mM of ASA. The observed increased in *B. cockerelli* mortality was not only linked to the reduction in plant infestation rate on the plants treated with 1 mM of ASA but also associated to lower *B. cockerelli* colonization preference observed in the choice study. Also, plants treated with 1 mM of ASA had lower Lso infection frequency than plants treated with 0 mM of ASA. Yet, the link between the reduction of *B. cockerelli* infestation rate and the reduction in Lso infection frequency could not be established since no significant differences were observed in the mean number of *B. cockerelli* on Lso-negative and Lso-positive plants. Thus, reduction in Lso infection found in plants treated with 1 mM of ASA could be the result of the enhanced plant defenses not only against the insect vectors but also plant defenses against the pathogens carried by the vectors. Priming *S. lycopersicum* plants with 1 mM of ASA could enhance plant SAR against the vectors and pathogens in this study.

In conclusion, this study suggests that the dynamic role of plant induced resistance against *B. cockerelli* and Lso was mediated by the ASA treatment. At 1 mM, ASA enhanced plant resistance against *B. cockerelli* colonization as evidenced by the reduced *B. cockerelli* infestation preference in choice studies and the reduced infestation rate in the no-choice study. These reductions of infestation rate on and preference for ASA treated plants were linked to a significant reduction of *B. cockerelli* survival in the survival study. This implies that 1 mM of ASA enhanced plant resistance to the *B. cockerelli*. This concentration also reduced frequency of Lso infection in plants, but it did not confer full protection since plants can still be infected with Lso. The full mechanism of plant induced resistance mediated by ASA is yet clear but ASA as a derivative of salicylate acid up-regulated the expression *PR1,* a marker gene for salicylate defense. Further studies are may be needed to evaluate the mechanism associated with effect of ASA on salicylate defense and on plant resistant against *B. cockerelli*. This is a first look on the effectiveness of ASA on plant protection against the *B. cockerelli* and '*Candidatus* Liberibacter solanacearum'. This study showed that ASA treatment on plants reduced *B. cockerelli* number and Lso infection detected in plants.

CHAPTER IV

DEHYDRATION STRESS AFFECTS *SOLANUM LYCOPERSICUM* SUSCEPTIBILITY INFESTATION AND COLONIZATION BY *BACTERICERA COCKERELLI*

4.1 Introduction

Dehydration (or drought) stress (DS) reduces plant growth and yield (Farooq *et al.*, 2009). Aside from inducing physiological changes potentially affecting crop development and yield such as closing of stomata, DS can promote the outbreaks of phytophagous insects (Mattson & Haack, 1987; Showler, 2014; White, 1969). Several mechanisms might be responsible for these insect outbreaks. For instance, DS significantly impacts protein quality and quantity in plants, as well as the accumulation of ions, sugars and defensive secondary metabolites (Mattson & Haack, 1987; Showler, 2014; Showler & Castro, 2010). In particular, in response to DS, proline accumulates in leaves and stems (Hsiao, 1973; Lombardini, 2006; Manivannan *et al.*, 2007; Showler, 2014; Showler & Castro, 2010). The accumulation of proline and other free amino acids in plants can enhance insect development and affect insect preference. Different studies showed that DS affects insect attraction to host plants. *Spodoptera exigua* and *Eoreuma loftini* adults preferred to oviposit on plants under DS (Showler & Castro, 2010; Showler & Moran, 2003). In both studies, dehydration-stressed plants had a higher concentration of free amino acids than the control plants suggesting that the insect attraction to plants under DS could be mediated by the increase of plant free amino acids. The attraction of leaf-chewers' to plants under DS was also linked to plant volatile organic compounds (VOC). Dehydration-stressed plants had higher concentration of 19 out of 55 detectable VOCs; and the oviposition preference of female cabbage moths (*Mamestra brassicae*) for stressed plants was associated to the increase of VOCs (Weldegergis *et al.*, 2015). For example, *Pieris napi* larvae had higher body mass and food conversion efficiency when feeding on stressed plants from the low-water regime (Bauerfeind & Fischer, 2013). Therefore, DS can render plants more susceptible to insect colonization.

Although results from a number of studies support the notion that DS can positively affect leaf-chewing herbivores, dehydration stress can also negatively affect insect performance (Showler & Moran, 2003). Similarly, its effect on phloem-feeding herbivores remains controversial. For instance, DS was shown to have positive (Hale *et al.*, 2003; Oswald & Brewer, 1997; Tariq *et al.*, 2012), negative (Johnson *et al.*, 2011; Simpson *et al.*, 2012), or neutral (Bethke *et al.*, 1998; King *et al.*, 2006; Pons & Tatchell, 1995) effects on aphids. The impact of water deficit on herbivores may dependent on the plant species (Showler, 2001; Wearing & Vanemden, 1967), leaf age (Wearing, 1972), insect species (Oswald & Brewer, 1997), and the level, duration, and type of water stress (Banfield-Zanin & Leather, 2014; Huberty & Denno, 2004; Thomas & Hodkinson, 1991). Empirical studies have shown that the effect of DS on phloem-feeding herbivores is complex since both positive and negative effects on insect populations were attributed to water stress (Huberty & Denno, 2004; Simpson et al., 2012; Tariq et al., 2012).

Three hypotheses were proposed to explain the relationship among water stress, plant quality and herbivore performance. While the plant stress hypothesis suggests that water stress enhances herbivore performance and population by increasing the availability of nutrients in plants (White, 1969), the plant vigor hypothesis argues that vigorous plants with high osmotic potential are more suitable hosts for herbivores than drought-stressed plants (Cornelissen *et al.*, 2008; Price, 1991). On the contrary, the plant vigor and pulsed hypothesis asserts that phloem-feeders perform better on intermittently water-stressed plants than continuously water-stressed plants and that plants that experienced intermittent dehydration stress tend to attract more phytophagous insects than continuously stressed plants due to the intermittent increase of nitrogen availability (Huberty & Denno, 2004). The three hypotheses use different aspects of the plant physiological response to explain the indirect effect of water stress on the insect population, but these hypotheses are not mutually exclusive. Based on extensive review of the water stress literatures, defining the type of water deficit stress and the effect it has on plant physiological response is important in the study of plant susceptibility to insect colonization.

Considering the increased severity of water deficit (McCabe & Wolock, 2015) and the outbreaks of insects and diseases (Creeden *et al.*, 2014; Elderd & Reilly, 2014; Hart *et al.*, 2014), studying the effect of DS on plant susceptibility to phloem-feeding insects is needed. Several phloem-feeding insects are vectors of plant diseases causing agricultural and economic losses (Hogenhout *et al.*, 2008; Ng & Falk, 2006; Weintraub & Beanland, 2006). The published studies primarily focused on the effect of water stress on plant susceptibility to aphids. The impact of water stress on plant susceptibility to *B. cockerelli*, also phloem feeding insects, is yet to be determined. *B. cockerelli* have become important pests worldwide since they transmit several bacterial pathogens responsible for devastating diseases such as huanglongbing (Bove, 2006; Grafton-Cardwell *et al.*, 2013) and zebra chip (Munyaneza, 2012). Water stress could be one of the influential factors that contribute to the outbreak of these insect vectors and bacterial diseases.

In this study, the dynamic role of DS on *Solanum lycopersicum* (tomato) susceptibility to *Bactericera cockerelli* (psyllid) was investigated. *Bactericera cockerelli* (Hemiptera: Triozidae) vectors Gram-negative pathogen, '*Candidatus* Liberibacter solanacearum' (Lso) (Hansen et al., 2008; Liefting et al., 2008) that infects several solanaceous plants (Liefting et al., 2009; Munyaneza, 2012) including *S. lycopersicum*. Dehydration stress could influence plant susceptibility to *B. cockerelli* and affect the epidemiology of Lso-related disease. Different studies including choice, no-choice, survival, and fitness experiments were conducted to evaluate the effect of DS on *S. lycopersicum* susceptibility to the colonization by *B. cockerelli*. The short and long term effects of *S. lycopersicum* susceptibility to *B. cockerelli* harboring Lso were evaluated. Results from this study can provide an insight on how DS affects plant susceptibility to insect pests and the pathogens they carry. The results may also provide insights for ways to improve current pest and disease management practices when plants are under drought stress.

4.2 Materials and methods

4.2.1 Plant source and water treatments

Tomato plants, *S. lycopersicum* cv. Money Maker (Thompson & Morgan), were grown from seeds in Sun Gro® Metro-Mix 900 soil. They were provided adequate water and fertilizer as directed (Miracle-Gro® Water Soluble Tomato Plant Food, 24-8-16 NPK). Plants were grown under L16:D8 photoperiod throughout their development. Four-week-old plants were individually transplanted into 3.5-inch square pots with dry soil and were subjected to one of three treatments: (1) control, (2) low dehydration stress, or (3) moderate dehydration stress. Plants in these treatments received a weekly water regime of 200 mL, 100 mL, and 50 mL, and are henceforth labeled as “C”, “LDS”, and “MDS” respectively. The weekly water regimes were maintained during the entire study.

4.2.2 Plant water potential and plant relative water content studies

The effects of the water treatments on plant water potential and plant relative water content (RWC) were verified two weeks post-treatment initiation, when plants were six weeks old. To test plant water potential, the bottom-most leaf was excised and plant water potential was immediately measured using a calibrated pressure chamber (Model 615, PMS Instrument Company) according to the manufacturer’s instructions. The pressure measured by the pressure chamber is the force required to push sap out of the cut end of the leaf, which is inversely proportional to plant water potential. The inverse relationship ($r^2 = -0.99$) between *S. lycopersicum* water potential (Ψ_w) and chamber pressure is well-documented and has been used in previous studies of plant water stress (Boyer, 1967; Duniway, 1971; Hsiao, 1973; Pardossi *et al.*, 1991; Thompson *et al.*, 2007). Plant water potential was used as plant water stress index. For plant RWC measurements, the same bottom-most leaf was used. Fresh, turgid and dried leaf weights were measured to calculate plant RWC as published (Pardossi et al., 1991). Briefly, fresh leaf biomass was measured after the excision. Leaf turgid biomass was measured after floating in distilled water for 24 hrs at 25 °C under dim light. Leaf dried biomass was measured after drying in an oven for 48 hrs at 65 °C.

4.2.3 Insects

Laboratory *B. cockerelli* colonies of central haplotype populations were maintained on *S. lycopesicum* cv. Money Maker in separate 14” X 14” X 24” insect cages (BioQuip) at room temperature and a photoperiod of 16:8 (Light: Dark) hours. Diagnostic PCRs were routinely performed to test for Lso infection (Nachappa et al. 2012). These colonies of insects were tested positive for Lso throughout the course of experiments.

4.2.4 Choice study

Based on the result from the plant water potential and plant RWC studies, a choice study was conducted using C and MDS plants. Plant water potential and RWC were tested at week 6, before proceeding to the insect bioassay. A plant from each treatment was placed in a 12” cube BioQuip observation cage. Plants of similar size with no symptoms of wilting were used to limit any confounding effect of visual cues that could potentially influence *B. cockerelli* colonization choice. Ten *B. cockerelli* adults were transferred into each cage and were allowed to settle and colonize their preferred host plant for two weeks at room temperature. The numbers of eggs and nymphs on each plant were counted weekly for two weeks. Four experimental trials were conducted. Each trial consisted of 8 choice arenas and lasted for two weeks from the day of the insect release. A total of 32 cages with 64 plants were included in the analysis. After the end of each experimental trial, plant roots were washed and root length was immediately measured to evaluate the symptoms of water stress between the treatments. Pictures of the plants and their roots were taken to contrast the effect of dehydration stress on root development. Then, root dry biomass was measured.

4.2.5 No-choice study

Similar to the choice study, C and MDS plants were used in the no-choice study. Each plant was individually caged in a 12” cube insect observation cage with ten *B. cockerelli* adults. The adult insects were allowed to feed, mate, and oviposit on each plant for three weeks. The eggs and nymphs on each plant were counted weekly and used as the *B. cockerelli* colonization indexes for one-week and two-week exposure times to insects. On week three, the numbers of emerging adults were monitored to assess *B. cockerelli* colonization and developmental success on the dehydration-stressed and control plants. In total, nine MDS and nine control plants were used in this experiment.

4.2.6 Batericera cockerelli *development, survivorship, and dispersion potential study*

A total of 72 *S. lycopersicum* plants (36 of control and 36 of MDS plants) were used to evaluate the effect of host plant water stress on *B. cockerelli* survival through different life stages. The experiments were conducted in four trials consisting of 18 plants per trial. Each experimental trial lasted for 28 days, the range of *B. cockerelli* development from egg to adult. After the water treatments and the assessment of plant water potential, five *B. cockerelli* female adults were caged in a leaf bag in each plant, and each plant was caged in a 12” cube cage. After two days, the females were removed from each plant, and the number of eggs on each plant was counted. The number of eggs and nymphs on each plant was recorded three times per week to monitor hatching and survival. The developmental stages of all the *B. cockerelli* on each plant were also recorded three times per week until all the nymphs on each plant became adults. Once nymphs developed into adults, newly emerged adults were counted and removed from the cage. Plants without viable eggs were removed from the analysis. Two plants that lost the leaf in which the adults had oviposited were excluded from the analyses. *Bactericera cockerelli* survival percentage was calculated based on the number of surviving *B. cockerelli* out of the initial number of first instar nymphs. Path analysis was conducted to evaluate whether *B. cockerelli* survival was directly or indirectly affected by plant water stress (based on water stress index), initial number of nymphs and *B. cockerelli* developmental time. *Bactericera cockerelli* developmental time was estimated based on the mean number of days from egg to each developmental stage (see below for statistics). *Bactericera cockerelli* dispersion potential was calculated based on the cumulative number of *B. cockerelli* adults at the time of the measurement. Dispersion potential is an estimate of number of adults that potentially can move to another host plant once the infected plant died.

4.2.7 Fitness study

Six populations of ten *B. cockerelli* adults were separately allowed to reproduce on C or MDS plants in 12” cube BioQuip observation cages for four weeks. After one generation on either C or MDS plants, newly emerged adults were sexed. Newly emerged virgin adult females and males from the same water treatment but different host plants were paired. Each couple was caged for nine days on an excised *S. lycopersicum* leaf placed in tubes with water. Excised leaves were obtained from independent plants grown under C conditions. The numbers of eggs and nymphs produced by each couple were counted and used as the fitness index. A total of 22 couples were evaluated.

4.2.8 Data analyses

The number of offspring on each plant was used as the *B. cockerelli* colonization index. The number of offspring represents the sum of eggs and nymphs. The higher the *B. cockerelli* colonization indexes, the more susceptible the plant is to insect herbivory.

All data analyses were conducted using JMP® Pro v.10 (SAS Institute Inc., Cary, NC, 1989-2013). Ratio associated data were transformed using arcsine transformation prior to conducting statistical analyses. Shapiro-Wilk W test was used to test for normality of each data set prior to conducting a statistical test. The data sets that met the normality assumption were analyzed using parametric tests (e.g., t-test or ANOVA), while the data sets that did not meet the normality assumption were analyzed using non-parametric tests (e.g., Wilcoxon or Kruskal-Wallis) to limit Type 1 Error. When a significant difference was detected ($P<0.05$) in a statistical test for more than two treatments, a post-hoc analysis was conducted to determine the difference among the treatments. The post-hoc tests were done according to the assumptions met for the type of statistical test. For example, the Dunn All Pairs for joint rank test was conducted as a post-hoc test following a Kruskal-Wallis non-parametric test. To evaluate the significant impact of the treatment, Cohen's *d* effect size test was conducted according to the equation of Cohen's $d = M1 - M2 / S_{pooled}$ where $S_{pooled} = \sqrt{((S_1^2 + S_2^2)/2)}$, M = mean, and S = standard deviation (Cohen, 1988). If two continuous variables are associating with each other in ways affecting the result of the study, a bivariate analysis was performed to determine the association between two variables. In an attempt to understand how the development time affected *B. cockerelli* survival, path analysis and regression analysis were performed using Fit Model tool by accounting the model effects that influence *B. cockerelli* survival. The normality of the model residuals was verified using the Shapiro-Wilk W test. The correlation matrix and the level of significance of each pairwise correlation were obtained through the multivariate platform in JMP. Path diagram was constructed using the statistical data for direct and indirect paths according to principle of path analysis and published studies (De Vida *et al.*, 2006; Mitchell, 2001).

4.3 Results

4.3.1 Plant water potential and plant relative water content study

Plant water potential (Fig. 4.1A) was significantly affected by the water treatments (Kruskal–Wallis, H = 39.78, 2 d.f., $P < 0.001$). Lower water treatment resulted in lower plant water potential corresponding to high water stress. The Dunn all pairs post-hoc tests showed that each comparison resulted in a significant difference in plant water potential ($P < 0.01$). MDS plants had the lowest water potential and Control plantss had the highest water potential. Based on the consideration of a 0.5 effect size as moderate and a 0.8 effect size as large (Cohen, 1988), the Cohen's effect size suggested a large effect size between the C and MDS plant groups ($d = 2.71$), the C and LDS plant groups ($d = 1.34$) and the LDS and MDS plant groups ($d = 1.63$). On average, plant water potential on MDS plants was 19.36% lower than on LDS plants and 36.57% lower than on Control plants. Based on *S. lycopersicum* plant water potential, MDS and LDS plants were under DS. Although the water treatment had a significant effect on plant water potential two weeks after initiated, wilting as a symptom of severe DS was not observed in any of the treated plant, even between MDS and control plants (Fig. 4.2).

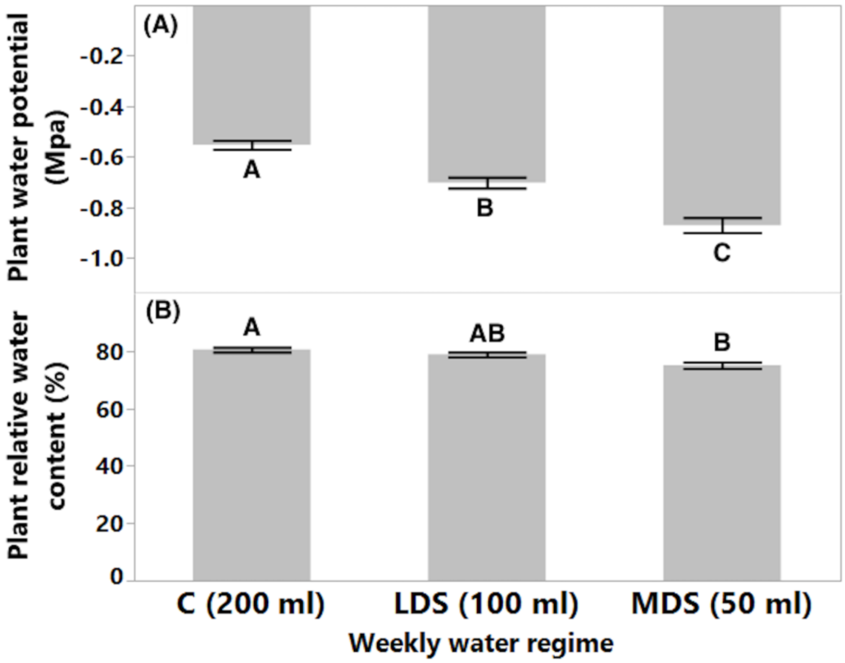

Figure 4.1 Mean (± SEM) plant water potential and relative water content two weeks after water regime initiation. (A) The water treatment had a significant effect on plant water potential ($P < 0.01$). (B) The water treatment had a significant effect on plant relative water content ($P < 0.01$). Different letters represent significant differences in post-hoc tests. Based on these plant osmotic stress indexes, plants treated with 50 mL, 100 mL and 200 mL were within the range of moderate dehydration stress (MDS), low dehydration stress (LDS), and unstressed control (C) plants, respectively.

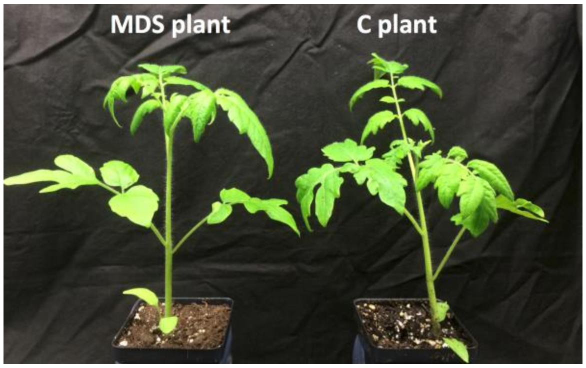

Figure 4.2 Plants in the MDS (50 mL water per week) and C (control 200 mL water per week) treatments after two weeks of water treatment.

In addition to plant water potential, the water treatments also significantly affected plant RWC (Kruskal–Wallis, H = 12.65, 2 d.f., $P < 0.01$, Fig. 4.1B). MDS plants had significantly lower plant RWC than control plants in the Dunn All Pairs test ($P < 0.01$), which confirmed that MDS plants were under water stress. MDS plants on average had 6.9% lower plant RWC than control plants. The effect size between the two treatments was large ($d = 1.15$). No significant effect of the treatment was found between C and LDS plants ($P = 0.789$) and between LDS and MDS plants ($P = 0.059$). Thus, based on both indexes, MDS plants were under higher DS. Bivariate analysis of 65 plants under different weekly water regime showed a significant positive correlation between plant water potential and RWC (r = 0.57, N = 65, $P < 0.001$), which suggests that both plant osmotic stress indexes are in agreement with each other. Plants with high water potential had higher RWC.

4.3.2 Choice study

A choice study was conducted to evaluate whether *B. cockerelli* prefer to colonize MDS plants over control plants of similar appearance (Fig. 4.2). No significant treatment effect was found on the number of eggs (Fig. 4.3A) after one week (t (62) = 1.03, $P = 0.305$) and after two weeks (t (62) = 1.50, $P = 0.142$), on the number of nymphs (Fig. 4.3B) after one week (t (62) = 0.01, $P = 0.996$) and two weeks (t (62) = 1.25, $P = 0.217$), or on total number of eggs and nymph combined (offspring, Fig. 4.3C) after one week (t (62) = 0.82, $P = 0.414$) and two weeks (t (62) = 0.12, $P = 0.908$).

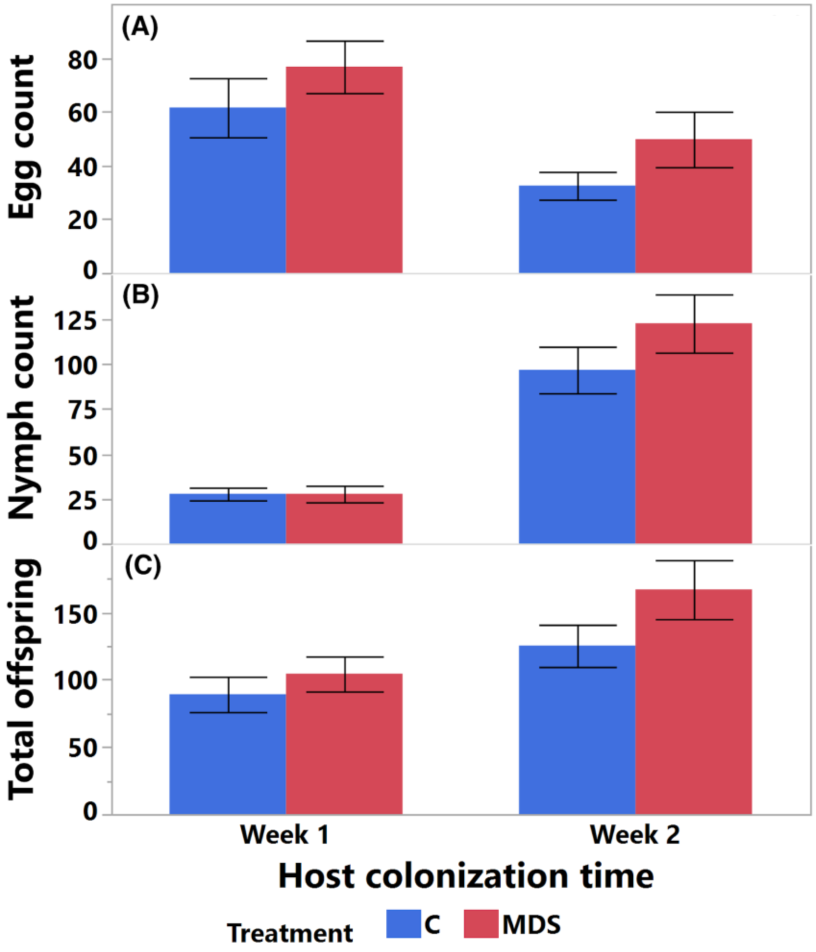

Figure 4.3 Effect of dehydration stress on *B. cockerelli* colonization preference on *S. lycopersicum* plants. (A) Mean (± SEM) *B. cockerelli* eggs on host plants. (B) Mean (± SEM) *B. cockerelli* nymphs on host plants. (C) Mean (± SEM) *B. cockerelli* offspring (eggs and nymphs) on host plants. MDS = moderate dehydration stressed plants. C = control plants. Symbol * represents significant difference between the treatments at $P < 0.01$.

The effect of the water treatment on root biomass and length was evaluated to verify the effect of the dehydration stress. Dehydration stress did not significantly affect root dried weight (t (60) = 0.30, $P = 0.763$, Fig. 4.4A) but significantly affected root length ($P < 0.01$, Fig. 4.4B and 4.5A). With a large effect size ($d = 1.52$), MDS plants on average had significantly longer root length than control plants. In response to dehydration stress, MDS plants also had more root hairs than control plants (e.g., Figure 4.5B). MDS plants had thinner and longer roots adapted for plants with water stress to seek for water in the soil. Interestingly, plant water potential was inversely correlated plant root length (r = -0.59, N = 62, *P* < 0.001) indicating that higher water stress resulted in longer roots. There was no significant correlation between plant water potential and plant dried root weight (r = -0.14, N = 62, *P* = 0.337).

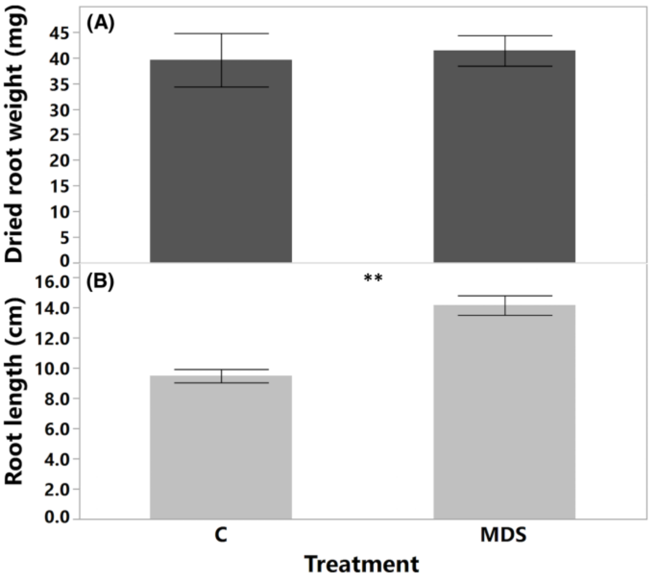

Figure 4.4 The impact of dehydration stress on *S. lycopersicum* root. (A) Mean (± SEM) plant root weight. (B) Mean (± SEM) plant root length. Symbol ** represents significant differences between the treatments at *P* < 0.01. MDS = moderate dehydration stressed plants. C = control plants.

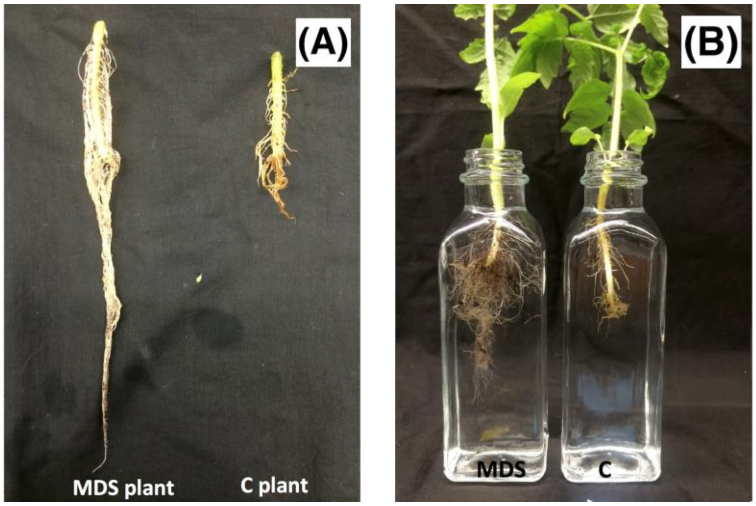

Figure 4.5 Dehydration stress effect on *S. lycopersicum* plant root length and architecture. (A) An example root image of MDS and control plants showing a difference in root length. (B) An example of root image of MDS and control plants showing a difference in root architecture. MDS = moderate dehydration stressed plants. C = control plants. While MDS plants had long, thin, and dense root, control plants had short, thick and uncrowded root.

4.3.3 No-choice study

A no-choice test was conducted to evaluate plant susceptibility to *B. cockerelli* colonization under dehydration stress. No significant difference was found between the number of eggs found on control plants and on MDS plants after one week (t (16) = 1.34, $P = 0.21$) and after two weeks (t (16) = 1.22, $P = 0.24$, Fig. 4.6A). However, the number of nymphs was significantly higher on MDS plants than on C after one week (t (16) = 3.76, $P < 0.01$) and after two weeks (t (16) = 1.94, $P = 0.035$, Fig. 4.6B). The significant differences found between the C and MDS plants were large with the effect size of $d = 1.77$ for week 1 and effect size of $d = 0.93$ for week 2. When the number of eggs and nymphs on each plant were combined to evaluate treatment effect on the number of offspring, MDS plants had significantly higher number of offspring than control plants after one week (*t* (16) = 2.09, *P* = 0.03, Fig. 4.6C) and two weeks (*t* (16) = 1.91, *P* = 0.037, Fig. 4.6D) of exposure times. The treatment also had a large effect on the number of offspring after one week (*d* = 0.99) and two weeks (*d* = 0.91). Thus, MDS plants were more susceptible to *B. cockerelli* than control plants since the colonization index was higher.

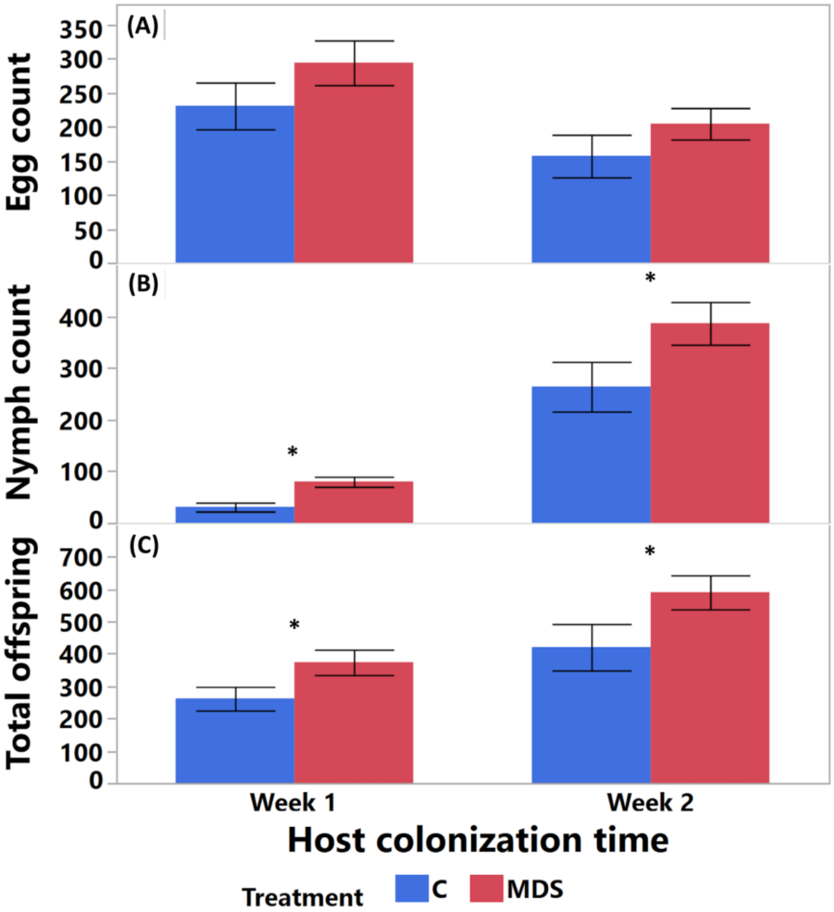

Figure 4.6 Dehydration stress on *S. lycopersicum* plant susceptibility to *B. cockerelli*. (A) Mean (± SEM) eggs on host plants. (B) Mean (± SEM) nymphs on host plants. (C) Mean ± SEM offspring (eggs +nymphs) on host plants. Symbol ** represents significant differences between the treatments at P < 0.01. MDS = moderate dehydration stressed plants. C = control plants.

After three weeks, MDS plants had a significantly higher number of newly emerged adults than control plants (*t* (16) = 2.02, *P* = 0.030, Fig. 4.7). The treatment had a moderate effect size (*d* = 0.96). On average, the MDS plants had 59% more *B. cockerelli* per plant than the control plants. Thus, plants under DS not only had higher number of *B. cockerelli* nymphs but also higher number of *B. cockerelli* adults than well-watered plants.

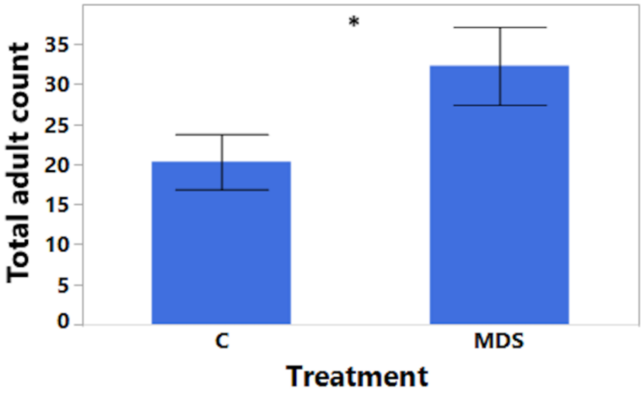

Figure 4.7 The emergence of adult *B. cockerelli* offspring on host plants in no-choice study after three weeks. Symbol * represents significant difference between the treatments.

4.3.4 Bactericera cockerelli *development, survivorship, and dispersion potential study*

The development and survival of *B. cockerelli* were evaluated by monitoring the development of nymphs from eggs to adults on C or MDS plants. Results showed that 74.9% of eggs hatched and 67.8% of the initial nymph population reached adulthood. Egg hatching occurred between day 5 and 12. The mean numbers of initial nymphs on control plants and MDS plants were 49.4 and 58.2 nymphs per plant, respectively. No significant difference was found on the percentage of egg hatching (*t* (64) = 0.518, *P* = 0.606*)* and number of initial nymphs among the two treatments (*t* (64) = 1.19, *P* = 0.24) accepting the null hypothesis that the number of initial nymphs per plant were equivalent.

Percentage of nymphal survival was higher on MDS plants than on control plants throughout the experiment (Fig. 4.8**,** P<0.01). Cohen's *d* test (Cohen, 1988) showed an increase in the effect size of the treatment from medium to large (*d* = 0.70-1.55) between day 12 and day 28, suggesting that the DS enhanced plant susceptibility to *B. cockerelli* colonization by gradually and significantly enhancing *B. cockerelli* survival percentage. Detailed statistic can be found in Table 4.1. The difference of *B. cockerelli* survival between MDS and control plants increased from 9.0% on day 12 to 37.8% on day 28. Nymphal mortality decreased as nymphs developed: under both treatments higher mortality was recorded earlier during development. However, MDS plants had lower percent mortality than control plantss. While less than 20% of the nymphs on MDS plants died up to day 19, almost 40% of the nymphs on control plants died up to day 19. By day 19, approximately 59% of *B. cockerelli* were fifth instar nymphs and 40 % of *B. cockerelli* on the plants were adults, irrespective of the water treatment.

Table 4.1 Mean (± SEM) *B. cockerelli* survival and the treatment effect size.

Developmental time	**Treatment**	**n**	**Mean**	**Std Error**	***t*-ratio**	***P*-value**	***Cohen's d***
Day 12	C	34	83.8305	1.8631	2.67	0.0096	0.70
	MDS	30	91.3224	1.9834			
Day 16	C	34	72.5585	2.6601	3.59	0.0006	0.92
	MDS	30	86.5427	2.8319			
Day 19	C	34	61.6569	2.4878	5.72	<0.0001	1.47
	MDS	30	82.7136	2.6485			
Day 21	C	34	58.7328	2.4806	6.03	<0.0001	1.53
	MDS	30	80.748	2.6408			
Day 23	C	34	57.9578	2.4264	6	<0.0001	1.55
	MDS	30	79.8912	2.5831			
Day 26	C	34	57.4527	2.4228	5.99	<0.0001	1.55
	MDS	30	79.3251	2.5793			
Day 28	C	34	57.415	2.4277	5.93	<0.0001	1.55
	MDS	30	79.1043	2.5844			

MDS = moderate dehydration stressed plants. C = control plants

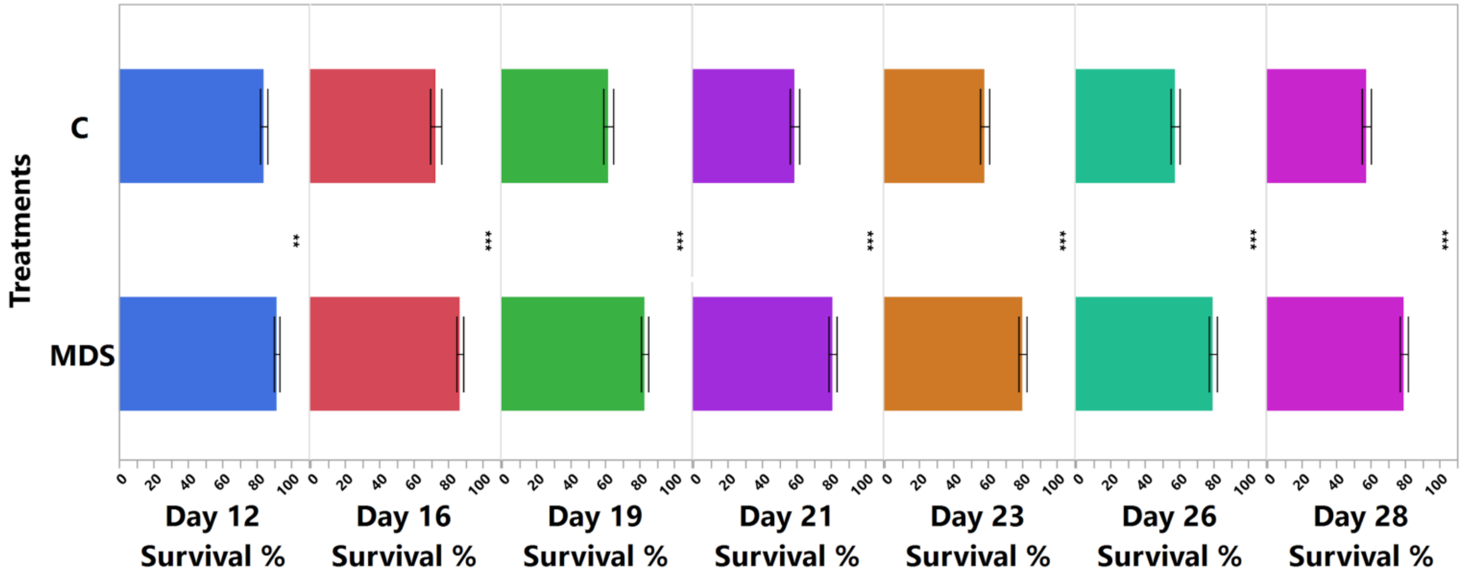

Figure 4.8 The effect of water stress on *B. cockerelli* percent survival at different days since oviposition. The bar graphs show mean (± SEM) of *B. cockerelli* percent survival on water stress (MDS) and control (C) plants. *P <0.05, **P <0.01,***P <0.001. Statistics were based on the arcsine-transformed data for proportional data. All data were normally distributed as verified by the Shapiro-Wilk W test.

The path diagram showed that plant DS has a strong positive effect on the overall survival of *B. cockerelli* (Fig. 4.9). Particularly, a positive correlation between plant water stress measured as function of chamber pressure and nymphal survival was found ($P < 0.001$). Also, the result from the multivariate regression model performed for the path diagram suggests that time of development to 2nd instar stage was negatively correlated to *B. cockerelli* overall survival to adults after accounting for the number of initial nymphs, the development time for each *B. cockerelli* life stage, and the plant water stress. The longer the time for *B. cockerelli* to develop to the second instar, the lower the *B. cockerelli* survival ($P = 0.0028$). The time of development to 2nd instar was also significantly influenced by the time of development to 1st instar ($P < 0.001$). Also, number of initial nymphs was negatively correlated with *B. cockerelli* survival ($P < 0.05$). Plant DS neither had a significant impact on the initial number of nymphs nor affected the *B. cockerelli* development time.

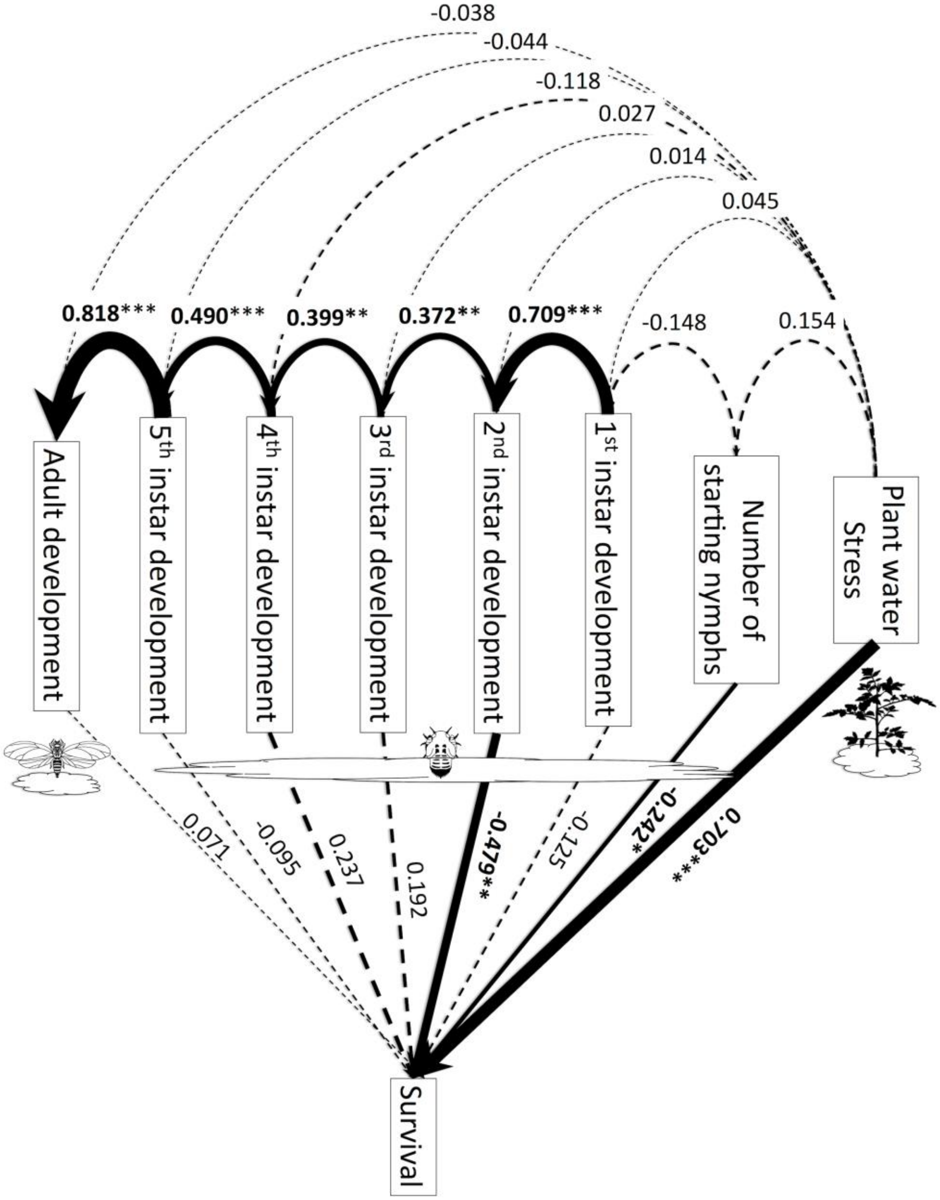

Figure 4.9 Path diagram of the model effects contributing to *B. cockerelli* survival. Solid lines denote significant effects, and dashed lines denote non-significant effects. The width of each line is proportional to the strength of the relationship. While positive numbers represent positive correlations, negative numbers represent negative correlations. *P <0.05, **P <0.01,***P <0.001.

The number of emerging adults on host plants can be used to estimate *B. cockerelli* dispersion potential. Results showed that water stress significantly enhanced *B. cockerelli* dispersion potential (P < 0.01, Fig. 4.10). The dispersion potential increased as more nymphs completed development overtime. Adult emergence occurred from day 19 to day 28. By day 19, on average 19 adults had emerged on MDS plants and 11 adults on control plants. DS plants consistently and significantly had higher dispersion potential than control plants. Thus, water stress not only increased plant susceptibility to colonization by enhancing *B. cockerelli* survival but could also potentially promote the dispersal of the insect vector

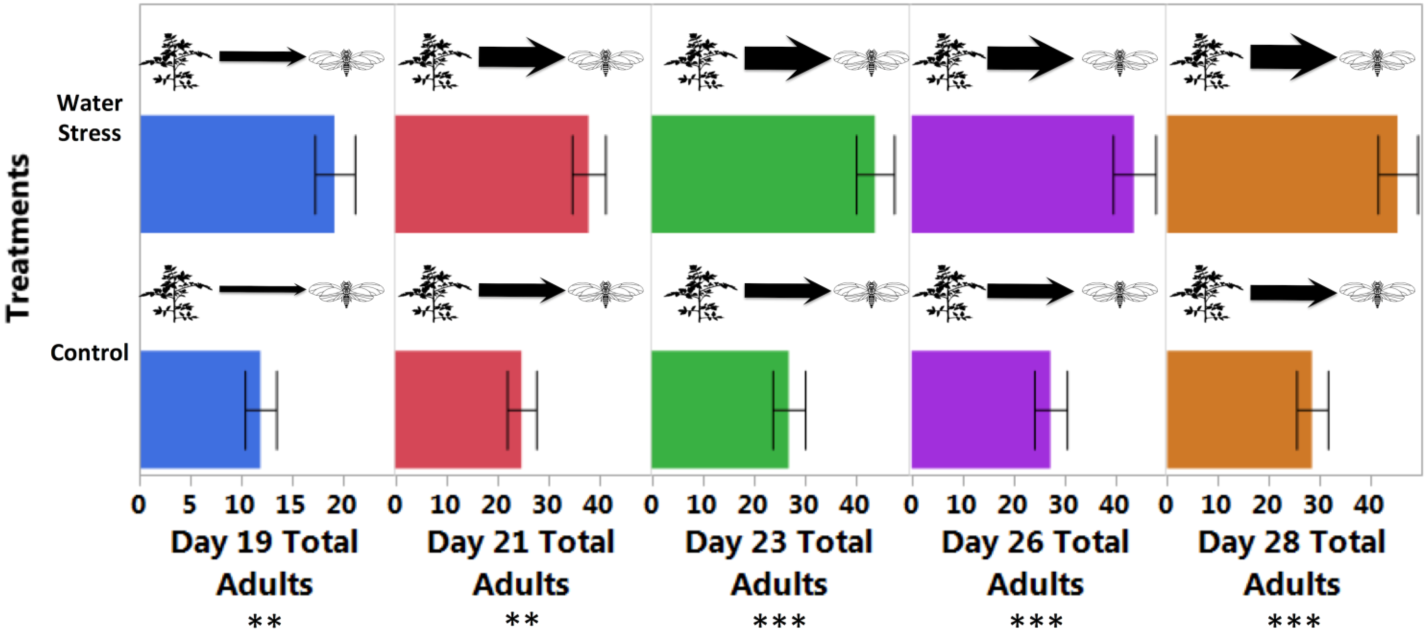

Figure 4.10 The effect of plant osmotic stress on the number of *B. cockerelli* adults as a function of their dispersal potential. Width of each arrow is proportional to cumulative number of *B. cockerelli* and the strength of the dispersal potential. *P <0.05, **P <0.01, ***P <0.001.

4.3.5 Fitness study

To evaluate if DS during nymphal development affected adult fitness, the fitness of *B. cockerelli* that developed from egg to adult on MDS and control plants was evaluated by comparing the number of eggs and nymphs they produced on leaves from control plants. There were no significant differences in the number of offspring (eggs + nymph) ($Z = 0.851$, $P = 0.395$), number of eggs ($Z = 0.788$, $P = 0.431$), or number of nymphs ($Z = 0.650$, $P = 0.516$) produced by couples that developed on C or MDS plants.

4.4 Discussion

Plant physiological response to water stress is complex. From mild to severe, water stress affects plant physiology in the following sequence: reduction of shoot and leaf growth, reduction of protein synthesis, reduction of cell division, accumulation of abscisic acid, reduction of transpiration and of CO_2 assimilation, accumulation of proline, and finally wilting (Hsiao, 1973; Lombardini, 2006). Abscisic acid (ABA) accumulation in plants has been used as indicator of plant physiological responses to water stress (Fujita *et al.*, 2011; Hartung *et al.*, 2005; Osakabe *et al.*, 2014), but the most efficient way to evaluate plant water stress is to analyze plant water potential. The accumulation ABA begins when plant water potential drops between -0.3 MPa and -0.7 MPa depending on the plant species (Lombardini, 2006; Hsiao, 1973). In *S. lycopersicum*, ABA drastically accumulates when plant water potential is at approximately -0.6 MPa and continues to accumulate as the plant reduces transpiration to limit water loss (Lombardini, 2006; Thompson et al., 2007). Based on the analysis of plant water potential in this study, plants in the 50 mL (Ψ_w = -0.87 MPa), 100 mL (Ψ_w = -0.70 MPa), and 200 mL (Ψ_w = -0.55 MPa) water regime groups were considered moderately water-stressed (MDS), low water-stressed (LDS), and unstressed (C), respectively. Evidenced by their low water potential (< -0.60 MPa), plants in the 50 mL and 100 mL water groups were considered water-stressed. Although plants in the 50 mL and 100 mL water groups respectively received four folds and two folds lower weekly water than the plants in 200 mM water group, the reduction of weekly water did not affect the plant appearance. None of the plants showed symptoms of wilting during the experiment. Therefore, the differences in visual cues that could potentially affect *B. cockerelli* colonization were at least limited. Wilting is only expected when plants experience severe dehydration stress (Hsiao, 1973; Lombardini, 2006). In this study, we focused on understanding the effect of dehydration stress on plant susceptibility to *B. cockerelli* colonization. Controlling plant physical appearance is imperative to limit the confounding effect of visual cues and isolate the effect of plant physiological stress on host selection preference by insects.

Dehydration stress in plants is influenced by a number of factors including but not limited to plant water potential and plant relative water content (Hsiao, 1973; Lombardini, 2006; Tariq et al., 2012). Plant relative water content is used as an indicator of plant water status (Hsiao, 1973; Tariq et al., 2012); the higher the drought stress (DS) treatment the lower the relative content (Tariq et al., 2012). Thus, plant RWC was used as a second index to validate plant water stress. MDS plants had significantly lower RWC than control plants validating that water stressed plant had lower plant RWC. The result of bivariate analysis evaluating the association between plant water potential and plant RWC suggests that the two responding variables were highly correlated. Other studies also indicated the association between plant water potential and RWC (Lombardini, 2006), especially in *S. lycopersicum* (Pardossi et al., 1991). Since low dehydration stress may not induce a large change in plant physiological response affecting the insects, LDS plants were excluded from that insect experiments. MDS and control plants were used in the insect studies to evaluate the effect of *S. lycopersicum* dehydration stress on plant susceptibility to *B. cockerelli* colonization. All plants used for the studies involving *B. cockerelli* were tested to verify their plant water potential. The results from all the studies were consistent with the study of plant water potential.

In the choice study, *B. cockerelli* did not preferentially colonize plants under DS since there was no significant difference in the number of eggs and nymphs between MDS and control plants. When *B. cockerelli* adults were restricted to colonize one host plant in the no-choice study, MDS plants had significantly higher number of nymphs than control plants suggesting that dehydration stress may render *S. lycopersicum* more susceptible to *B. cockerelli* colonization. However, no significant difference was found in the number of eggs, implying that eggs laying by *B. cockerelli* adults may not be the contributing factor to plant susceptibility to *B. cockerelli*. In the survival study, *B. cockerelli* nymphs had significantly higher percent survival on MDS plants than on control plants. Thus, the higher nymphal survival on MDS plants could contribute to the higher number of nymphs, suggesting higher plant susceptibility to *B. cockerelli*. Also, MDS plants had significantly more nymphs that developed into adults than control plants making MDS plants a better host for colonization and repopulation. On average, there were 17 more *B. cockerelli* adults per MDS plant than adults per control plant. This adult survival result is also in agreement with the result found in the no-choice study where significantly higher number of adults was found on MDS plants than on control plants. However, it is imperative to note that the effect of DS did not affect the fecundity of *B. cockerelli*. Population of *B. cockerelli* on MDS plants and on control plants may lay similar number of eggs after multiple generations, but the population of *B. cockerelli* on MDS plants may be larger than that on control plants due to higher nymphal survival.

Studies showed that dehydration stress could elicit an accumulation of nutrients and free amino acids in plants (Manivannan et al., 2007) that favor insect growth and development (Showler, 2014) since plant phloem sap is nitrogen limited (Mattson, 1980). The accumulation of the α-amino acid proline in the plant in response to dehydration stress (Gadallah, 1995; Manivannan et al., 2007) could be a plausible reason why MDS plants had significantly higher nymphal survival than the control plants. Prolonged dehydration can increase nitrogen availability in plants and affect phloem-feeding insects (Lombardini, 2006; Manivannan et al., 2007; Showler & Moran, 2003). Therefore, water limitation could have induced dehydration stress in plants and improved plant quality for *B. cockerelli* resulting in decreased mortality. Similar to the results from this study, other studies found that water stress increased plant susceptibility to phloem-feeding insects (Oswald & Brewer, 1997; Tariq et al., 2012). Aphids (*Brevicoryne brassicae* and *Myzus persicae*) had greater fecundity and higher intrinsic rate of increase on moderate water stressed plants than on unstressed plants (Tariq et al., 2012). Interestingly, the frequency and intensity of water stress had different effects on host plant and subsequently on phloem-feeding insects. While moderate and intermittent water stress improved host plant quality and provided benefits for phloem-feeding insects, severe (both intermittent and continuous) water stress lowered host plant quality and had a detrimental impact on phloem-feeding insects (Banfield-Zanin & Leather, 2014; Sconiers & Eubanks, 2017). The impact of the frequency and intensity of water stress on plants and plant susceptibility to insects was extensively reviewed as noted previously (Huberty & Denno, 2004). Thus, it is imperative to note that the susceptibility of *S. lycopersicum* to *B. cockerelli* observed in this study only pertains to intermittent and moderate dehydration stress. Continuous and serve dehydration stress could result in different outcomes since other factors such as wilting, production of reactive oxygen species, VOCs and defense compounds could affect insects (Farooq et al., 2009; Gill *et al.*, 2012; Weldegergis et al., 2015). In summary, the collective results from this study support the plant vigor and pulsed hypothesis (Huberty & Denno, 2004) and are in agreement with the plant stress hypothesis (White, 1969).

The differences in host plant quality could also be mediated by plant root response to different intensity of water stress. Moderate water stress increase plant root length and distribution to enhance water absorption but severe water stress can reduce plant root length and distribution to conserve water (Franco *et al.*, 2008; Franco *et al.*, 2011). Under moderate water stress, plants may accelerate root growth and increase root length as observed in the MDS plants. The increase in root elongation and root hydraulic conductivity to obtain water is a common plant response to the lack of water (Sekiya &

Araki, 2013). Also, the increase of abscisic acid under dehydration stress is a common root response (Thompson et al., 2007). Abscisic acid plays an important role in turgor regulation in tomato roots (Griffiths *et al.*, 1996). This type of root response may allow plants to tolerate moderate drought stress in the root while releasing free amino acids in the shoot as the consequence of DS. The significant relationship between plant water potential and plant root length found in this study also support other studies that the increase of water stress could be associated with the increase in plant root length with the exception of severe water stress (Franco et al., 2008; Franco et al., 2011).

In conclusion, DS enhanced plant susceptibility to *B. cockerelli* by influencing nymphal survival and adult dispersion potential, which could affect Lso disease outbreak. The increase in frequency and severity of drought in certain regions could render plants more susceptible to insect colonization and outbreaks, affecting the epidemiology of vector-borne diseases. Future studies should be aimed at understanding the effect of DS on plant susceptibility to other *B. cockerelli* haplotypes (Swisher et al., 2014; Swisher et al., 2013a) and to Lso infection. Since Lso infection can influence *B. cockerelli* host selection behavior (Davis et al., 2012; Mas et al., 2014) the effect of DS in plant susceptibility to Lso-free *B. cockerelli* should also be assessed.

CHAPTER V

GLOBAL GENE REGULATION IN PLANT (*SOLANUM LYCOPERSICUM*) RESPONDING TO VECTOR (*BACTERICERA COCKERELLI*) FEEDING AND PATHOGEN (‘*CANDIDATUS* LIBERIBACTER SOLANACEARUM’) INFECTION

5.1 Introduction

Within the last two decades, bacteria in the genus *Liberibacter* have emerged worldwide as serious pathogens of citrus, solanaceous and apiaceous plants (Haapalainen, 2014). In the United States, *Liberibacter* species cause millions of dollars in agricultural losses annually, ‘*Candidatus* Liberibacter asiaticus’ caused a total estimated loss of $4.5 billion between 2006 and 2011 to the Florida citrus industry and ‘*Candidatus* Liberibacter solanacearum’ (Lso) infecting potatoes caused an estimated loss of more than $25 million between 2003 and 2005 in Texas (CNAS, 2006; Hodges & Spreen, 2012; Munyaneza, 2012).

‘*Candidatus* Liberibacter solanacearum’ is a phloem-limited, Gram-negative, bacterial pathogen (Munyaneza, 2012). In the Americas and New Zealand, this phytopathogen is vectored by the potato psyllid *Bactericera cockerelli* (Munyaneza et al., 2007) and infects solanaceous plants including tomato, pepper, eggplant, tamarillo, and cape gooseberry (Liefting et al., 2008; Liefting et al., 2009; Munyaneza *et al.*, 2009a).

Previous studies on citrus-‘*Candidatus* Liberibacter americanus’ interaction have identified changes in the plant primary and secondary metabolism, in particular in the carbohydrate metabolism (Mafra *et al.*, 2013). More recently, the citrus transcriptome in response to the vector *Diaphorina citri* and '*Candidatus* Liberibacter asiaticus' was analyzed comparing plants response to early and late infection. The early infection was characterized by the down-regulation of defense genes, while changes in the expression of genes involved in carbohydrate metabolism, hormone signaling and plant defense were identified later during the infection (Zhong *et al.*, 2016). While citrus response to *Liberibacter* infection has been extensively studied, much less is known concerning the transcriptomic responses of solanaceous plants to Lso infection. In *Solanum tuberosum*, increased levels of phenolic compounds, and of peroxidase and polyphenol oxidase activities were measured following Lso infection (Wallis et al., 2012). In *S. lycopersicum*, Lso infection resulted in the up-regulation of allene oxide synthase and proteinase inhibitor 2 genes in the jasmonate defense pathway and the up-regulation of phenylalanine lyase 5 and pathogenesis-related 1 genes in the salicylate defense pathway (Casteel et al., 2012). Yet little is known about the global plant transcriptomic response to Lso infection. Most of the effort on the plant host were focused on the epidemiology and breeding for resistance. Studying plant responses to the vector and the pathogen can reveal crucial aspects of plant defense and disease development. In particular, understanding plant innate immune response to vector colonization and pathogen infection could lead to novel strategies for the management of Liberibacter diseases.

In this study, the transcriptional response of *S. lycopersicum* to *B. cockerelli* and Lso was evaluated over time using Illumina HiSeq RNA sequencing. We focused on evaluating the plant immune and metabolic responses using a combination of bioinformatics and empirical approaches to monitor the changes in gene expression in plants colonized by Lso-negative *B. cockerelli* and by Lso-positive *B. cockerelli* over the course of four weeks. The progression of *B. cockerelli* colonization and Lso infection on the exposed plants were monitored alongside untreated control plants. The expression of genes associated with plant defenses and metabolic responses was verified by quantitative RT-PCR, and protein assays were performed to link changes in protein activity to the up-regulation of defense genes. This study is the first global gene expression analysis on tomato-Liberibacter interaction. Overall, the findings of this study contribute to the understanding of *S. lycopersicum* responses to *B. cockerelli* and Lso at the molecular level.

5.2 Materials and methods

5.2.1 Insect source

Lso-negative and Lso-positive *B. cockerelli* colonies of Northwestern-haplotype were maintained on tomato plants in separate rooms under the 16:8 light to dark cycle at room temperature. *Bactericera cockerelli* colonies were tested regularly by diagnostic PCR to evaluate Lso infection as previously published (Nachappa et al., 2011). On average, 80 to 100% of the insects tested positive in the Lso-positive colony. Both Lso haplotypes, Lso A and Lso B (Wen *et al.*, 2009), infect the Lso-positive colony. None of the insects tested positive in the Lso-negative colony.

5.2.2 Plant material

Tomato plants, *Solanum lycopersicum* cv. Moneymaker (Thompson & Morgan), were grown from seed in Sun Gro® Metro-Mix 900 soil and transplanted into 4-inch square pots four weeks later. Plants were watered and fertilized weekly according to the label rate of the Miracle-Gro® Water Soluble Tomato Plant Food (18-18-21 NPK). All experiments were conducted at room temperature and with a 16:8 light to dark cycle.

5.2.3 Experimental design and sample collection

Experiments were designed to evaluate *S. lycopersicum* transcriptional responses to *B. cockerelli* herbivory and Lso infection at three time points: one week (T1, infestation stage), two weeks (T2, colonization stage), and four weeks (T3, repopulation stage). There were three *B. cockerelli* treatments within each time point: plants exposed to Lso-negative *B. cockerelli* (P), plants exposed to Lso-positive *B. cockerelli* (L), and control plants (no *B. cockerelli*, C). Six-week-old plants of similar size were individually caged and randomly assigned to one of the three insect treatments (C, P, and L) within one of three the time points: T1, T2, or T3. Each plant in the *B. cockerelli* treatments (L and P) was exposed to 5 one-day-old-adult females and 5 one-day-old-adult males from either the Lso-negative (P) or from the Lso-positive colonies (L). Control plants I were caged similarly as the infested plants, but without *B. cockerelli*. Seven days after their release, the *B. cockerelli* adults were collected and the progenies were allowed to develop on the plants.

Leaf tissues were collected only once from each plant, therefore independent plants were used for each time point. Plant tissues from the top-most fully-expanded leaf were collected and immediately flash-frozen in liquid nitrogen. After leaf samples were collected, each plant was kept until the end of the experiment in order to collect plant tissues for DNA extraction to verify the presence or absence of Lso. Lso in plants can be easily detected four weeks after *B. cockerelli* infestation (Levy et al., 2011). T1 was considered the infestation stage when the ten *B. cockerelli* in each cage were mating, settling, laying eggs, and feeding on the host plant. T2 was considered the colonization stage when the emerged nymphs fed on the host plant. T3 was considered the repopulation stage when new adults emerged while the remaining nymphs were developing. For the plants in cages with Lso-positive *B. cockerelli*, each time point represents a different stage in Lso infection.

5.2.4 Verification of Lso infection in plants

DNA from 0.1 g of plant tissues was extracted and used for diagnostic PCR to verify the presence or absence of Lso in all the plants as previously published (Levy et al., 2011). Forward and reverse primers targeting Lso *16S ribosomal RNA* gene were used for Lso detection (Nachappa et al., 2011) and primers targeting tomato *elongation factor 1* (*EF1*) (Nachappa et al., 2014) were used as internal control. Fifty nanograms of nucleic acid from each plant were used as template in the diagnostic PCR.

5.2.5 RNA extraction, library preparation, sequencing and analyses

The flash-frozen tissues were ground to fine powder for the total RNA extraction using Plant Rneasy Mini Kit (Qiagen, Valencia, CA) according to the manufacturer's instructions. The RNA samples were treated with Rnase-Free Dnase to eliminate genomic DNA contamination during the extraction (Qiagen, Valencia, CA). Any remaining DNA contaminant was removed using TURBO DNA-free^{TM} Kit (Life Technologies, Carlsbad, CA, USA). RNAs for the 27 samples were submitted to the AgriLife Genomic and Bioinformatic Center. Libraries were made following the TruSeq RNA sample preparation protocol. Sequencing of libraries was performed using Illumina SE 135 bp using the HiSeq 2500 platform. Three libraries failed with this approach and were later re-sequenced using Illumina PE 125 bp, however, one L sample at T1 yielded a low quality library and was not used in this analysis. Three biological replicates per treatment within each time point were sequenced using three lanes with the exception of L treatment at T1. Sequence cluster identification, quality prefiltering, base calling and uncertainty assessment were done in real time using Illumina's HCS 2.2.38 and RTA 1.18.61 software with default parameter settings. Sequencer basecall (.bcl) files were formatted into fastq files using bcl2fastq 1.8.4 script configureBclToFastq.pl. The sequence raw reads were cleaned using cutadapt 1.0 to remove barcode tags and adaptors. Individual samples were processed with FastQC, and the QC reports were checked as final confirmation of sequence quality.

5.2.6 Bioinformatic data analysis and gene annotation

The processed sequences were uploaded to Discovery Environment (DE) web interface and platform at CyVerse (www.iplantcollaborative.org) (Goff *et al.*, 2011). Tuxedo RNA-Seq apps (TopHat2, Cufflinks2, Cuffmerge2, Cuffdiff2) within DE interface were used to map sequences against the *S. lycopersicum* genome, Ensembl 14 (Sato *et al.*, 2012), to assemble transcripts, to create full transcriptome, and to identify differentially expressed genes (DEGs) according to the published protocol (Trapnell *et al.*, 2012). The analyses were done with the default false discovery rate (FDR = 0.05) and adjusted with Benjamini-Hochberg correction for multiple comparisons.

Transcriptomes were compared among treatments. Each treatment consisted of three biological replicates except one for which a low quality library was obtained. Transcriptomes of plants from C and P treatments were compared to evaluate plant response to herbivory. Transcriptomes of plants from C and L treatments were compared to evaluate plant response to herbivory and infection. Transcriptomes of plants from P and L treatments were compared to evaluate the difference in plant responses to Lso-negative and Lso-positive *B. cockerelli*. Each comparison was done with respect to each time point (T1, T2, T3). In total, nine comparisons were performed.

DEGs in each of the nine comparative transcriptomes were annotated using UniProt Knowledgebase (Bateman *et al.*, 2015) and further validated using tomato genome database at www.solgenomics.net (Fernandez-Pozo *et al.*, 2015). GO term enrichment analyses of up-regulated and down-regulated DEGs were performed using

PhytoMine (Goodstein *et al.*, 2012) with Holm-Bonferroni correction method to identify significantly enriched GO terms.

5.2.7 Comparing transcriptome results to RT-qPCR results

An aliquot of 500 ng of the total RNA from each sample was used for reverse transcription using Thermo Fisher Scientific Verso^{TM} cDNA Kit. The cDNA was diluted 5 times before it was used for analysis by quantitative real-time PCR (qRT-PCR). Each reaction consisted of 1 μL cDNA, 5 μL SensiFAST SYBR Hi-ROX mix (Bioline), 0.4 μL of 400 nM of each primer, and 3.2 μL of molecular grade water. Quantitative RT-PCR was performed in an Applied Biosystem 7300 Real-Time PCR System with the following parameters: 2 mins at 95 °C, followed by 40 cycles of 5s at 95 °C and 30s at 60 °C. The melting curve for each reaction was generated to test amplicon specificity at the last step. All RT-qPCR reactions were performed in three technical and three biological replicates. The relative expression of each gene was analyzed using the ΔΔCT method (Riedel *et al.*, 2014) using GADPH as gene reference. The primers (Table 5.1) were designed using *S. lycopersicum* transcript sequence and Primer3 (Rozen & Skaletsky, 2000). The transcript sequences can be found in the tomato genome database (Fernandez-Pozo et al., 2015). The amplification efficiency for each primer set was calculated using LinRegPCR (Ruijter et al., 2009). The relative expression of each gene was statistically tested. Gene expression data from RT-qPCR and from the transcriptome analyses were compared and Pearson product-moment correlation test was performed to evaluate the similarity in gene expression obtained using the RNA-seq (fold change from Cuffdiff) and RT-qPCR (ΔΔCT) methods.

Table 5.1 Primers for genes of interest.

Primers	Gene description	SNG Gene aliases	Primer sequence 5’-3’	Product size (bp)	Type of primers
GADPH_F	Glyceraldehyde-3-phosphate dehydrogenase	Solyc04g009030.2.1	CCTCCGTGTTCCCACCCCTA	178	Reference
GADPH_R			CACGTCACTGCACCGGAAGT		
SWEET_F	Sugar transporter SWEET	Solyc03g097610.2	TGCACCAAAGAAAGCCAGGGT	180	Target
SWEET_R			ACAATGCCTAAGGGTGCAACA		
HR_F	Hypersensitive response assisting protein	Solyc07g006560.2	CCCAAAGACATGTGGAAGGAAGC	174	Target
HR_R			TGTAGCAGAGTCACAAGGGACA		
PR10_F	Pathogenesis-related protein 10	Solyc09g090980.2	GCTGCTGGAGATGGAGGTTGT	161	Target
PR10_R			GCGTAGACAGAAGGATTAGCGAGG		
ACRE65_F	Avr9/Cf-9 rapidly elicited protein 65	Solyc03g082370.1	TCAGATCAAAAGACCGCCGCT	142	Target
ACRE65_R			CAAAACAGTGAACGCCGTCGAA		
PI1_F	Proteinase inhibitor I	Solyc09g089510.2	TCATGGCCTGAACTTGTTGGGA	178	Target
PI1_R			AGGGAGTAACTCGAACAATGCGT		

5.2.8 Protein assays

Plant leaves from P, L, or C plants at T1, T2, and T3 were collected, weighted and flash frozen. Peroxidase (POD) and polyphenol oxidase (PPO) activity assays were conducted according to the previously published protocol (Thaler et al., 1996). Briefly, 100 mg of frozen plant tissues were crushed in a microcentrifuge tube and homogenized in 1 mL of cold phosphate protein buffer (0.1 M $(K_2H/KH_2)PO_4$ buffer at pH 7) containing 7% polyvinyl-polypyrrolidone. The solution was then mixed with 0.4 mL of 10% triton X-100 and centrifuged at 10,000 g for ten minutes. The resultant supernatant was used for the assays. For PPO assays, 10 µL of protein extract were added to 60 µL of caffeic acid solution (78.9 mg of caffeic acid in 15 mL of 0.1 M $(K_2H/KH_2)PO_4$ buffer at pH 8). For POD assays, 10 µL of protein extract were added to 90 µL guiacol solution (60 µL guiacol and 20 µL 30% hydrogen peroxide in 20 mL of 0.1 M (K_2H/KH_2)PO_4 buffer at pH 8). Changes in absorbance were measured in a microplate reader (Tecan Infiniti Pro 200) at 470 nm in a kinetic loop for 10 mins using three technical replicates. The activity of the enzymes is expressed in delta OD/min/mg of protein. Protein quantification was performed using the Bradford protein assay method with bovine serum albumin as the protein standard. The standard curve was generated using 5 µL of protein standard and 250 µL of 1x Coomassie protein assay reagent (Thermal Scientific Inc.) in the microplate standard assay. The protein extracted from each plant was quantified in triplicate to evaluate the protein concentration for the calculation of the enzyme activity as indicated above.

5.3 Results

5.3.1 Lso infection in plants

Results from diagnostic PCR tests performed at the end of the experiment (4 weeks post infestation) indicated that all plants in the C and P treatments were negative for Lso, and all plants in the L treatment were positive for Lso infection.

5.3.2 Transcriptome analyses

A total of 27 purified RNA samples from three treatments and three time points were submitted for sequencing: three biological replicates per treatment-time. One L library at T1 failed twice and no more tissues were available for a third trial. From the 26 successfully sequenced libraries, a total of 558.9 million reads were obtained. On average, 80.98% of the reads mapped to the tomato genome and there were 17,965 assembled transcripts per library (Table 5.2).

Table 5.2 Number of reads mapped on to the So*lanum lycopersicum* genome and number of known transcripts assembled.

Library ID	Time	Treat-ment	Input read	Mapped read (percent of read)	Multiple alignments (percent of mapped reads)	Number of known tomato genes expressed (FPKM>0)
C1	T1	Control	12,663,523	8,708,476 (68.8%)	380,312 (4.4%)	17,240
C2	T2	Control	23,158,716	18,933,582 (81.8%)	579,588 (3.1%)	18,108
C3	T3	Control	16,449,666	13,271,207 (80.7%)	414,790 (3.1%)	17,382
C4	T1	Control	36,238,643	29,322,635 (80.9%)	829,069 (2.8%)	18,945
C5*	T2	Control	27,156,529	25,634,706 (94.4%)	815,860 (3.2%)	18,464
C6*	T3	Control	17,339,436	15,997,964 (92.3%)	573,664 (3.6%)	17,957
C7	T1	Control	15,089,619	12,137,778 (80.4%)	316,887 (2.6%)	17,840
C8	T2	Control	14,649,185	11,844,774 (80.9%)	293,276 (2.5%)	17,874
C9	T3	Control	18,198,266	13,377,164 (73.5%)	410,775 (3.1%)	17,962
P1	T1	Psyllid (Lso -)	32,624,707	25,186,305 (77.2%)	774,097 (3.1%)	18,276
P2	T2	Psyllid (Lso -)	20,889,499	15,203,153 (72.8%)	448,050 (2.9%)	17,496
P3	T3	Psyllid (Lso -)	22,688,753	20,475,731 (90.2%)	600,819 (2.9%)	18,053
P4	T1	Psyllid (Lso -)	17,182,550	13,786,703 (80.2%)	420,607 (3.1%)	18,042
P5	T2	Psyllid (Lso -)	16,240,822	13,042,309 (80.3%)	374,869 (2.9%)	17,815
P6	T3	Psyllid (Lso -)	16,663,633	13,404,255 (80.4%)	336,386 (2.5%)	17,941
P7	T1	Psyllid (Lso -)	17,118,776	13,244,944 (77.4%)	374,174 (2.8%)	17,687
P8	T2	Psyllid (Lso -)	58,642,355	49,548,712 (84.5%)	1,311,827 (2.6%)	18,861
P9	T3	Psyllid (Lso -)	29,204,270	24,135,240 (82.6%)	665,100 (2.8%)	18,438

Table 5.2 continued.

Library ID	**Time**	**Treat-ment**	**Input read**	**Mapped read (percent of read)**	**Multiple alignments (percent of mapped reads)**	**Number of known tomato genes expressed (FPKM>0)**
L1	T1	Psyllid (Lso +)	25,963,836	21,190,469 (81.6%)	617,196 (2.9%)	18,241
L2	T2	Psyllid (Lso +)	13,538,452	10,406,108 (76.9%)	304,659 (2.9%)	17,530
L3	T3	Psyllid (Lso +)	16,357,509	2,626,452 (77.2%)	342,693 (2.7%)	17,877
L4	T1	Psyllid (Lso +)	22,975,568	8,547,608 (80.7%)	554,158 (3.0%)	18,024
L5	T2	Psyllid (Lso +)	21,672,664	16,299,554 (75.2%)	425,899 (2.6%)	17,973
L6	T3	Psyllid (Lso +)	16,972,694	14,810,226 (87.3%)	356,112 (2.4%)	17,762
L8	T2	Psyllid (Lso +)	14,372,124	10,548,704 (73.4%)	230,919 (2.2%)	17,742
L9	T3	Psyllid (Lso +)	14,850,996	10,958,219 (73.8%)	232,458 (2.1%)	17,564
Average			21,496,261	17,409,345 (80.98%)	499,394	17,965

* mark the libraries sequenced with 125PE. T1, T2, and T3 represent one, two, and four weeks after infestation, respectively.

5.3.3 Gene ontology of all expressed genes

Gene ontology (GO) term analysis of the 100 most expressed genes from each library was performed. Terms associated with photosynthesis were enriched in all libraries as expected for leaf samples: among the Biological Process terms (GO:0015979, GO:0019685, GO:0019684, GO:0019253, GO:0009765, GO:0009853, GO:0018298, GO:0015977) and among the Molecular Function terms (GO:0016168 and GO:0016984).

5.3.4 Significantly differentially expressed genes (DEGs)

For each time point, three transcriptome comparisons were performed: C vs P (plants exposed to no insect vs to Lso-negative *B. cockerelli*), C vs L (plants exposed to no insect vs plants exposed to Lso-positive *B. cockerelli*) and P vs L (plants exposed to Lso-negative vs plants exposed to Lso-positive *B. cockerelli*). Depending on the comparison, there were between 24 and 341 DEGs (Table 5.3). In the C vs P comparison, over 65% of the DEGs were up-regulated at T1, T2, and T3 in response to *B. cockerelli* herbivory (Fig. 5.1). Similarly, larger percentages of the DEGs were up-regulated than down-regulated in the comparative transcriptomes of P vs L and C vs L at T2 and T3 (Fig. 5.2 and Fig.5.3**)**. However, the P vs L and C vs L comparative transcriptomes at T1 showed a larger percentage of the DEGs down-regulated than up-regulated.

Table 5.3 Significantly differentially expressed genes (DEGs)

Time	**Treatment comparisons**	**Treatment effects**	**Number of DEGs**	**Number (%) of up regulated DEGs**	**Number (%) of down regulated DEGs**
T1	C vs P	Herbivory	85	79 (92.9%)	6 (7.1%)
T2	C vs P	Herbivory	29	19 (65.5%)	10 (34.5%)
T3	C vs P	Herbivory	93	65 (69.9%)	28 (30.1%)
T1	C vs L	Combination	24	6 (25%)	18 (75%)
T2	C vs L	Combination	106	75 (70.8%)	31 (29.2%)
T3	C vs L	Combination	341	189 (55.4%)	152 (44.6%)
T1	P vs L	Infection	139	7 (5%)	132 (95%)
T2	P vs L	Infection	127	78 (61.4%)	49 (38.6%)
T3	P vs L	Infection	138	97 (70.3%)	41 (29.7%)

T1, T2, and T3 represent one, two, and four weeks after infestation, respectively.

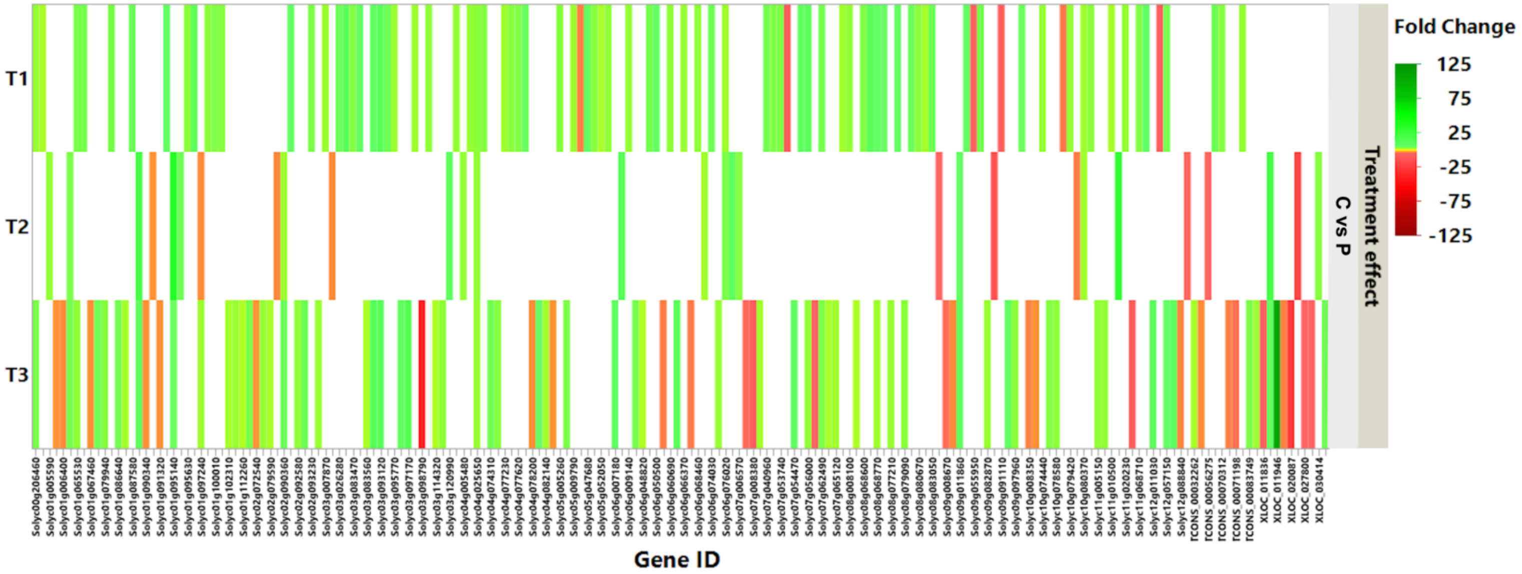

Figure 5.1 Heat map of significantly differentially expressed genes (DEGs) detected in comparative transcriptomes between plants exposed to no insect and to Lso-negative *B. cockerelli*. Green represents up-regulated genes. Red represents down-regulated genes. Fold change increases according to the darkness of each color. White represents genes that were not differentially expressed at a specific time point but were differentially expressed in other time points. T1, T2, and T3 represent one, two, and four weeks after infestation, respectively.

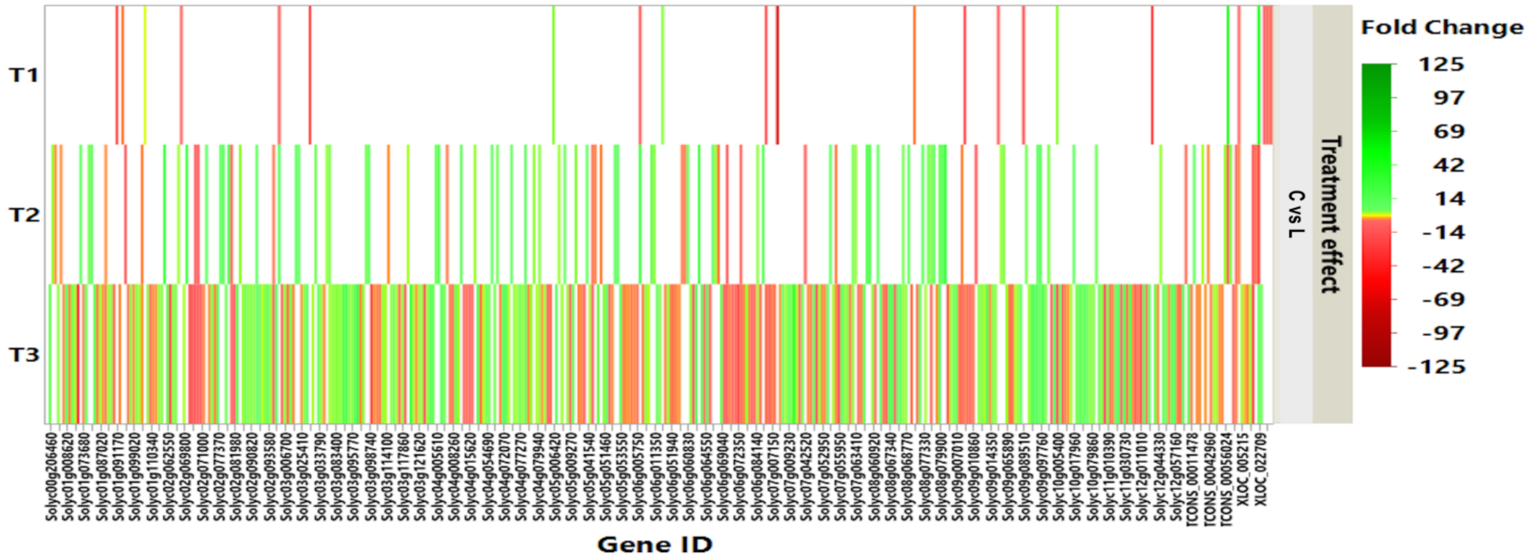

Figure 5.2 Heat map of significantly differentially expressed genes (DEGs) detected in the comparative transcriptomes between plants exposed to no insect and to Lso-positive *B. cockerelli*. Green represents up-regulated genes. Red represents down-regulated genes. Gene expression in fold change increases according to the darkness of each color. White represents the genes that were not differentially expressed at a specific time point but were differentially expressed in other time points. T1, T2, and T3 represent one, two, and four weeks after infestation, respectively.

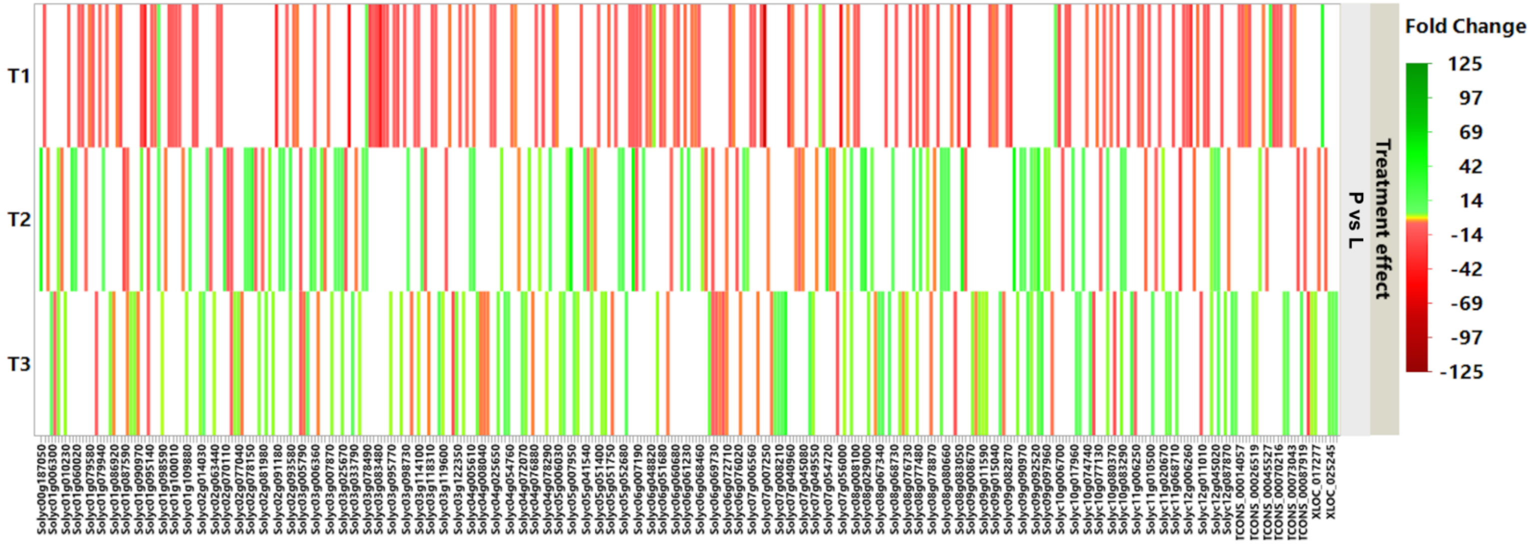

Figure 5.3 Heat map of significantly differentially expressed genes (DEGs) detected in the comparative transcriptomes between plants exposed to Lso-negative and to Lso-positive *B. cockerelli*. Green represents up-regulated genes. Red represents down-regulated genes. Gene expression in fold change increases according to the darkness of each color. White represents the genes that were not differentially expressed at a specific time point but were differentially expressed in other time points. T1, T2, and T3 represent one, two, and four weeks after infestation, respectively.

The results of all the comparative transcriptomes revealed that changes in plant gene expression under each treatment and time point were unique (Fig. 5.4). Only one gene, Solyc03g026280 (CBF1), was differentially expressed in all three comparisons at T1. No DEG was shared among the three comparisons at T2 and T3. The rest of the genes were significantly differentially expressed in either one or two comparisons. Lists of DEGs identified at each time point were tabulated (C vs P: Table A.5, C vs L: Table A.6, and P vs L: Table A.7).

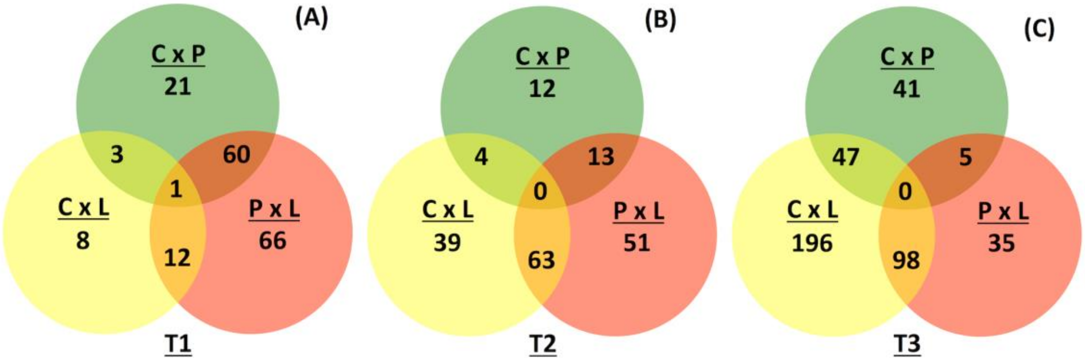

Figure 5.4 Venn diagrams of significantly differentially expressed genes (DEG) between tomato plants within their specified treatments according to the time point. (A) DEGs after one week (T1). (B) DEGs after two weeks (T2). (C) DEGs after four weeks (T3). C: control plants, P: plants infested with Lso-negative *B. cockerelli*, L: plants infested with Lso-positive *B. cockerelli*. C and P plants tested negative for Lso. L plants tested positive for Lso.

5.3.5 C vs P comparative transcriptome

The gene ontology (GO) terms of DEGs in the C vs P comparison were identified (Table A.8). The enrichment analyses of GO term were performed for each time point ($P < 0.05$, Table 5.4) and used to evaluate plant induced response. At T1, 13 biological process (BP) and 2 molecular function (MF) GO terms were significantly enriched among the up-regulated DEGs. These GO terms were associated with the function of gene transcription and metabolic processes. Specifically, these GO terms were associated with *WRKY* and *ethylene-responsive transcription factors* (*ERF*) genes which regulate plant defenses and immunity (Table 5.5). Among the down-regulated DEGs at T1, only one BP and one MF GO terms were significantly enriched. These GO terms were associated with photosynthesis.

Table 5.4 Significantly enriched gen ontology (GO) terms associated with the up- and down-regulated genes in the C vs P comparative transcriptomes.

Time	Exposure Period	Group	Category	GO Term	p-Value
T1	1 week	Up	BP	Regulation of transcription, DNA-dependent (GO:0006355)	0.017
T1	1 week	Up	BP	Regulation of RNA biosynthetic process (GO:2001141)	0.017
T1	1 week	Up	BP	Regulation of RNA metabolic process (GO:0051252)	0.017
T1	1 week	Up	BP	Regulation of biosynthetic process (GO:0009889)	0.019
T1	1 week	Up	BP	Regulation of macromolecule biosynthetic process (GO:0010556)	0.019
T1	1 week	Up	BP	Regulation of cellular biosynthetic process (GO:0031326)	0.019
T1	1 week	Up	BP	Regulation of cellular macromolecule biosynthetic process (GO:2000112)	0.019
T1	1 week	Up	BP	Regulation of gene expression (GO:0010468)	0.025
T1	1 week	Up	BP	Regulation of nucleobase-containing compound metabolic process (GO:0019219)	0.028
T1	1 week	Up	BP	Regulation of nitrogen compound metabolic process (GO:0051171)	0.028
T1	1 week	Up	BP	Regulation of macromolecule metabolic process (GO:0060255)	0.028
T1	1 week	Up	BP	Regulation of primary metabolic process (GO:0080090)	0.033
T1	1 week	Up	BP	Regulation of cellular metabolic process (GO:0031323)	0.036
T1	1 week	Up	CC	No significant enrichment	NA
T1	1 week	Up	MF	Nucleic acid binding transcription factor activity (GO:0001071)	1.14E-04
T1	1 week	Up	MF	Sequence-specific DNA binding transcription factor activity (GO:0003700)	1.14E-04
T1	1 week	Down	BP	Photosynthetic electron transport in photosystem II (GO:0009772)	0.018341
T1	1 week	Down	CC	No significant enrichment	NA
T1	1 week	Down	MF	Electron transporter in photosynthesis activity (GO:0045156)	0.009411

Table 5.4 continued.

Time	**Exposure Period**	**Group**	**Category**	**GO Term**	**p-Value**
T2	2 weeks	Up	BP	No significant enrichment	NA
T2	2 weeks	Up	CC	No significant enrichment	NA
T2	2 weeks	Up	MF	Ribonuclease T2 activity (GO:0033897)	0.013363
T2	2 weeks	Up	MF	Endoribonuclease activity, producing 3'-phosphomonoesters (GO:0016892)	0.016685
T2	2 weeks	Up	MF	Endonuclease activity with DNA or RNA (GO:0016894)	0.016685
T2	2 weeks	Down	BP	No significant enrichment	NA
T2	2 weeks	Down	CC	No significant enrichment	NA
T2	2 weeks	Down	MF	No significant enrichment	NA
T3	4 weeks	Up	BP	Cellular glucan metabolic process (GO:0006073)	9.88E-06
T3	4 weeks	Up	BP	Glucan metabolic process (GO:0044042)	9.88E-06
T3	4 weeks	Up	BP	Cellular carbohydrate metabolic process (GO:0044262)	1.46E-05
T3	4 weeks	Up	BP	Cellular polysaccharide metabolic process (GO:0044264)	1.46E-05
T3	4 weeks	Up	BP	Polysaccharide metabolic process (GO:0005976)	2.39E-05
T3	4 weeks	Up	CC	Apoplast (GO:0048046)	1.62E-06
T3	4 weeks	Up	CC	Extracellular region (GO:0005576)	7.20E-06
T3	4 weeks	Up	CC	Cell wall (GO:0005618)	1.14E-04
T3	4 weeks	Up	CC	External encapsulating structure (GO:0030312)	1.39E-04
T3	4 weeks	Up	CC	Cell periphery (GO:0071944)	0.001315
T3	4 weeks	Up	MF	Xyloglucan:xyloglucosyl transferase activity (GO:0016762)	1.25E-07
T3	4 weeks	Up	MF	Transferase activity, transferring glycosyl groups (GO:0016757)	0.008476
T3	4 weeks	Up	MF	Transferase activity, transferring hexosyl groups (GO:0016758)	0.022509
T3	4 weeks	Down	BP	No significant enrichment	NA

Table 5.4 continued.

Time	**Exposure Period**	**Group**	**Category**	**GO Term**	**p-Value**
T3	4 weeks	Down	CC	No significant enrichment	NA
T3	4 weeks	Down	MF	No significant enrichment	NA

NA = not applicable. P-value was adjusted for multiple comparisons by the Holm-Bonferroni method. Biological process (BP, blue). Cellular component (CC, green). Molecular function (MF, red). C: control plants. P: plants infested with Lso-negative *B. cockerelli*. T1, T2, and T3 represent one, two, and four weeks after infestation, respectively.

Table 5.5 List of DEGs identified in the C vs P comparative transcriptomes involved in plant induced defenses, photosynthesis, and sugar metabolism.

Gene name	Gene Description	Time	Direction	Function	Supporting literature DOI
Solyc03g082370.1	Avr9/Cf-9 rapidly elicited protein 65	T1	UP	Plant hypersensitive response	10.1105/tpc.104.026013
CZFP1 (Solyc04g077980)	C2H2-type zinc finger protein	T1	UP	Plant defense and disease resistance	10.1371/journal.pone.0042578
GRAS4 (Solyc01g100200)	GRAS family transcription factor	T1	UP	Plant disease resistance and abiotic stress response, axillary shoot meristem formation	10.3389/fpls.2016.00353
HSC70.1 (Solyc06g076020)	Heat shock cognate protein 70-1	T1	UP	Plant induced defense	10.1016/S0981-9428(01)01284-0
Solyc01g097240.2	Pathogenesis-related protein 4B	T1	UP	Plant systemic defenses	10.3103/S1068367411040082, 10.1007/978-94-007-1933-0_17, 10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
Solyc01g091590.2	SRC2 protein (plant immunity)	T1	UP	Hypersensitive response	10.1093/jxb/erv161
SAP6 (Solyc08g079700)	Stress-associated protein 6	T1	UP	Responding to stress	
Solyc05g009790.1	Transcriptional factor B3	T1	UP	Plant defenses	
Solyc06g066370.2	WRKY transcription factor 1	T1	UP	Plant defense and immunity	10.1104/pp.109.138990
Solyc06g068460.2	WRKY transcription factor 1	T1	UP	Plant defense and immunity	10.1104/pp.109.138990
Solyc08g006320.2	WRKY transcription factor 3	T1	UP	Plant defense and immunity	10.1104/pp.109.138990
Solyc03g095770.2	WRKY transcription factor 6	T1	UP	Plant defense and immunity	10.1104/pp.109.138990
Solyc09g014990.2	WRKY-like transcription factor	T1	UP	Plant defense and immunity	10.1104/pp.109.138990
WRKY3 (Solyc01g095630)	WRKY3 (response to wounding)	T1	UP	Plant defense and immunity	10.1104/pp.109.138990
LE-ACS6 (Solyc08g008100)	1-aminocyclopropane-1-carboxylic acid synthase gene (LEACS6)	T1	UP	Regulates ethylene production	10.1104/pp.123.3.979

Table 5.5 continued.

Gene name	Gene Description	Time	Direction	Function	Supporting literature DOI
ERF3 (TCONS_00070312)	Ethylene response factor 3	T1	UP	Responding to ethylene	10.1186/1471-2229-12-190, 10.1105/tpc.12.5.771
ERF1 (Solyc06g065820)	Ethylene responsive transcription factor (ERF1)	T1	UP	Responding to ethylene	10.1186/1471-2229-12-190, 10.1105/tpc.12.5.771
DDTFR10/A (Solyc05g052040)	Ethylene responsive transcription factor 1a	T1	UP	Responding to ethylene	10.1186/1471-2229-12-190, 10.1105/tpc.12.5.771
Solyc08g078190.1	Ethylene responsive transcription factor 1a	T1	UP	Responding to ethylene	10.1186/1471-2229-12-190, 10.1105/tpc.12.5.771
Solyc05g052050.1	Ethylene responsive transcription factor 1a	T1	UP	Responding to ethylene	10.1186/1471-2229-12-190, 10.1105/tpc.12.5.771
Solyc10g006130.1	Ethylene responsive transcription factor 3a	T1	UP	Responding to ethylene	10.1186/1471-2229-12-190, 10.1105/tpc.12.5.771
Solyc07g053740.1	Ethylene-responsive transcription factor 4	T1	UP	Responding to ethylene	10.1186/1471-2229-12-190, 10.1105/tpc.12.5.771
CBF1 (Solyc03g026280)	C-repeat binding factor 1	T1	UP	Protect of PSII and PSI	10.1111/j.1438-8677.2010.00365.x
TXET-B2 (Solyc07g056000)	Xyloglucan endotransglucosylase/hydrolase 7	T1	UP	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
Solyc03g093110.2	Xyloglucan endotransglucosylase/hydrolase 9	T1	UP	Cell wall remodeling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
Solyc03g093120.2	Xyloglucan endotransglucosylase/hydrolase 9	T1	UP	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
Solyc09g055950.1	Photosystem II D2 protein	T1	DOWN	Photosynthesis	
Solyc12g039030.1	Photosystem Q(B) protein	T1	DOWN	Photosynthesis	
HSC70.1 (Solyc06g076020)	Heat shock cognate protein 70-1	T2	UP	Plant induced defense	10.1016/S0981-9428(01)01284-0
Solyc07g006560.2	Hypersensitive response assisting protein	T2	UP	Hypersensitive response	10.1007/s11103-005-1002-3
LEMMI9 (Solyc01g095150)	Late embryogenesis abundant protein	T2	UP	Hypersensitive response	

Table 5.5 continued.

Gene name	**Gene Description**	**Time**	**Direction**	**Function**	**Supporting literature DOI**
Solyc11g018800.1	Peroxidase 2 (POD2)	T2	UP	Plant defenses	10.1023/A:1014904815352, 10.2478/jppr-2014-0057
CHI3 (Solyc02g082920)	Acidic 26 kDa endochitinase	T2	DOWN	Defense against pathogen	10.1111/j.1365-3040.2005.01471.x, 10.1155/2012/137037
ARG2 (Solyc01g091170)	Arginase 2	T2	DOWN	Plant induced defenses, reduce herbivore protein digestion	10.1074/jbc.M407151200, 10.1073/pnas.0509026102
TOMQ`B (Solyc10g079860)	Glucan endo-1,3-beta-D-glucosidase	T2	DOWN	Defense against pathogen, similar to PR gene	10.1007/BF00029854, 10.5958/j.2229-4473.26.2s.141
Solyc09g007010.1	Pathogenesis-related protein (PR1)	T2	DOWN	Plant defenses and systemic acquired resistance	10.1007/978-94-007-1933-0_17, 10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7, 10.1007/s10658-014-0394-9
Solyc01g097240.2	Pathogenesis-related protein 4B	T2	DOWN	Plant systemic defenses	10.1007/978-94-007-1933-0_17, 10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
AS1 (Solyc06g007180)	Asparagine synthetase	T3	UP	Plant defense responses to microbial pathogens	10.1111/j.1365-313X.2011.04622.x, 10.1093/pcp/pch092
Solyc02g064680.2	Calcium-transporting ATPase	T3	UP	Receptor-mediated signaling in plant immune responses and development	10.1104/pp.111.192575
Solyc09g082870.1	Calcium-transporting ATPase	T3	UP	Receptor-mediated signaling in plant immune responses and development	10.1104/pp.111.192575

Table 5.5 continued.

Gene name	**Gene Description**	**Time**	**Direction**	**Function**	**Supporting literature DOI**
Solyc04g078340.2	Cytochrome P450	T3	UP	Production of plant allelochemicals	10.1016/j.bbapap.2010.09.012, 10.1248/bpb.35.824, 10.1098/rstb.2012.0426, 10.1146/annurev-arplant-042809-112305
Solyc04g080820.2	Cytokinin oxidase/dehydrogenase	T3	UP	Controlling local cytokinin levels	10.1007/s10265-003-0096-4, 10.1016/j.jplph.2014.06.021
Solyc01g097240.2	Pathogenesis-related protein 4B	T3	UP	Plant defenses against bacterial pathogen	10.1007/978-94-007-1933-0_17, 10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
Solyc02g092580.2	Peroxidase (POD)	T3	UP	Plant defense against bacterial pathogen	10.1155/2012/137037, 10.1023/A:1014904815352, 10.2478/jppr-2014-0057
ERF1 (Solyc06g065820)	Ethylene response factor 1 (ERF1)	T3	UP	Responding to ethylene	10.1186/1471-2229-12-190
LEXET2 (Solyc07g009380)	Xyloglucan endotransglucosylase/hydrolase 2	T3	UP	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
Solyc12g011030.1	Xyloglucan endotransglucosylase/hydrolase 7	T3	UP	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
TXET-B2 (Solyc07g056000)	Xyloglucan endotransglucosylase/hydrolase 7	T3	UP	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
Solyc03g093110.2	Xyloglucan endotransglucosylase/hydrolase 9	T3	UP	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
Solyc03g093120.2	Xyloglucan endotransglucosylase/hydrolase 9	T3	UP	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844

Table 5.5 continued.

Gene name	Gene Description	Time	Direction	Function	Supporting literature DOI
BR1 (Solyc09g092520)	Xyloglucan endotransglycosylase	T3	UP	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
ARPI (Solyc11g021060.1)	Auxin-related proteinase inhibitor (ARPI)	T3	DOWN	Plant defenses	10.1104/pp.104.2.811, 10.1007/BF00021815
Solyc04g082710.2	Cathepsin B-like cysteine proteinase 3	T3	DOWN	Hypersensitive response and plant disease resistance	10.1111/j.1365-313X.2007.03226.x
Solyc01g067460.1	Glutaredoxin family protein	T3	DOWN	Anti-oxidant defense	10.1016/j.bbamcr.2007.10.017
Solyc01g006290.2	Peroxidase (POD)	T3	DOWN	Plant defense against bacterial pathogen	10.1155/2012/137037, 10.1023/A:1014904815352, 10.2478/jppr-2014-0057
TD (Solyc09g008670)	Threonine dehydratase (Threonine deaminase)	T3	DOWN	Induced by wounding and JA, plant defense, degrade essential amino acid in herbivory midgut	10.1073/pnas.0509026102
Solyc01g090340.2	Ethylene responsive transcription factor 1b	T3	DOWN	Responding to ethylene	10.1186/1471-2229-12-190
Solyc02g072540.2	Non-specific serine/threonine protein kinase	T3	DOWN	Hypersensitive response, resistance to bacterial disease in tomato, Avr disease resistance	10.1016/0092-8674(95)90208-2, 10.1105/tpc.104.161010, 10.1074/jbc.273.25.15860

Table 5.5 continued.

C: control plants. P: plants infested with Lso-negative *B. cockerelli*. T1, T2, and T3 represent one, two, and four weeks after infestation, respectively.

At T2, 3 MF GO terms were significantly enriched among the up-regulated DEGs, they were associated with nuclease activity (Table 5.4). These GO terms were associated with genes involved in plant hypersensitive response affecting plant defenses. Also in association with plant defenses, a peroxidase gene was up-regulated in response to *B. cockerelli* (Table 5.5). Interestingly, five genes associated with plant defenses were down-regulated.

Similar to the analysis of T2, no GO term was enriched among the down-regulated DEGs at T3. But, there were five BP, five cellular component (CC), and three MF GO terms significantly enriched among the up-regulated DEGs **(**Table 5.4**)**. The enriched GO terms were associated with polysaccharide metabolism and cell wall processes. The up-regulated DEGs associated with these GO terms were xyloglucan hydrolase genes. These genes not only play important roles in polysaccharide metabolic processes but also important role in cell wall remodeling and plant defenses (Table 5.5). Other plant defense genes such as cytochrome P450, pathogenesis-related, and Calcium-transporting ATPase were also up-regulated. Interestingly, peroxidase genes were among the up-regulated and down-regulated DEGs. Other down-regulated DEGs involved in plant defense were Auxin-related proteinase inhibitor (ARPI) and Threonine dehydratase.

5.3.6 C vs L comparative transcriptome

The GO terms associated with the DEGs identified in the C vs L comparison were identified (Table A.9). In the C vs L comparisons, the number of DEGs increased with time (Table 5.3). At T1, the C vs L comparative transcriptome had the lowest number of DEGs out of the nine comparisons. Significant enrichments of GO terms associated with photosynthesis were found among the down-regulated genes but no significantly enrichment was found among the GO terms of up-regulated genes (Table 5.6). Plants exposed to Lso-positive *B. cockerelli* also down-regulated plant defense genes such as arginase, asparagine synthetase, Avr9/Cf-9 rapidly elicited 65, metallocarboxypeptidase inhibitor, and threonine dehydratase (Table 5.7).

Table 5.6 Significantly enriched gene ontology (GO) terms associated with the up- and down-regulated genes in the C vs L comparative transcriptomes

Time	Exposure Period	Group	Category	GO Term	p-Value
T1	1 week	Up	BP	No significant enrichment	NA
T1	1 week	Up	CC	No significant enrichment	NA
T1	1 week	Up	MF	No significant enrichment	NA
T1	1 week	Down	BP	Photosynthetic electron transport in photosystem II (GO:0009772)	0.009179
T1	1 week	Down	BP	Photosynthetic electron transport chain (GO:0009767)	0.049913
T1	1 week	Down	CC	No significant enrichment	NA
T1	1 week	Down	MF	Electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity (GO:0045156)	0.023495
T1	2 weeks	Up	BP	No significant enrichment	NA
T2	2 weeks	Up	CC	No significant enrichment	NA
T2	2 weeks	Up	MF	Endopeptidase inhibitor activity (GO:0004866)	0.019659
T2	2 weeks	Up	MF	Peptidase inhibitor activity (GO:0030414)	0.019659
T2	2 weeks	Up	MF	Peptidase regulator activity (GO:0061134)	0.019659
T2	2 weeks	Up	MF	Endopeptidase regulator activity (GO:0061135)	0.019659
T2	2 weeks	Down	BP	Photosynthesis, light harvesting (GO:0009765)	1.10E-04
T2	2 weeks	Down	BP	Photosynthesis, light reaction (GO:0019684)	0.004516
T2	2 weeks	Down	CC	No significant enrichment	NA
T2	2 weeks	Down	MF	No significant enrichment	NA
T3	4 weeks	Up	BP	Cellular glucan metabolic process (GO:0006073)	0.023358
T3	4 weeks	Up	BP	Glucan metabolic process (GO:0044042)	0.023358
T3	4 weeks	Up	BP	Cellular polysaccharide metabolic process (GO:0044264)	0.033654
T3	4 weeks	Up	CC	Extracellular region (GO:0005576)	9.54E-05
T3	4 weeks	Up	CC	Apoplast (GO:0048046)	1.48E-04

Table 5.6 continued.

Time	Exposure Period	Group	Category	GO Term	p-Value
T3	4 weeks	Up	CC	Cell wall (GO:0005618)	0.009209
T3	4 weeks	Up	CC	External encapsulating structure (GO:0030312)	0.011086
T3	4 weeks	Up	MF	Xyloglucan:xyloglucosyl transferase activity (GO:0016762)	1.55E-04
T3	4 weeks	Up	MF	Hydrolase activity, hydrolyzing O-glycosyl compounds (GO:0004553)	0.006246
T3	4 weeks	Up	MF	Hydrolase activity, acting on glycosyl bonds (GO:0016798)	0.010895
T3	4 weeks	Up	MF	Heme binding (GO:0020037)	0.034246
T3	4 weeks	Up	MF	Sequence-specific DNA binding (GO:0043565)	0.036988
T3	4 weeks	Down	BP	Photosynthesis, light harvesting (GO:0009765)	1.99E-15
T3	4 weeks	Down	BP	Photosynthesis, light reaction (GO:0019684)	3.58E-10
T3	4 weeks	Down	BP	Photosynthesis (GO:0015979)	2.99E-07
T3	4 weeks	Down	BP	Generation of precursor metabolites and energy (GO:0006091)	4.72E-05
T3	4 weeks	Down	CC	No significant enrichment	NA
T3	4 weeks	Down	MF	Hydrolase activity, acting on ester bonds (GO:0016788)	0.017596

C: control plants. L: plants infested with Lso-positive *B. cockerelli*. T1, T2, and T3 represent one, two, and four weeks after infestation, respectively. NA = not applicable. P-value was adjusted for multiple comparisons by the Holm-Bonferroni method Biological process (BP, blue). Cellular component (CC, green). Molecular function (MF, red).

Table 5.7 List of DEGs identified in the C vs L comparative transcriptomes involved in plant defense, photosynthesis, and sugar metabolism.

Gene name	Gene Description	Time	Direction	Function	Supporting literature DOI
ARG2 (Solyc01g091170)	Arginase 2	T1	DOWN	Plant induced defenses, reduce herbivore protein digestion	10.1074/jbc.M407151200, 10.1073/pnas.0509026102
AS1 (Solyc06g007180)	Asparagine synthetase	T1	DOWN	Plant defense responses to microbial pathogens	10.1111/j.1365-313X.2011.04622.x, 10.1093/pcp/pch092
Solyc03g082370.1	Avr9/Cf-9 rapidly elicited protein 65	T1	DOWN	Plant hypersensitive response	10.1105/tpc.104.026013
Solyc07g007250.2	Metallocarboxypeptidase inhibitor (wound-induced)	T1	DOWN	Wound-induced plant defense	10.1016/S0014-5793(98)01447-1
Solyc09g089510.2	Proteinase inhibitor I	T1	DOWN	Defense against insects by inhibiting insect proteinase to reduce digestion	10.1007/BF02028503
TD (Solyc09g008670)	Threonine dehydratase (Threonine deaminase)	T1	DOWN	Induced by wounding and JA, plant defense, degrade essential amino acid in herbivory midgut	10.1073/pnas.0509026102, 10.1073/pnas.1016157108
Solyc09g055950.1	Photosystem II D2 protein	T1	DOWN	Photosynthesis	
Solyc12g039030.1	Photosystem Q(B) protein	T1	DOWN	Photosynthesis	
CBF1 (Solyc03g026280)	C-repeat binding factor 1	T1	DOWN	Protect of PSII and PSI	10.1111/j.1438-8677.2010.00365.x
AS1 (Solyc06g007180)	Asparagine synthetase 1	T2	UP	Plant defense responses to microbial pathogens	10.1111/j.1365-313X.2011.04622.x, 10.1093/pcp/pch092
Solyc04g078340.2	Cytochrome P450	T2	UP	Production of allelochemicals	10.1016/j.bbapap.2010.09.012, 10.1248/bpb.35.824, 10.1098/rstb.2012.0426, 10.1146/annurev-arplant-042809-112305
Solyc10g083690.2	Cytochrome P450	T2	UP	Production of allelochemicals	10.1016/j.bbapap.2010.09.012, 10.1248/bpb.35.824, 10.1098/rstb.2012.0426, 10.1146/annurev-arplant-042809-112305

Table 5.7 continued.

Gene name	Gene Description	Time	Direction	Function	Supporting literature DOI
Solyc04g080820.2	Cytokinin oxidase/dehydrogenase	T2	UP	Controlling local cytokinin levels	10.1007/s10265-003-0096-4, 10.1016/j.jplph.2014.06.021
Solyc03g078490.2	Glycosyltransferase	T2	UP	Plant defense, Mi-Mediated resistance, cell wall synthesis, carbohydrate biosynthesis	10.1104/pp.106.090241
Solyc07g006560.2	Hypersensitive response assisting protein	T2	UP	Hypersensitive response	10.1007/s11103-005-1002-3
Solyc08g079900.1	Pathogenesis related protein P69G	T2	UP	Multiple defenses against pathogens	10.1007/978-94-007-1933-0_17, 10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
PR-5 (Solyc08g080660)	Pathogenesis-related protein 5 (PR-5)	T2	UP	Plant defenses and systemic acquired resistance	10.1007/978-94-007-1933-0_17, 10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
Solyc02g092580.2	Peroxidase (POD)	T2	UP	Plant defense against bacterial pathogen	10.1023/A:1014904815352, 10.2478/jppr-2014-0057
Solyc03g025380.2	Peroxidase (POD)	T2	UP	Plant defense against bacterial pathogen	10.1023/A:1014904815352, 10.2478/jppr-2014-0057
Solyc04g071890.2	Peroxidase (POD)	T2	UP	Plant defense against bacterial pathogen	10.1023/A:1014904815352, 10.2478/jppr-2014-0057
Solyc02g078650.2	Polyphenol oxidase (PPO)	T2	UP	Plant defense against bacterial pathogen	10.1023/A:1014904815352

Table 5.7 continued.

Gene name	Gene Description	Time	Direction	Function	Supporting literature DOI
Solyc08g074680	Polyphenol oxidase (PPO)	T2	UP	Plant defense against bacterial pathogen	10.1023/A:1014904815352
Solyc03g020010.1	Kunitz-type trypsin inhibitor alpha chain	T2	UP	Plant induced defense against insects and pathogens	10.1104/pp.107.106229, 10.1104/pp.98.3.995, 10.1126/science.175.4023.776, 10.3390/ijms10062860
Solyc03g098730.1	Kunitz trypsin inhibitor	T2	UP	Plant induced defense against insects and pathogens	10.1104/pp.107.106229, 10.1104/pp.98.3.995, 10.1126/science.175.4023.776, 10.3390/ijms10062860
Solyc07g054720.1	Proteinase inhibitor type-2 CEVI57	T2	UP	Plant induced defense against insects and pathogens	10.1104/pp.107.106229, 10.1104/pp.98.3.995, 10.1126/science.175.4023.776, 10.3390/ijms10062860
Solyc09g090970.2	Similar to pathogenesis-related protein STH-2	T2	UP	Plant defenses	10.1007/978-94-007-1933-0_17, 10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
Solyc05g009790.1	Transcriptional factor B3	T2	UP	Plant defenses	
Solyc07g063410.2	NAC domain protein (No apical meristem protein)	T2	UP	Regulate No apical meristem (NAM) protein	10.1016/j.tplants.2004.12.010
Solyc05g007770.2	NAC domain transcription factor (No apical meristem protein)	T2	UP	Regulate No apical meristem (NAM) protein	10.1016/j.tplants.2004.12.010
Solyc04g005610.2	NAC domain transcription factor (No apical meristem protein)	T2	UP	Regulate No apical meristem (NAM) protein	10.1016/j.tplants.2004.12.010
Solyc08g021820.2	Auxin responsive gene	T2	UP	Responding to auxin	10.1073/pnas.1400074111

Table 5.7 continued.

Gene name	**Gene Description**	**Time**	**Direction**	**Function**	**Supporting literature DOI**
Solyc03g006360.2	Auxin-repressed gene	T2	UP	Responding to auxin	10.1007/s11240-013-0321-3
Solyc08g029000.2	Lipoxygenase (LOX)	T2	UP	Biosynthesis of Jasmonic Acid (JA), plant induced defenses	10.1104/pp.010787, http://10.1371/journal.pgen.1003964
BR1 (Solyc09g092520)	Xyloglucan endotransglycosylase	T2	UP	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
Solyc06g069730.2	Chlorophyll a-b binding protein 4	T2	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
Solyc02g070980.1	Chlorophyll a/b binding protein	T2	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
Solyc02g070990.1	Chlorophyll a/b binding protein	T2	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
Solyc03g005790.2	Chlorophyll a/b-binding protein	T2	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
PSBS (Solyc06g060340)	Chloroplast photosystem II-associated protein	T2	DOWN	Photosynthesis	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
Solyc07g042520.2	Sucrose synthase 4	T2	DOWN	Cleaves sucrose reversibly to UDP-glucose and fructose and is found in the cytosol	10.1080/10409230008984165, 10.1007/s00425-011-1356-5

Table 5.7 continued.

Gene name	Gene Description	Ti-me	Dire-ction	Function	Supporting literature DOI
Solyc09g008320.2	Xyloglucan endotransglucosylase/hydrolase 12	T2	DOWN	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
Solyc06g072710.2	RNA polymerase sigma factor	T2	DOWN	Required for the initiation of RNA synthesis	10.1016/S0923-2508(02)01368-2
Solyc06g065560.1	3-ketoacyl-CoA synthase	T3	UP	Synthesis of cuticular waxes	10.1104/pp.114.246348
CHI3 (Solyc02g082920)	Acidic 26 kDa endochitinase	T3	UP	Defense against pathogen	10.1111/j.1365-3040.2005.01471.x, 10.1155/2012/137037
ASC-1 (Solyc03g114600.2)	Alternaria stem canker resistance protein 1 (ASC1)	T3	UP	The plant disease resistance gene Asc-1 prevents disruption of sphingolipid metabolism during AAL-toxin-induced programmed cell death	
Solyc03g082370.1	Avr9/Cf-9 rapidly elicited protein 65 (hypersensitive response)	T3	UP	Plant hypersensitive response	10.1105/tpc.104.026013
Solyc01g008620.2	Beta-1 3-glucanase	T3	UP	Plant defense	1457981 JA 10.1104/pp. 126.3.1299, 10.1590/S1516-89132006000700004, 10. 1104/pp.103.024687
Solyc02g064680.2	Calcium-transporting ATPase	T3	UP	Receptor-mediated signaling in plant immune responses and development	10.1104/pp.111.192575
Solyc09g082870.1	Calcium-transporting ATPase	T3	UP	Receptor-mediated signaling in plant immune responses and development	10.1104/pp.111.192575
CATHDINH (Solyc03g098790.1)	Cathepsin D Inhibitor (chymotrypsin inhibitor 21)	T3	UP	Plant induced defenses	10.1104/pp.106.086587
Solyc01g006300.2	CEVI-1 Peroxidase	T3	UP	Phenolics-mediated resistance against necrotrophic phytopathogens	10.1155/2012/137037, 10.1023/A:1014904815352 , 10.2478/jppr-2014-0057

Table 5.7 continued.

Gene name	Gene Description	Ti-me	Dire-ction	Function	Supporting literature DOI
Solyc05g053550.2	Chalcone synthase 2	T3	UP	Key gene of the flavonoid/isoflavonoid biosynthesis	10.1007/s11101-011-9211-7
Solyc03g122350.2	Cytochrome P450	T3	UP	Production of Allelochemicals	10.1016/j.bbapap.2010.09.012, 10.1248/bpb.35.824, 10.1098/rstb.2012.0426, 10.1146/annurev-arplant-042809-112305
Solyc04g078290.2	Cytochrome P450	T3	UP	Production of Allelochemicals	10.1016/j.bbapap.2010.09.012, 10.1248/bpb.35.824, 10.1098/rstb.2012.0426, 10.1146/annurev-arplant-042809-112305
Solyc04g078340.2	Cytochrome P450	T3	UP	Production of Allelochemicals	10.1016/j.bbapap.2010.09.012, 10.1248/bpb.35.824, 10.1098/rstb.2012.0426, 10.1146/annurev-arplant-042809-112305
Solyc07g014670.2	Cytochrome P450	T3	UP	Production of Allelochemicals	10.1016/j.bbapap.2010.09.012, 10.1248/bpb.35.824, 10.1098/rstb.2012.0426, 10.1146/annurev-arplant-042809-112305
Solyc11g030730.1	Cytochrome P450	T3	UP	Production of Allelochemicals	10.1016/j.bbapap.2010.09.012, 10.1248/bpb.35.824, 10.1098/rstb.2012.0426, 10.1146/annurev-arplant-042809-112305
Solyc12g042480.1	Cytochrome P450	T3	UP	Production of Allelochemicals	10.1016/j.bbapap.2010.09.012, 10.1248/bpb.35.824, 10.1098/rstb.2012.0426, 10.1146/annurev-arplant-042809-112305

Table 5.7 continued.

Gene name	Gene Description	Ti-me	Dire-ction	Function	Supporting literature DOI
Solyc04g080820.2	Cytokinin oxidase/dehydrogenase	T3	UP	Controlling local cytokinin levels	10.1007/s10265-003-0096-4, 10.1016/j.jplph.2014.06.021
GGPS1 (Solyc11g011240)	Geranylgeranyl pyrophosphate synthase 1	T3	UP	Plant induced defenses	10.1007/s00425-006-0301-5
TOMQ`B (Solyc10g079860)	Glucan endo-1,3-beta-D-glucosidase	T3	UP	Defense against pathogen, similar to PR gene	10.1007/BF00029854, 10.5958/j.2229-4473.26.2s.141
Solyc03g078490.2	Glycosyltransferase	T3	UP	Plant defense, Mi-Mediated resistance, cell wall synthesis, carbohydrate biosynthesis	10.1104/pp.106.090241
Solyc12g096960.1	Major allergen Mal d 1.0502/Pathogenesis-related protein STH-2	T3	UP	Multiple defenses against pathogens	10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
Solyc09g091000.2	Major allergen Mal d 1//Pathogenesis-related protein STH-2	T3	UP	Multiple defenses against pathogens	10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
PTI5 (Solyc02g077370)	Pathogenesis-related genes transcriptional activator (PTI5)	T3	UP	Multiple defenses against pathogens	10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7

Table 5.7 continued.

Gene name	Gene Description	Time	Direction	Function	Supporting literature DOI
Solyc09g007010.1	Pathogenesis-related protein (PR1)	T3	UP	Plant defenses and systemic acquired resistance	10.1007/978-94-007-1933-0_17, 10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7, 10.1007/s10658-014-0394-9
Solyc09g090980.2	Pathogenesis-related protein 10 (PR10)	T3	UP	Multiple defenses against pathogens	10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
Solyc09g090990.2	Pathogenesis-related protein 10 (PR10)	T3	UP	Multiple defenses against pathogens	10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
Solyc01g097240.2	Pathogenesis-related protein 4B	T3	UP	Plant defenses against bacterial pathogen	10.1007/978-94-007-1933-0_17, 10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
Solyc02g092580.2	Peroxidase (POD)	T3	UP	Plant defense against bacterial pathogen	10.1155/2012/137037, 10.1023/A:1014904815352, 10.2478/jppr-2014-0057
Solyc03g006700.2	Peroxidase (POD)	T3	UP	Plant defense against bacterial pathogen	10.1155/2012/137037, 10.1023/A:1014904815352, 10.2478/jppr-2014-0057

Table 5.7 continued.

Gene name	Gene Description	Time	Direction	Function	Supporting literature DOI
Solyc06g050440.2	Peroxidase (POD)	T3	UP	Plant defense against bacterial pathogen	10.1155/2012/137037, 10.1023/A:1014904815352, 10.2478/jppr-2014-0057
Solyc11g018800.1	Peroxidase 2 (POD2)	T3	UP	Plant defense against bacterial pathogen	10.1155/2012/137037, 10.1023/A:1014904815352, 10.2478/jppr-2014-0057
Solyc08g067340.2	WRKY transcription factor	T3	UP	Plant defense and immunity	10.1104/pp.109.138990
Solyc03g095770.2	WRKY transcription factor 6	T3	UP	Plant defense and immunity	10.1104/pp.109.138990
Solyc08g067360.2	WRKY transcription factor 9	T3	UP	Plant defense and immunity	10.1104/pp.109.138990
Solyc09g014990.2	WRKY-like transcription factor	T3	UP	Plant defense and immunity	10.1104/pp.109.138990
Solyc08g079900.1	Pathogenesis related protein P69G	T3	UP	Plant defenses	10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
Solyc10g076480.1	Ammonium transporter	T3	UP	Increase nitrogen up-take for plant growth	10.1016/S0005-2736(00)00136-X
HT2 (Solyc09g075820.2)	Hexose transporter (HT2), sugar transporter	T3	UP	Sugar transporter, or Solute carrier family 2	10.1111/j.1365-3040.2008.01919.x
Solyc03g097610.2	Sugar transporter SWEET	T3	UP	Transport hexoses and sucrose	10.1111/nph.12445, 10.1038/nature15391, 10.1016/j.tibs.2015.05.005
ERF1 (Solyc06g065820)	Ethylene response factor 1 (ERF1)	T3	UP	Responding to ethylene	10.1186/1471-2229-12-190
ACO4 (Solyc07g049550)	1-aminocyclopropane-1-carboxylate oxidase 4 (ACC oxidase 4)	T3	UP	Ethylene biosynthesis, up-regulated in response to pathogen infection	10.1007/s10658-014-0394-9, 10.1007/s11738-012-1096-6, 10.1104/pp.121.4.1257
Solyc03g113520.2	Beta-1 3-galactosyltransferase-like protein	T3	UP	Secondary Cell Wall Biogenesis	10.1002/9780470015902.a0020102, 10.1104/pp.104.055087

Table 5.7 continued.

Gene name	**Gene Description**	**Time**	**Direction**	**Function**	**Supporting literature DOI**
Wiv-1 (Solyc10g083290)	Cell-wall invertase	T3	UP	Carbohydrate partitioning and regulation of sink-source interaction	10.1104/pp.108.127977, 10.3389/fpls.2014.00293, 10.1093/jxb/erg055
LEXET2 (Solyc07g009380)	Xyloglucan endotransglucosylase/hydrolase 2	T3	UP	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
Solyc12g011030.1	Xyloglucan endotransglucosylase/hydrolase 7	T3	UP	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
TXET-B2 (Solyc07g056000)	Xyloglucan endotransglucosylase/hydrolase 7	T3	UP	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
Solyc03g093120.2	Xyloglucan endotransglucosylase/hydrolase 9	T3	UP	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
BR1 (Solyc09g092520)	Xyloglucan endotransglycosylase	T3	UP	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
Solyc02g072540.2	Non-specific serine/threonine protein kinase	T3	DOWN	Hypersensitive response, resistance to bacterial disease in tomato, Avr disease resistance	10.1016/0092-8674(95)90208-2, 10.1105/tpc.104.161010, 10.1074/jbc.273.25.15860
ARPI (Solyc11g021060.1)	Auxin-related proteinase inhibitor (ARPI)	T3	DOWN	Plant defenses	10.1104/pp.104.2.811, 10.1007/BF00021815
LEEXP2 (Solyc06g049050)	Expansin	T3	DOWN	Cell Wall Remodeling and plant defense	10.3389/fpls.2015.00323
Solyc07g014730.2	Phospholipase A2	T3	DOWN	Involves in Auxin signal transduction	10.1016/j.plantsci.2012.11.002, 10.3389/fpls.2012.00056, 10.1105/tpc.110.074211
TD (Solyc09g008670)	Threonine dehydratase (Threonine deaminase)	T3	DOWN	Induced by wounding and JA, plant defense, degrade essential amino acid in herbivory midgut	10.1073/pnas.0509026102

Table 5.7 continued.

Gene name	**Gene Description**	**Time**	**Direction**	**Function**	**Supporting literature DOI**
Solyc06g053840.2	Auxin responsive protein, IAA1	T3	DOWN	Plant growth, leaf formation, shoot and root initiation	
IAA7 (Solyc06g053830.2)	Auxin responsive protein, IAA7	T3	DOWN	Plant growth, leaf formation, shoot and root initiation	
Solyc12g009200.1	Chlorophyll a-b binding protein	T3	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
Solyc07g063600.2	Chlorophyll a-b binding protein 13	T3	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
Solyc08g067330.1	Chlorophyll a-b binding protein 3C-like	T3	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
Solyc06g069730.2	Chlorophyll a-b binding protein 4	T3	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
CAB1B (Solyc02g070950)	Chlorophyll a/b binding protein	T3	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
CAB1B (Solyc02g070970)	Chlorophyll a/b binding protein	T3	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
CAB1D (Solyc02g071000)	Chlorophyll a/b binding protein	T3	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373

Table 5.7 continued.

Gene name	**Gene Description**	**Time**	**Direction**	**Function**	**Supporting literature DOI**
CAB5 (Solyc12g006140)	Chlorophyll a/b binding protein	T3	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
Solyc02g070980.1	Chlorophyll a/b binding protein	T3	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373,
Solyc02g070990.1	Chlorophyll a/b binding protein	T3	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
Solyc02g071000.1	Chlorophyll a/b binding protein	T3	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
Solyc03g005790.2	Chlorophyll a/b-binding protein	T3	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
GTS1 (Solyc04g014510)	Glutamine synthetase	T3	DOWN	Nitrogen assimilation	10.1093/jexbot/53.370.979, 10.1093/pcp/pch092
Solyc11g010410.1	1-aminocyclopropane-1-carboxylate oxidase	T3	DOWN	Ethylene biosynthesis	10.1007/s11738-012-1096-6, 10.1104/pp.121.4.1257
Solyc09g008320.2	Xyloglucan endotransglucosylase/hydrolase 12	T3	DOWN	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
Solyc06g072710.2	RNA polymerase sigma factor	T3	DOWN	Required for the initiation of RNA synthesis	10.1016/S0923-2508(02)01368-2

C: control plants. L: plants infested with Lso-positive *B. cockerelli*. T1, T2, and T3 represent one, two, and four weeks after infestation, respectively.

At T2, 70.8% of the DEGs were up-regulated (Table 5.3). Among those DEGs, four GO terms associated with peptidase inhibitory activity were significantly enriched (Table 5.6). These four enriched GO terms were associated with proteinase inhibitor genes which are involved in plant defense. Other up-regulated plant defense genes were cytochrome P450, asparagine synthetase, glycosyltransferase, peroxidase, polyphenol oxidase, lipoxygenase, endotransglycosylase, NAC domain transcription factor and pathogenesis-related (Table 5.7). Among the down-regulated genes, there were two enriched GO terms associated with plant photosynthesis. Down-regulation of photosynthesis genes such as chlorophyll a/b-binding can be associated with disease development and result in leaf chlorosis.

At T3, the C vs L comparative transcriptome had the greatest number of DEGs compared to the other comparative transcriptomes. In this comparison, there were ten times more DEGs than at T1 and over twice as many as in the P vs L comparative transcriptome at T3. Twelve GO terms were significantly enriched among the up-regulated genes and four GO terms were significantly enriched among the down-regulated genes (Table 5.6). The enriched GO terms among the up-regulated genes were primarily associated with WRKY transcription factor, peroxidase, xyloglucan hydrolase and cytochrome P450 genes, which are involved in plant defenses. Other notable up-regulated defense genes were cell-wall invertase, pathogenesis related, glycosyltransferase, glucan endo-1,3-beta-D-glucosidase, cathepsin D inhibitor, calcium-transporting ATPase, beta-1 e-glucanase, Avr9/Cf-9 rapidly elicited, alternarian stem canker resistance, and acidic 26 kDa endochitinase. Despite the up-regulation defense genes, genes potentially associated with disease development were also up-regulated, such as sugar transporter SWEET and Hexose transporter. The enriched GO terms among the down-regulated genes were associated with twelve chlorophyll a/b binding genes (**Table 6**). Other down-regulated genes were threonine dehydratase, auxin responsive, phospholipase A2, glutamine synthetase, and ACC oxidase.

5.3.7 P vs L comparative transcriptome

The GO associated with the DEGs in the P vs L comparison were identified (Table A.10). At T1, there were 139 DEGs in the P vs L comparison, 132 of them were down-regulated on plants exposed to Lso-positive *B. cockerelli* compared to plants exposed to Lso-negative *B. cockerelli*. Two MF GO terms associated with twelve transcription factors were enriched among the down-regulated genes (Table 5.8). Coincidentally, ten of the twelve down-regulated transcription factors in the P vs L comparative transcriptome were up-regulated in C vs P comparative transcriptome at T1 (Table 5.9). Other down-regulated genes included at least 26 known defense genes (Table 5.10) including jasmonate ZIM-domain, MAPK kinase 4, matrix metalloproteinase, metallocarboxypeptidase inhibitor, peroxidase 4 and proteinase inhibitor. Interestingly, only two known defense genes were up-regulated in the P vs L comparative transcriptomes. The two genes were glycosyltransferase and expansin, which play a role in restructuring plant cell walls.

Table 5.8 Significantly enriched gene ontology (GO) terms associated with the up- and down-regulated genes in the P vs L comparative transcriptomes

Time	Exposure Period	Group	Category	GO Term	p-Value
T1	1 week	Up	BP	No significant enrichment	NA
T1	1 week	Up	CC	No significant enrichment	NA
T1	1 week	Up	MF	No significant enrichment	NA
T1	1 week	Down	BP	No significant enrichment	NA
T1	1 week	Down	CC	No significant enrichment	NA
T1	1 week	Down	MF	Nucleic acid binding transcription factor activity (GO:0001071)	0.002967
T1	1 week	Down	MF	Sequence-specific DNA binding transcription factor activity (GO:0003700)	0.002967
T1	2 weeks	Up	BP	Response to biotic stimulus (GO:0009607)	0.034777
T2	2 weeks	Up	CC	No significant enrichment	NA
T2	2 weeks	Up	MF	Endopeptidase inhibitor activity (GO:0004866)	0.016218
T2	2 weeks	Up	MF	Peptidase inhibitor activity (GO:0030414)	0.016218
T2	2 weeks	Up	MF	Peptidase regulator activity (GO:0061134)	0.016218
T2	2 weeks	Up	MF	Endopeptidase regulator activity (GO:0061135)	0.016218
T2	2 weeks	Down	BP	Photosynthesis, light harvesting (GO:0009765)	2.33E-05
T2	2 weeks	Down	BP	Photosynthesis, light reaction (GO:0019684)	0.002455
T2	2 weeks	Down	CC	No significant enrichment	NA
T2	2 weeks	Down	MF	No significant enrichment	NA
T3	4 weeks	Up	BP	No significant enrichment	NA
T3	4 weeks	Up	CC	No significant enrichment	NA
T3	4 weeks	Up	MF	No significant enrichment	NA
T3	4 weeks	Down	BP	Photosynthesis, light harvesting (GO:0009765)	5.80E-04
T3	4 weeks	Down	BP	Photosynthesis, light reaction (GO:0019684)	0.023307

Table 5.8 continued.

Time	Exposure Period	Group	Category	GO Term	p-Value
T3	4 weeks	Down	CC	No significant enrichment	NA
T3	4 weeks	Down	MF	No significant enrichment	NA

P: plants infested with Lso-negative *B. cockerelli*. L: plants infested with Lso-positive *B. cockerelli*. T1, T2, and T3 represent one, two, and four weeks after infestation, respectively. NA = not applicable. P-value was adjusted for multiple comparisons by the Holm-Bonferroni method. Biological process (BP, blue). Cellular component (CC, green). Molecular function (MF, red).

Table 5.9 Similar genes associated with significantly enriched GO terms in the C vs P and P vs L comparative transcriptomes

Gene ID	Gene Descriptions	C vs P	P vs L
Solyc05g052050.1	Ethylene responsive transcription factor 1a	Up	Down
Solyc08g078190.1	Ethylene responsive transcription factor 1a	Up	Down
Solyc10g006130.1	Ethylene responsive transcription factor 3a	Up	Down
Solyc07g053740.1	Ethylene-responsive transcription factor 4	Up	Down
Solyc04g007000.1	Ethylene-responsive transcription factor 4	N.S.	Down
Solyc07g055710.2	Heat stress transcription factor A3	Up	N.S.
Solyc05g009790.1	Transcriptional factor B3	Up	Down
Solyc06g066370.2	WRKY transcription factor 1	Up	Down
Solyc06g068460.2	WRKY transcription factor 1	Up	Down
Solyc08g006320.2	WRKY transcription factor 3	Up	Down
Solyc03g095770.2	WRKY transcription factor 6	Up	Down
Solyc09g014990.2	WRKY-like transcription factor	Up	Down
Solyc10g009550.2	WRKY transcription factor	N.S.	Down

Table 5.10 List of DEGs identified in the P vs L comparative transcriptomes involved in plant defense, photosynthesis, and sugar metabolism.

Gene name	Gene Description	Ti-me	Direc-tion	Function	Supporting literature DOI
Solyc03g078490.2	Glycosyltransferase	T1	UP	Plant defense, Mi-Mediated resistance, cell wall synthesis, carbohydrate biosynthesis	10.1104/pp.106.090241
LEEXP2 (Solyc06g049050)	Expansin	T1	UP	Cell wall remodeling and plant defense	10.4172/22263
ARG2 (Solyc01g091170)	Arginase 2	T1	DOWN	Plant induced defenses, reduce herbivore protein digestion	10.1074/jbc.M407151200, 10.1073/pnas.0509026102
AS1 (Solyc06g007180)	Asparagine synthetase	T1	DOWN	Plant defense responses to microbial pathogens	10.1111/j.1365-313X.2011.04622.x, 10.1093/pcp/pch092
CZFP1 (Solyc04g077980)	C2H2-type zinc finger protein	T1	DOWN	Plant defense and Disease resistance	10.1371/journal.pone.0042578
Solyc02g064680.2	Calcium-transporting ATPase	T1	DOWN	Receptor-mediated signaling in plant immune responses and development	10.1104/pp.111.192575
Solyc09g082870.1	Calcium-transporting ATPase	T1	DOWN	Receptor-mediated signaling in plant immune responses and development	10.1104/pp.111.192575
GRAS4 (Solyc01g100200)	GRAS family transcription factor	T1	DOWN	Plant disease resistance and abiotic stress response, axillary shoot meristem formation	10.3389/fpls.2016.00353
Solyc07g042170.2	Jasmonate ZIM-domain protein 3	T1	DOWN	Regulate pathogen-induced cell death for plant defense	10.1371/journal.pone.0075728
LEMKK4 (TCONS_00023686)	MAPK kinase 4	T1	DOWN	Pto-mediated defense response of tomato	10.1074/jbc.M410323200
Solyc04g005040.1	Matrix metalloproteinase	T1	DOWN	Up-regulate in response to bacterial pathogens	10.1186/s12870-015-0536-z
Solyc07g007250.2	Metallocarboxypeptidase inhibitor (wound-induced)	T1	DOWN	Wound-induced plant defense	10.1016/S0014-5793(98)01447-1

Table 5.10 continued.

Gene name	Gene Description	Time	Direction	Function	Supporting literature DOI
Solyc04g071890.2	Peroxidase 4 (POD4)	T1	DOWN	Plant defense against bacterial pathogen	10.1155/2012/137037, 10.1023/A:1014904815352, 10.2478/jppr-2014-0057
Solyc09g089510.2	Proteinase inhibitor I	T1	DOWN	Defense against insects by inhibiting insect proteinase to reduce digestion	10.1007/BF02028503
Solyc01g091590.2	SRC2 protein (plant immunity)	T1	DOWN	Hypersensitive response	10.1093/jxb/erv161
SAP6 (Solyc08g079700)	Stress-associated protein 6	T1	DOWN	Responding to stress	
TD (Solyc09g008670)	Threonine dehydratase (Threonine deaminase)	T1	DOWN	Induced by wounding and JA, plant defense, degrade essential amino acid in herbivory midgut	10.1073/pnas.0509026102, 10.1073/pnas.1016157108
Solyc05g009790.1	Transcriptional factor B3	T1	DOWN	Plant defenses	
Solyc06g066370.2	WRKY transcription factor 1	T1	DOWN	Plant defense and immunity	10.1104/pp.109.138990
Solyc06g068460.2	WRKY transcription factor 1	T1	DOWN	Plant defense and immunity	10.1104/pp.109.138990
Solyc08g006320.2	WRKY transcription factor 3	T1	DOWN	Plant defense and immunity	10.1104/pp.109.138990
Solyc09g014990.2	WRKY-like transcription factor	T1	DOWN	Plant defense and immunity	10.1104/pp.109.138990
WRKY3 (Solyc01g095630)	WRKY3 (response to wounding)	T1	DOWN	Plant defense and immunity	10.1104/pp.109.138990
LE-ACS6 (Solyc08g008100)	1-aminocyclopropane-1-carboxylic acid synthase gene (LEACS6)	T1	DOWN	Regulates ethylene production	10.1104/pp.123.3.979
ERF3 (TCONS_00070312)	Ethylene response factor 3	T1	DOWN	Responding to ethylene	10.1186/1471-2229-12-190
ERF1 (Solyc06g065820)	Ethylene responsive transcription factor (ERF1)	T1	DOWN	Responding to ethylene	10.1186/1471-2229-12-190
DDTFR10/A (Solyc05g052040)	Ethylene responsive transcription factor 1a	T1	DOWN	Responding to ethylene	10.1186/1471-2229-12-190
Solyc08g078190.1	Ethylene responsive transcription factor 1a	T1	DOWN	Responding to ethylene	10.1186/1471-2229-12-190

Table 5.10 continued.

Gene name	Gene Description	Time	Direction	Function	Supporting literature DOI
Solyc10g006130.1	Ethylene responsive transcription factor 3a	T1	DOWN	Responding to ethylene	10.1186/1471-2229-12-190
Solyc07g053740.1	Ethylene-responsive transcription factor 4	T1	DOWN	Responding to ethylene	10.1186/1471-2229-12-190
CBF1 (Solyc03g026280)	C-repeat binding factor 1	T1	DOWN	Protect of PSII and PSI	10.1111/j.1438-8677.2010.00365.x
Solyc12g011030.1	Xyloglucan endotransglucosylase/hydrolase 7	T1	DOWN	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
TXET-B2 (Solyc07g056000)	Xyloglucan endotransglucosylase/hydrolase 7	T1	DOWN	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
TXET-B1 (Solyc12g017240)	Xyloglucan endotransglucosylase/hydrolase 7	T1	DOWN	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
Solyc03g093110.2	Xyloglucan endotransglucosylase/hydrolase 9	T1	DOWN	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
ARG2 (Solyc01g091170)	Arginase 2	T2	UP	Plant induced defenses, reduce herbivore protein digestion	10.1074/jbc.M407151200, 10.1073/pnas.0509026102
AS1 (Solyc06g007180)	Asparagine synthetase 1	T2	UP	Plant defense responses to microbial pathogens	10.1111/j.1365-313X.2011.04622.x, 10.1093/pcp/pch092
Solyc01g008620.2	Beta-1 3-glucanase	T2	UP	Plant defense	1457981 JA 10.1104/pp.126.3.1299, 10.1590/S1516-89132006000700004, 10.1104/pp.103.024687
Solyc04g078340.2	Cytochrome P450	T2	UP	Production of Allelochemicals	10.1016/j.bbapap.2010.09.012, 10.1248/bpb.35.824, 10.1098/rstb.2012.0426, 10.1146/annurev-arplant-042809-112305

Table 5.10 continued.

Gene name	Gene Description	Time	Direction	Function	Supporting literature DOI
Solyc10g083690.2	Cytochrome P450	T2	UP	Production of Allelochemicals	10.1016/j.bbapap.2010.09.012, 10.1248/bpb.35.824, 10.1098/rstb.2012.0426, 10.1146/annurev-arplant-042809-112305
Solyc12g042480.1	Cytochrome P450	T2	UP	Production of Allelochemicals	10.1016/j.bbapap.2010.09.012, 10.1248/bpb.35.824, 10.1098/rstb.2012.0426, 10.1146/annurev-arplant-042809-112305
Solyc04g080820.2	Cytokinin oxidase/dehydrogenase	T2	UP	Controlling local cytokinin levels	10.1007/s10265-003-0096-4, 10.1016/j.jplph.2014.06.021
TOMQ`B (Solyc10g079860)	Glucan endo-1,3-beta-D-glucosidase (PR)	T2	UP	Defense against pathogen, similar to PR gene	10.1007/BF00029854, 10.5958/j.2229-4473.26.2s.141
Solyc01g059980.2	Glucan endo-1,3-beta-glucosidase B (PR)	T2	UP	Defense against pathogen, similar to PR gene	10.1007/BF00029854, 10.5958/j.2229-4473.26.2s.141
Solyc03g078490.2	Glycosyltransferase	T2	UP	Plant defense, Mi-Mediated resistance, cell wall synthesis, carbohydrate biosynthesis	10.1104/pp.106.090241
Solyc09g091000.2	Major allergen Mal d 1//Pathogenesis-related protein STH-2	T2	UP	Defenses against pathogens	
Solyc08g079900.1	Pathogenesis related protein P69G	T2	UP	Multiple defenses against pathogens	10.1007/978-94-007-1933-0_17, 10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
Solyc09g007010.1	Pathogenesis-related protein (PR1)	T2	UP	Plant defenses and systemic acquired resistance	10.1007/978-94-007-1933-0_17, 10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7, 10.1007/s10658-014-0394-9

Table 5.10 continued.

Gene name	Gene Description	Time	Direction	Function	Supporting literature DOI
Solyc09g090980.2	Pathogenesis-related protein 10 (PR10)	T2	UP	Multiple defenses against pathogens	10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
Solyc01g097240.2	Pathogenesis-related protein 4B	T2	UP	Plant defenses against bacterial pathogen	10.1007/978-94-007-1933-0_17, 10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
PR-5 (Solyc08g080660)	Pathogenesis-related protein 5 (PR-5)	T2	UP	Plant defenses and systemic acquired resistance	10.1007/978-94-007-1933-0_17, 10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
Solyc02g092580.2	Peroxidase (POD)	T2	UP	Plant defense against bacterial pathogen	10.1023/A:1014904815352, 10.2478/jppr-2014-0057
Solyc03g006700.2	Peroxidase (POD)	T2	UP	Plant defense against bacterial pathogen	10.1023/A:1014904815352, 10.2478/jppr-2014-0057
Solyc03g025380.2	Peroxidase (POD)	T2	UP	Plant defense against bacterial pathogen	10.1023/A:1014904815352, 10.2478/jppr-2014-0057
Solyc02g078650.2	Polyphenol oxidase (PPO)	T2	UP	Plant defense against bacterial pathogen	10.1023/A:1014904815352
Solyc09g090970.2	Similar to pathogenesis-related protein STH-2	T2	UP	Plant defenses	10.1007/978-94-007-1933-0_17, 10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
Solyc05g007770.2	NAC domain transcription factor (No apical meristem protein)	T2	UP	Regulate No apical meristem (NAM) protein	10.1016/j.tplants.2004.12.010
Solyc04g005610.2	NAC domain transcription factor (No apical meristem protein)	T2	UP	Regulate No apical meristem (NAM) protein	10.1016/j.tplants.2004.12.010
ACS3 (Solyc02g091990)	1-aminocyclopropane-1-carboxylate synthase 3 (ACS3)	T2	UP	Ethylene biosynthesis	10.1105/tpc.001768, 10.1104/pp.121.4.1257
Solyc08g021820.2	Auxin responsive gene	T2	UP	Responding to auxin	10.1073/pnas.1400074111

Table 5.10 continued.

Gene name	Gene Description	Time	Direction	Function	Supporting literature DOI
Solyc03g006360.2	Auxin-repressed gene	T2	UP	Responding to auxin	10.1007/s11240-013-0321-3
Solyc08g029000.2	Lipoxygenase (LOX)	T2	UP	Biosynthesis of Jasmonic Acid (JA), plant induced defenses	10.1104/pp.010787, http://10.1371/journal.pgen.1003964
Solyc03g020010.1	Kunitz-type trypsin inhibitor alpha chain	T2	UP	Plant induced defense against insects and pathogens	10.1104/pp.107.106229, 10.1104/pp.98.3.995, 10.1126/science.175.4023.776, 10.3390/ijms10062860
Solyc03g098730.1	Kunitz trypsin inhibitor	T2	UP	Plant induced defense against insects and pathogens	10.1104/pp.107.106229, 10.1104/pp.98.3.995, 10.1126/science.175.4023.776, 10.3390/ijms10062860
Solyc07g054720.1	Proteinase inhibitor type-2 CEVI57	T2	UP	Plant induced defense against insects and pathogens	10.1104/pp.107.106229, 10.1104/pp.98.3.995, 10.1126/science.175.4023.776, 10.3390/ijms10062860,10.1016/j.plaphy.2004.03.006, 10.1073/pnas.92.10.4106
Solyc09g089540.2	Proteinase inhibitor I	T2	UP	Plant induced defense against insects and pathogens	10.1104/pp.107.106229, 10.1104/pp.98.3.995, 10.1126/science.175.4023.776, 10.3390/ijms10062860
Solyc10g083290 (Wiv-1)	Cell-wall invertase	T2	UP	Carbohydrate partitioning and regulation of sink-source interaction	10.1104/pp.108.127977, 10.3389/fpls.2014.00293, 10.1093/jxb/erg055
BR1 (Solyc09g092520)	Xyloglucan endotransglycosylase	T2	UP	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
HSC70.1 (Solyc06g076020)	Heat shock cognate protein 70-1	T2	DOWN	Plant induced defense	10.1016/S0981-9428(01)01284-0
Solyc12g009200.1	Chlorophyll a-b binding protein	T2	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373

Table 5.10 continued.

Gene name	**Gene Description**	**Time**	**Direction**	**Function**	**Supporting literature DOI**
Solyc06g069730.2	Chlorophyll a-b binding protein 4	T2	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
Solyc02g070980.1	Chlorophyll a/b binding protein	T2	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
Solyc02g070990.1	Chlorophyll a/b binding protein	T2	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
Solyc03g005790.2	Chlorophyll a/b-binding protein	T2	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
PSBS (Solyc06g060340)	Chloroplast photosystem II-associated protein	T2	DOWN	Photosynthesis	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
Solyc11g010410.1	1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase)	T2	DOWN	Ethylene biosynthesis	10.1007/s11738-012-1096-6, 10.1104/pp.121.4.1257
Solyc07g042520.2	Sucrose synthase 4	T2	DOWN	Cleaves sucrose reversibly to UDP-glucose and fructose and is found in the cytosol	10.1080/10409230008984165, 10.1007/s00425-011-1356-5
Solyc09g008320.2	Xyloglucan endotransglucosylase/hydrolase 12	T2	DOWN	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
Solyc06g072710.2	RNA polymerase sigma factor	T2	DOWN	Required for the initiation of RNA synthesis	10.1016/S0923-2508(02)01368-2
CHI3 (Solyc02g082920)	Acidic 26 kDa endochitinase	T3	UP	Defense against pathogen	10.1111/j.1365-3040.2005.01471.x, 10.1155/2012/137037
Solyc01g008620.2	Beta-1 3-glucanase	T3	UP	Plant defense	1457981 JA 10.1104/pp.126.3.1299, 10.1590/S1516-89132006000700004, 10.1104/pp.103.024687

Table 5.10 continued.

Gene name	Gene Description	Ti-me	Direc-tion	Function	Supporting literature DOI
CATHDINH (Solyc03g098790.1)	Cathepsin D Inhibitor (chymotrypsin inhibitor 21)	T3	UP	Plant induced defenses	10.1104/pp.106.086587
Solyc01g006300.2	CEVI-1 Peroxidase	T3	UP	Phenolics-mediated resistance against necrotrophic phytopathogens	10.1155/2012/137037, 10.1023/A:1014904815352, 10.2478/jppr-2014-0057
Solyc05g053550.2	Chalcone synthase 2	T3	UP	Key gene of the flavonoid/isoflavonoid biosynthesis	10.1007/s11101-011-9211-7
RCR3 (Solyc02g076980)	Cysteine proteinase	T3	UP	Plant defense and resistance	10.1126/science.1111404
Solyc03g122350.2	Cytochrome P450	T3	UP	Production of Allelochemicals	10.1016/j.bbapap.2010.09.012, 10.1248/bpb.35.824, 10.1098/rstb.2012.0426, 10.1146/annurev-arplant-042809-112305
Solyc04g078290.2	Cytochrome P450	T3	UP	Production of Allelochemicals	10.1016/j.bbapap.2010.09.012, 10.1248/bpb.35.824, 10.1098/rstb.2012.0426, 10.1146/annurev-arplant-042809-112305
Solyc11g030730.1	Cytochrome P450	T3	UP	Production of Allelochemicals	10.1016/j.bbapap.2010.09.012, 10.1248/bpb.35.824, 10.1098/rstb.2012.0426, 10.1146/annurev-arplant-042809-112305
Solyc12g042480.1	Cytochrome P450	T3	UP	Production of Allelochemicals	10.1016/j.bbapap.2010.09.012, 10.1248/bpb.35.824, 10.1098/rstb.2012.0426, 10.1146/annurev-arplant-042809-112305

Table 5.10 continued.

Gene name	Gene Description	Time	Direction	Function	Supporting literature DOI
GGPS1 (Solyc11g011240)	Geranylgeranyl pyrophosphate synthase 1	T3	UP	Plant induced defenses	10.1007/s00425-006-0301-5
TOMQ`B (Solyc10g079860)	Glucan endo-1,3-beta-D-glucosidase	T3	UP	Defense against pathogen, similar to PR gene	10.1007/BF00029854, 10.5958/j.2229-4473.26.2s.141
Solyc03g078490.2	Glycosyltransferase	T3	UP	Plant defense, Mi-Mediated resistance, cell wall synthesis, carbohydrate biosynthesis	10.1104/pp.106.090241
Solyc12g096960.1	Major allergen Mal d 1.0502/Pathogenesis-related protein STH-2	T3	UP	Multiple defenses against pathogens	10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
Solyc09g091000.2	Major allergen Mal d 1//Pathogenesis-related protein STH-2	T3	UP	Multiple defenses against pathogens	10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
Solyc08g079900.1	Pathogenesis related protein P69G	T3	UP	Plant defenses	10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
Solyc09g090990.2	Pathogenesis-related protein 10 (PR10)	T3	UP	Multiple defenses against pathogens	10.1094/MPMI.2003.16.6.467, 10.15406/apar.2015.03.00077, 10.1016/0300-9084(93)90100-7
Solyc06g050440.2	Peroxidase (POD)	T3	UP	Plant defense against bacterial pathogen	10.1155/2012/137037, 10.1023/A:1014904815352, 10.2478/jppr-2014-0057
Solyc09g097810.2	Systemic acquired resistance protein (SAR8.2)	T3	UP	Involves in hypersenstive response and the development of systemic acquired resistance	10.1104/pp.16.00269
Solyc08g067340.2	WRKY transcription factor	T3	UP	Plant defense and immunity	10.1104/pp.109.138990
Solyc03g095770.2	WRKY transcription factor 6	T3	UP	Plant defense and immunity	10.1104/pp.109.138990
Solyc08g067360.2	WRKY transcription factor 9	T3	UP	Plant defense and immunity	10.1104/pp.109.138990
Solyc03g097610.2	Sugar transporter SWEET	T3	UP	Transport hexoses and sucrose	10.1111/nph.12445, 10.1038/nature15391, 10.1016/j.tibs.2015.05.005

Table 5.10 continued.

Gene name	Gene Description	Time	Direction	Function	Supporting literature DOI
ACO4 (Solyc07g049550)	1-aminocyclopropane-1-carboxylate oxidase 4 (ACC oxidase 4)	T3	UP	Ethylene biosynthesis, up-regulated in response to pathogen infection	10.1007/s10658-014-0394-9, 10.1007/s11738-012-1096-6, 10.1104/pp.121.4.1257
Wiv-1 (Solyc10g083290)	Cell-wall invertase	T3	UP	Carbohydrate partitioning and regulation of sink-source interaction	10.1104/pp.108.127977, 10.3389/fpls.2014.00293, 10.1093/jxb/erg055
XTH6 (Solyc11g066270)	Xyloglucan endotransglucosylase-hydrolase 6	T3	UP	Cell wall remodelling and plant defenses	10.3389/fpls.2015.00323, 10.1055/s-2004-817959, 10.1104/pp.110.156844
Solyc08g067330.1	Chlorophyll a-b binding protein 3C-like	T3	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
Solyc06g069730.2	Chlorophyll a-b binding protein 4	T3	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
Solyc02g071000.1	Chlorophyll a/b binding protein	T3	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
Solyc03g005790.2	Chlorophyll a/b-binding protein	T3	DOWN	Photosynthesis: captures and delivers excitation energy to PS I and II	10.1016/j.scienta.2013.05.022, 10.1016/0005-2728(94)90148-1, 10.1105/tpc.114.127373
GTS1 (Solyc04g014510)	Glutamine synthetase	T3	DOWN	Nitrogen assimilation	10.1093/jexbot/53.370.979, 10.1093/pcp/pch092
Solyc06g072710.2	RNA polymerase sigma factor	T3	DOWN	Required for the initiation of RNA synthesis	10.1016/S0923-2508(02)01368-2

P: plants infested with Lso-negative *B. cockerelli*. L: plants infested with Lso-positive *B. cockerelli*. T1, T2, and T3 represent one, two, and four weeks after infestation, respectively.

At T2, there were 127 DEGs. Compared to T1, there was a shift in gene regulation since at T2, 61% of the DEGs were up-regulated and 38% were down-regulated. At T2, 61% of the DEGs were up-regulated and 38% were down-regulated (Table 5.3). Five GO terms associated with plant response to biotic stimulus and plant defenses were significantly enriched among the up-regulated genes and two GO terms associated with photosynthesis were enriched among the down-regulated genes (Table 5.8). The up-regulated genes playing a role in plant defenses were cytochrome P450, The up-regulated genes playing a role in plant defenses were cytochrome P450, glucan endo-1,3-beta-D-glucosidase, glycosyltransferase, pathogenesis related, peroxidase, polyphenol oxidase, proteinase inhibitor, lipoxygenase, NAC domain transcription factor, and cell wall remodeling genes (Table 5.10). The down-regulated genes were mainly involved in photosynthesis. The down-regulation of chloroplast photosystem and chlorophyll a/b binding genes is usually associated with leaf chlorosis and disease development.

At T3, there were 97 up-regulated and 41 down-regulated genes. No significant GO term was enriched among the up-regulated genes. Two GO terms associated with photosynthesis were enriched among the down-regulated genes (Table 5.8). At both T2 and T3, GO terms associated with photosynthesis were over-represented among the down-regulated genes in the P vs L comparative transcriptomes. Additionally, a gene required for the initiation of RNA synthesis, RNA polymerase sigma factor, was down-regulated at both time points. Other up-regulated genes in common between the T2 and T3 comparative transcriptomes included cytochrome P450, 1,3-beta-D-glucosidase, glycosyltransferase, pathogenesis-related, proteinase inhibitor, peroxidase (Table 5.10). Other up-regulated genes playing roles in plant defense and immunity at T3 were WRKY transcription factor, systemic acquired resistance, geranylgeranyl pyrophosphate synthase, cysteine proteinase gene, beta-1 3-glucanase, and acidic 26 kDa endochitinase. Despite the up-regulation of defense genes, genes commonly associated with bacterial diseases such as the sugar transporter SWEET and cell-wall invertase were also up-regulated in the P vs L comparative transcriptome.

5.3.8 Comparing transcriptome results to RT-qPCR results

The transcriptional profile of five genes was compared by RT-qPCR (Table 5.11**)**. The selected genes were associated with either plant defenses or disease development. The bioinformatic and the RT-qPCR methods revealed similar expression profile for 13 out of 16 comparisons and for 9 out 16 comparisons similar significance difference. The relative gene expression obtained by RNA-seq and RT-qPCR methods were compared. The Pearson product-moment correlation test showed a significant correlation between the result from the RNA-seq and the RT-qPCR methods ($r = 0.67$, $n = 16$, $p = 0.004$).

Table 5.11 Comparison of the gene expression profile of 5 genes obtained by RNA-seq and by RT-qPCR

Gene ID	Gene	Time	Comparison	Transcriptome (Fold change)	RT-qPCR (ddCT)	Transcriptome q-value	RT-qPCR p-value
Solyc03g082370.1	ACRE65	T1	P vs L	-19.68	-16.81	0.013	0.049
Solyc09g089510.2	PI1	T1	C vs P	1.37	1.32	1.000	0.252
Solyc09g089510.2	PI1	T1	P vs L	-24.12	-4.65	0.013	0.275
Solyc09g089510.2	PI1	T1	C vs L	-17.55	-3.51	0.013	0.275
Solyc09g090980.2	PR10	T2	C vs P	-2.21	-0.585	0.101	0.295
Solyc09g090980.2	PR10	T2	P vs L	6.46	28.26	0.013	0.564
Solyc09g090980.2	PR10	T2	C vs L	2.93	16.52	0.500	0.827
Solyc09g090980.2	PR10	T3	P vs L	2.16	9.75	0.074	0.039
Solyc09g090980.2	PR10	T3	C vs P	1.26	-1.35	0.998	0.413
Solyc09g090980.2	PR10	T3	C vs L	2.73	7.22	0.014	0.018
Solyc03g097610.2	SWEET	T3	P vs L	2.63	5.68	0.024	0.074
Solyc03g097610.2	SWEET	T3	C vs L	3.34	1.62	0.008	0.157
Solyc03g097610.2	SWEET	T3	C vs P	1.27	-3.51	0.998	0.053
Solyc07g006560.2	HR	T2	P vs L	1.28	-2.76	0.999	0.083
Solyc07g006560.2	HR	T2	C vs P	7.86	18.48	0.030	0.083
Solyc07g006560.2	HR	T2	C vs L	10.05	6.69	0.013	0.275

T1, T2, and T3 represent one, two, and four weeks after infestation, respectively.

5.3.9 Comparing transcriptome results to protein assay results

Since peroxidase (POD) genes were differentially up-regulated in four comparative transcriptomes, POD activities in leaves were compared among treatments. Differences in POD activity were found at T2 (ANOVA, F (2, 5) = 10.3, P = 0.0169) and at T3 (ANOVA, F (2, 6) = 5.69, P = 0.0411, Fig. 5.5A). At both time points, higher POD activity was measured in L plants compared to C and P plants. These results are in agreement with the expression profile of three POD genes (Solyc02g092580, Solyc03g006700.2, Solyc06g050440.2. Similarly, polyphenol oxidase (PPO) activity in plants at T2 was tested since the expression of PPO gene (Solyc02g078650.2) was up-regulated in L plants compared to C and P plants. Higher PPO protein activity was measured in L plants than P plants (t (6) = 2.75, p = 0.0479, Fig. 5.6A) at T2. This result was concurred with the result found in the gene expression at T2 (Fig. 5.6B). The PPO activity was also higher in L plants than C plants but statistical analysis was not possible since only samples from two C plants were available.

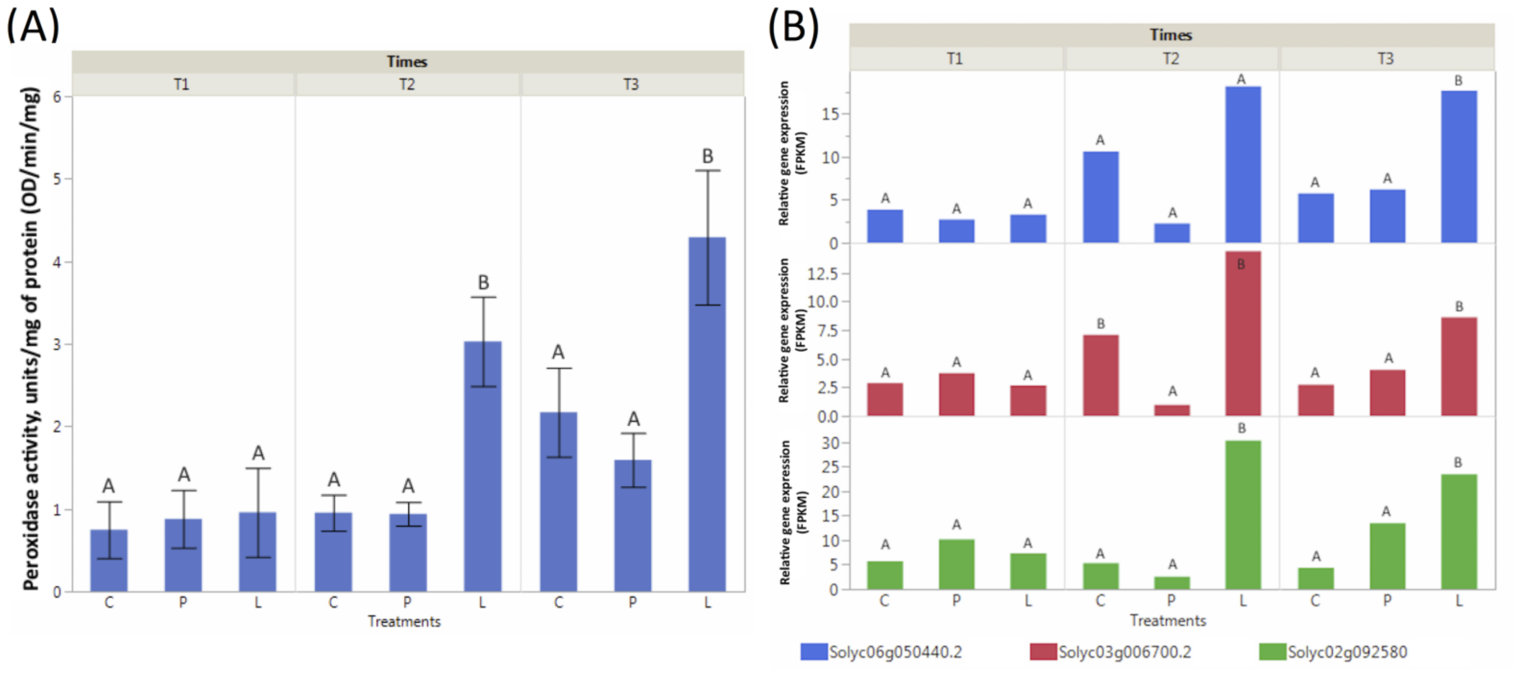

Figure 5.5 Comparison of plant peroxidase protein activity and gene expression.
(A) Peroxidase activities by colorimetric protein activity assay. (B) Expression of peroxidase genes by RNA-seq method. Leaves from plants exposed to either no *B. cockerelli* (C), to Lso-negative *B. cockerelli* (P), or to Lso-positive *B. cockerelli* (L) were compared at one week (T1), two weeks (T2), or four weeks (T3). Different letters represent significant different at $P <$ 0.05 for protein activity and at $q < 0.05$ for gene expression among the treatments within the specified exposure time. The expression of each gene was represented by the Fragments Per Kilobase of transcript per Million mapped reads (FPKM) value.

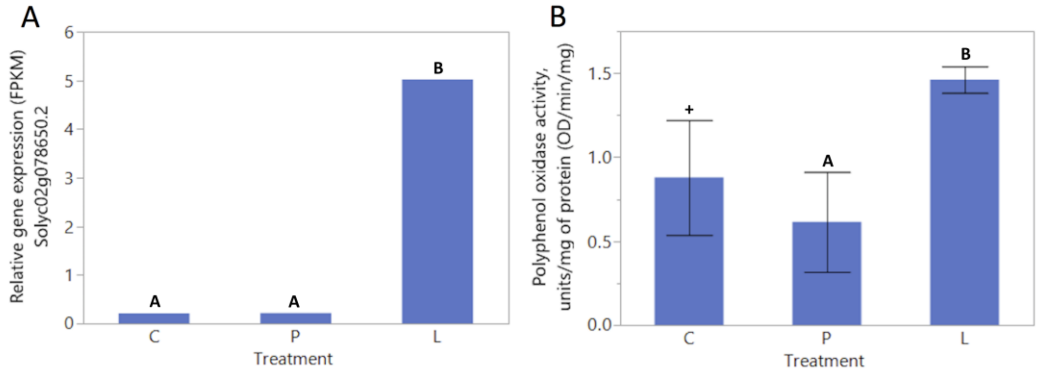

Figure 5.6 Comparison of plant polyphenol oxidase gene expression and protein activity. (A) Polyphenol oxidase activities by colorimetric protein activity assay. (B) Expression of polyphenol oxidase genes by RNA-seq method. Leaves from plants exposed to either no *B. cockerelli* (C), to Lso-negative *B. cockerelli* (P), or to Lso-positive *B. cockerelli* (L) were compared at week two (T2). Different letters represent significant different at $P < 0.05$ for protein activity and at $q < 0.05$ for gene expression. The expression of each gene was represented by the Fragments Per Kilobase of transcript per Million mapped reads (FPKM) value. + represents the treatment not able to test statistically.

5.4 Discussion

The emergence and spread of Lso pose a number of concerns regarding the future of food security and yet management methods including biological and chemical controls are not always effective (Munyaneza, 2012). In spite of the increasing number of publications on this topic, little is known regarding the changes in gene expression in host plants exposed to Lso-positive vectors, or the differences in plant responses against Lso-negative and Lso-positive *B. cockerelli.* This study is the first attempt to investigate and distinguish the differences among plant transcriptional responses to no insect, Lso-positive and Lso-negative *B. cockerelli*. The differences between plant responses to the vector and/or the pathogen were evaluated in a temporal manner to determine how the progression of *B. cockerelli* infestation and Lso infection affected plant gene expression.

In response to Lso-negative *B. cockerelli* (C vs P), plants responded by predominantly up-regulating the expression of defense genes. Interestingly, different genes were induced in response to adults at T1, nymphs at T2, and nymphs and adults at T3. This is not surprising since nymphs are less mobile than adults and tend to feed on the same plant during their development. Therefore, it is possible that the strategies used by each life-stage to feed on plants are different (Walling, 2008). Overall, fewer DEGs were identified in response to nymphs (T2) than to adults (T1 and T3). At T1, WRKY transcription factors and ethylene-responsive transcription factors (ERF) were induced in response to adults. WRKY transcription factors enhance plant immunity, which could be modulated by the phytohormones jasmonic acid (JA) and salicylic acid (SA) (Chen *et al.*, 2013; Pandey & Somssich, 2009). Similarly, ERF genes affect the ethylene (ET) pathway and enhance plant defense response against insects (Chen et al., 2013; Grennan, 2008; Gu *et al.*, 2000). JA, SA, and ET play important roles in plant defenses and immunity since they affect multiple defense genes (Karban & Baldwin, 1997; Walling, 2000). Coincidentally, Avr9/Cf-9 rapidly elicited protein 65 and SRC2 genes were up-regulated in plants in response to *B. cockerelli* at T1. These genes regulate plant hypersensitive response (HR) (Liu *et al.*, 2015; Rowland *et al.*, 2005). Modulated by nitric oxide and reactive oxygen species, HR regulates plant defenses upstream of the SA pathway (Walling, 2000). Interestingly, other genes affecting HR were up-regulated by nymphs (at T2) including HR assisting protein and peroxidase genes. At T3, several HR associated genes were down-regulated including Non-specific serine/threonine protein kinase and Cathepsin B-like cysteine proteinase 3. Bactericera cockerelli also affected the plant primary metabolism. In particular, genes involved in photosynthesis were down-regulated. For instance, the down-regulation of the genes encoding the photosystem II D2 and photosystem Q(B) proteins could result in leaf yellowing. Chlorosis is the main symptom of psyllid yellows which is associated with *B. cockerelli* feeding (Sengoda et al., 2010). Moreover, the regulation of photosynthesis genes could affect source-sink carbon partitioning (Roitsch, 1999). Indeed, genes associated with carbohydrate metabolism such as xyloglucan endotransglucosylase/hydrolase were up-regulated in plant response to *B. cockerelli* at T1 and T3. These genes are involved not only in polysaccharide metabolism but also are involved in pathways associated with ET (Munoz-Bertomeu *et al.*, 2013) and JA-ET-dependent defenses (Tian *et al.*, 2014; Walling, 2000).

Plant responses to Lso-positive *B. cockerelli* (C vs L) were markedly different. While similar number of DEGs were identified at each time point in the C vs P comparisons, a greater number of DEGs were identified in the C vs L transcriptomes as time passed. Second, over 65% of the DEGs were up-regulated independently of the time point in the C vs P comparisons but approximately 25%, 70% and 55% were up-regulated at T1, T2 and T3, respectively in the C vs L comparisons. These differences could result from the concomitant infection of the plants with Lso. Interestingly, photosynthesis-related genes were down-regulated independently of the time point. This is not surprising since chlorosis is a common symptom of Liberibacter infection in all crops. Plant defense genes, however, were regulated in a temporal dynamic manner. While down-regulated at T1, plant defense genes were up-regulated at T2 and T4. The down-regulation defense genes at early stage of *B. cockerelli* colonization and Lso infection could be detrimental to plants since quick defense response can deter *B. cockerelli* and restrict pathogen infection to minimize damage. Although plant defense genes such as cytochrome P450, pathogenesis-related, peroxidase, WRKY, and cell-wall invertase were up-regulated at T2 and T3 (Hamberger & Bak, 2013; Pandey & Somssich, 2009; Roitsch *et al.*, 2003), genes associated with plant disease such as sugar transporters SWEET, hexose transporter, and NAC domain transcription factor were also up-regulated suggesting that disease development was in its early stage (Chen *et al.*, 2010; Chen, 2014; Kocal *et al.*, 2008; Sherson *et al.*, 2003). A key difference in plant response to Lso-positive *B. cockerelli* and Lso-negative *B. cockerelli* was the abrupt change in the expression of plant defense and carbohydrate–related genes. The up-regulation of carbohydrate-related genes in response to pathogen infection could affect sink-source carbohydrate regulation in favor pathogen infection and disease development.

Since differences in expression profile of DEGs were found in the C vs P and C vs L comparative transcriptomes, plant responses to Lso-negative and Lso-positive *B. cockerelli* were compared. Interestingly, more DEGs were identified in P vs L comparison than in C vs P and C vs L comparisons at T1 and T2. At T1, 95% of the genes were down-regulated in response to Lso-positive *B. cockerelli* compared to that of Lso-negative *B. cockerelli*. Therefore, it is possible that upon infection Lso down-regulated of plant genes or modulates the ability of plants to respond to attacks. This modulation of plant responses by Lso might also positively or negatively affect the vector. It is difficult to differentiate Lso direct and indirect effects on *B. cockerelli* fitness, however *B. cockerelli* nymphs develop faster on potato and silverleaf nightshade if associated with Lso (Thinakaran *et al.*, 2015c).

The P vs L comparative transcriptome also showed that plants exposed to Lso-positive *B. cockerelli* had lower expression of photosynthesis-associated genes than plants exposed to Lso-negative *B. cockerelli* at T2 and T3. Several studies showed that *Liberibacter*-infected plants down-regulate photosynthetic activities as the disease develops (Nwugo *et al.*, 2013a; Nwugo *et al.*, 2013b; Xu *et al.*, 2015). Other studies also showed that infected plants down-regulate photosynthetic activities as a consequence of disease development (Berger *et al.*, 2007; Huang, 2001). The reduction of photosynthesis could be induced by the overexpression of cell wall invertase (Bonfig *et al.*, 2006; Kocal et al., 2008; Koch, 1996), a common plant response to a pathogen attack (Berger et al., 2007; Tauzin & Giardina, 2014). Results of the P vs L and C vs L comparative transcriptomes are in agreement and photosynthesis genes were down-regulated in Lso-positive plants.

Also, plants that were exposed to Lso-positive *B. cockerelli* and later tested positive for Lso infection overexpressed cell wall invertase and pathogen-related (PR) genes at T2 and T3. An extensive literature review of cell-wall-bound invertases reported that both cell wall invertase and PR genes were up-regulated in plants in response to pathogen infection (Roitsch et al., 2003) similar to the finding in our study. Due to the similarity in their overexpression in response to pathogen infection, researchers questioned whether the cell wall invertase genes have a similar role as the

PR genes in plant defenses despite their primary role in sugar metabolism (Roitsch et al., 2003). Cell wall invertase can limit sucrose export and inhibit photosynthesis in *S. lycopersicum* (Kocal et al., 2008) and in other plants (Koch, 1996). The association between the cell wall invertase and sugar transporter in plants was reviewed in details (Sherson et al., 2003). Interestingly, a similarity in the up-regulation of cell wall invertase gene and a sugar transporter gene was also found in our study. For example, a sugar transporter SWEET gene was overexpressed in response to the Lso infection. The connection between SWEET and cell wall invertase genes is not yet known. However, the up-regulation of SWEET gene is associated with plant response to pathogen. Particularly, SWEET protein and/or genes, which are involved in the phloem-loading process, can be manipulated by pathogens to provide nutrients to the pathogen (Chen, 2014) and probably allowing them access to the plant's sucrose pools (Roitsch et al., 2003). Similar to the C vs L comparative transcriptome, the P vs L comparative transcriptome revealed that SWEET gene, involved in phloem loading, was up-regulated in response to Lso. In *S. tuberosum*, symptoms associated with Lso infection include irregular sugar distribution in the roots (Chen, 2014), leaves (Wallis et al., 2015) and stem (Alvarado *et al.*, 2012). In citrus, HLB, a disease caused by *Candidatus* Liberibacter spp., disrupts the carbohydrate flow resulting in accumulation of starch in source tissues (Rosales & Burns, 2011; Xu et al., 2015). Thus, disease symptoms on plants could be a result of Lso manipulating one or more genes involved in photosynthesis, defenses, or sugar metabolism and transport. Since studies showed that these genes could interact with each other, Lso effects on one may trigger a cascade of responses involving other genes.

One of the challenges to understand citrus-*Liberibacter* interaction is the long latency period (months) of the disease. Therefore, the solanaceous plants-Lso systems, characterized by short latency periods (weeks), could help understand the early plant responses to the vector and the pathogen. Significant gene expression correlation was obtained between the transcriptome and the RT-qPCR analyses. However, for some genes, differential expression was identified in the comparative transcriptomes but not on the RT-qPCR analyses ($P>0.05$). This could be related to differences in sensitivity between the two methods. Further validation of the bioinformatics results was performed by assaying peroxidase and polyphenol oxidase activity since changes in the expression of genes encoding those proteins were identified among the treatments. The enzymatic assays were in accordance with the transcriptomic results.

Overall, the results from this study revealed similarities between *S. lycopersicum* and citrus responses to *Liberibacter* pathogens: up-regulation of ERF and WRKY transcription factors, induction of defense genes such as LOX and PR, as well as of invertases, HSP70 and MAPK genes (Fan *et al.*, 2011; Mafra et al., 2013; Zhong et al., 2016; Zhong *et al.*, 2015). Interestingly, the up-regulation of WRKY genes and other defense genes within their network was detected during the later stage of infection. However, the WRKY genes and other defense genes were down-regulated at the early stage of Lso infection.

In conclusion, *S. lycopersicum* regulated specific genes in response to Lso-positive and Lso-negative *B. cockerelli* and in response to different life-stages. Interestingly, the changes in gene expression supported the observed symptoms associated with *B. cockerelli* herbivory and/or Lso infection including chlorosis (down-regulation of photosynthesis-associated genes), disruption in sugar transport and carbon partitioning (regulation of sugar transporters and genes involved in carbohydrate metabolism), stunting (regulation of phytohormone-related genes and of NAC domain transcription factor genes). Based on the results presented here, plants perceived *B. cockerelli* herbivory and Lso infection and responded by activating defenses. However, those defenses did not stop the insect development or Lso infection. Therefore, we speculate that a complex molecular dialog was established among *S. lycoperisum, B. cockerelli* and Lso, characteristic of the evolutionary arms-race between plants and their attackers.

CHAPTER VI

SUMMARY AND CONCLUSIONS

Plant responses to insect vectors and bacterial pathogens are complex. Plant responses could involve in the regulation of genes and biochemical that modulate plant physiological processes. The phytohormones jasmonic acid and salicylic acid are keys regulators of plant defenses and immune responses. Lso-positive *B. cockerelli* not only up-regulated the genes required to synthesize JA and SA but also induced genes that were modulated by JA and SA (Casteel et al., 2012). The induction of these genes could be due to *B. cockerelli* and/or Lso, but the cause of induction was not clear since Casteel et. al. 2012 did not use Lso-negative *B. cockerelli*. Furthermore, the effectiveness of these induced defenses against Lso infection or *B. cockerelli* infestation was not evaluated. Thus, I tested the effectiveness of JA and SA defenses against *B. cockerelli* using the induction approach. My results showed that plants previously treated by the JA elicitor induced jasmonate defenses by up-regulated *PI2* gene but this jasmonate defense did not confer resistant against Lso-negative or Lso-positive *B. cockerelli*. Plants previously treated by a derivative of SA up-regulated *PR1* gene and induced salicylate defense. Interestingly, salicylate defense appeared to enhance plant resistance against Lso-positive *B. cockerelli* by reducing the survival, preference, and infestation rate of Lso-positive *B. cockerelli*. Salicylate induced plants also had lower frequency of Lso infection than the control plants. This suggests that plant salicylate defense could be effective for plants to defend against *B. cockerelli* and Lso. However, salicylate defenses might only delay *B. cockerelli* infestation or Lso infection.

Although plant innate defenses such as jasmonate and salicylate defenses could be induced in response to *B. cockerelli* and Lso (Casteel et al., 2012), the effect of plant induced defenses may be hinder when plants are under water stress. Since Lso was first documented in Texas where the prevalence of drought is high, water stress on crop plants could be a contributing factor that promoted the outbreak of *B. cockerelli* and Lso. Thus, the effect of water stress on plant susceptibility to *B. cockerelli* and Lso was tested. My results indicated that moderate water stress increased plant susceptibility to Lso-positive *B. cockerelli* in choice and no-choice experiment. Also, water-stressed plants enhancing *B. cockerelli* development and survival from egg to adult. The mechanism of plant susceptibility to Lso-positive *B. cockerelli* when plants were under water stress is not yet clear. However, water stress could affect plant defenses and can increase the quality of plants as a food source for insects.

Insect feeding and pathogen infection may not only affect jasmonate and salicylate defenses but also affect other defenses and metabolism. Changes in the level of phenolic compounds, sugars, and amino acids were detected in leaves, stems and tubers of Lso-positive plants when compared to Lso-negative plants (Wallis et al., 2015). To study the changes in plant primary and secondary metabolites, I performed a transcriptome analysis using plants exposed to no insects, to Lso-negative *B. cockerelli*, or to Lso-positive *B. cockerelli*. The comparative transcriptome revealed that plant induced responses to Lso-negative and Lso-positive *B. cockerelli* were unique and different in a temporal dynamic response. In response to Lso-negative *B. cockerelli* (e.g. C vs P), plants up-regulated defense genes continuously from week one to week four. In response Lso-positive *B. cockerelli* (e.g. C vs L and P vs L), plants down-regulated defense genes at week one and up-regulate defense genes at week two and week fours, but the up-regulation of defense genes at week two and four which was coincided with regulation of genes associated with the early signs of plant disease symptoms. For example, the unexpected down-regulation of photosynthesis genes could be early sign of plant developing chlorosis symptom whereas the abnormal up-regulation of sugar transporter genes could be the early sign of Lso disrupting plant sugar metabolism as found in potato plants with Zebra Chip.

Plant induced response to insect and pathogen is complex involving the interactions among genes, proteins, and chemicals. Plant induced defenses may be regulated by JA and SA, but the effectiveness of defense genes and/or compounds induced by these phytohormones depends not only on the type of insect or pathogen but also on the combination of insect and pathogen. Interestingly, insect and pathogen can affect plant innate defense. Plant induced defenses is multi-dimensional as found in the transcriptome study where the up-regulation or down-regulation of genes may depend on the time the plant was exposed to the insects and/or pathogen.

Results from these studies will contribute the current limited knowledge on how plant response to *B. cockerelli* and Lso. This perhaps could be a first step in the direction of finding plant defense genes to enhance plant resistance against the vector and pathogen. Also, knowledge on how water stress enhancing plant susceptible to *B.*

cockerelli harboring Lso will help farmer making effective management decisions for crop disease associated with Lso, especially in drought condition. Future studies on enhancing plants to continuously up-regulate defense genes effective against Lso-positive *B. cockerelli* can potentially reduce the incidence Lso infection. Functionally described and putatively described defense transcripts discovered in the comparative transcriptome open doors for genetic selection. Markers for defense genes can be designed to test plants and facilitate artificial selection for lines of plants that are more resistance to *B. cockerelli* harboring Lso. Also, unique transcript found exclusively in plant transcriptional response to *B. cockerelli* and Lso can be use to develop a marker gene and be used to help develop a biochemical assay for a quick diagnosis for Lso infection.

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APPENDIX

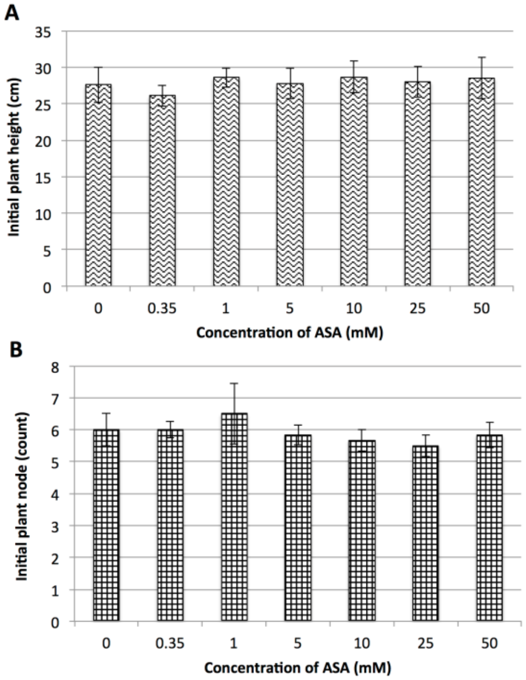

Figure A.1 Average plant height and node showing the similarity in initial plant size and growth

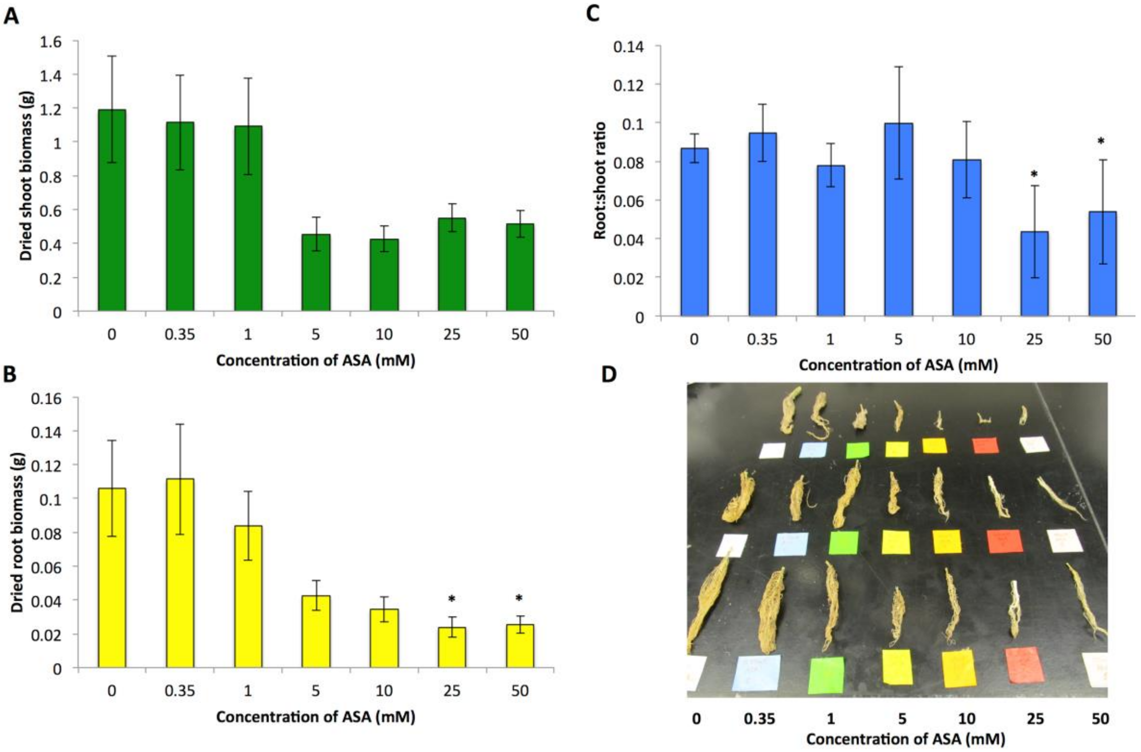

Figure A.2 Effect of ASA on *S. lycopersicum* shoot and root biomass in the choice study. (A) Mean (±SE) dried plant shoot biomass (*P* = 0.106). (B) Mean (±SE) dried plant root biomass (*P* = 0.0129). (C) Mean (±SE) plant root to shoot dry biomass ratio (*P* = 0.005). (D) Plant dried roots at the end of the experiment. Symbols * indicate significant differences at *P* < 0.05 following a post-hoc test comparing control (0 mM) to ASA (0.35 mM, 1 mM, 5 mM, 10 mM, 25mM, or 50 mM).

Table A.1 The effect of ASA on plant mortality across time points.

	ASA Concentration						
	0 mM	**0.35 mM**	**1 mM**	**5 mM**	**10 mM**	**25 mM**	**50 mM**
1 week	0 (0%)	0 (0%)	0 (0%)	1 (16.6%)	1 (16.6%)	4 (66.6%)	3 (50%)
2 weeks	0 (0%)	0 (0%)	0 (0%)	1 (16.6%)	2 (33.3%)	4 (66.6%)	6 (100%)
3 weeks	0 (0%)	0 (0%)	0 (0%)	2 (33.3%)	5 (83.3%)	5 (83.3%)	6 (100%)

The table shows the number and percentage of plant mortality according to the weekly treatment of ASA.

Table A.2 '*Candidatus* Liberibacter solanacearum' detection in plants from the choice experiment.

		ASA concentration			Total
		0 mM	**0.35 mM**	**1 mM**	
Lso infection	**Positive plants**	6 (100%)	4 (66.7%)	5 (83.3%)	15
	Negative plants	0 (0%)	2 (33%)	1 (16.7%)	3
	Total	6	6	6	18

Contingency table shows the number and percentage of plants that tested positive and negative for the presence of Lso in the ASA treatments.

Table A.3 '*Candidatus* Liberibacter solanacearum' detection in plants from the no-choice experiment.

		ASA concentration			Total
		0 mM	**0.35 mM**	**1 mM**	
Lso infection	**Positive plants**	9 (75%)	10 (83.3%)	4 (33.3%)	23
	Negative plants	3 (25%)	2 (16.7%)	8 (66.7%)	13
	Total	12	12	12	36

Contingency table shows the number and percentage of plants that tested positive and negative for the presence of Lso in the ASA treatments.

Table A.4 '*Candidatus* Liberibacter solanacearum' detection in plants separated by trial in the no-choice experiment

	Treatment	Lso-positive plants	Lso-negative plants
Trial 1	0 mM ASA	100%	0%
	0.35 mM ASA	100%	0%
	1 mM ASA	33.30%	66.70%
Trial 2	0 mM ASA	66.67%	33.33%
	0.35 mM ASA	66.67%	33.33%
	1 mM ASA	33.30%	66.70%
Trial 3	0 mM ASA	33.33%	66.67%
	0.35 mM ASA	66.67%	33.33%
	1 mM ASA	0.00%	100.00%
Trial 4	0 mM ASA	100%	0%
	0.35 mM ASA	100%	0%
	1 mM ASA	66.67%	33.33%

*Acetylsalicylic acid (ASA)

Table A.5 List of significantly differentially expressed genes (DEGs) in C vs P comparison

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc03g093120	Solyc03g093120.2	T1	T1_C	T1_P	12.13	UP	27.22	0.013452	*
Solyc03g082370	Solyc03g082370.1	T1	T1_C	T1_P	11.36	UP	481.49	0.013452	*
Solyc08g068680	AADC1A	T1	T1_C	T1_P	10.7	UP	6.28	0.023556	*
Solyc07g056000	TXET-B2	T1	T1_C	T1_P	9.97	UP	141.54	0.013452	*
Solyc09g014990	Solyc09g014990.2	T1	T1_C	T1_P	7.89	UP	26.3	0.013452	*
Solyc01g096510	Solyc01g096510.2	T1	T1_C	T1_P	7.74	UP	42.77	0.013452	*
Solyc03g093110	Solyc03g093110.2	T1	T1_C	T1_P	7.47	UP	29.37	0.013452	*
Solyc07g055710	Solyc07g055710.2	T1	T1_C	T1_P	7.43	UP	6.63	0.0403049	*
Solyc01g091590	Solyc01g091590.2	T1	T1_C	T1_P	6.86	UP	108.38	0.013452	*
Solyc05g047680	Solyc05g047680.2	T1	T1_C	T1_P	6.48	UP	7.3	0.0403049	*
Solyc12g009000	Solyc12g009000.1	T1	T1_C	T1_P	6.35	UP	22.23	0.013452	*
Solyc02g091180	Solyc02g091180.1	T1	T1_C	T1_P	6.3	UP	70.64	0.023556	*
Solyc06g050500	Solyc06g050500.2	T1	T1_C	T1_P	6.25	UP	21.31	0.013452	*
Solyc03g083480	Solyc03g083480.2	T1	T1_C	T1_P	5.9	UP	45.14	0.013452	*
Solyc08g068770	Solyc08g068770.1	T1	T1_C	T1_P	5.8	UP	137.37	0.013452	*
Solyc08g078190	Solyc08g078190.1	T1	T1_C	T1_P	5.25	UP	69.92	0.013452	*
Solyc08g077020	Solyc08g077020.1	T1	T1_C	T1_P	5.09	UP	138.92	0.013452	*
Solyc04g077980	CZFP1	T1	T1_C	T1_P	4.96	UP	223.67	0.013452	*
Solyc10g006700	Solyc10g006700.1	T1	T1_C	T1_P	4.89	UP	578.65	0.013452	*
Solyc01g087580	Solyc01g087580.2	T1	T1_C	T1_P	4.8	UP	132.8	0.023556	*
Solyc08g079700	SAP6	T1	T1_C	T1_P	4.78	UP	389.16	0.013452	*
Solyc03g026280	CBF1	T1	T1_C	T1_P	4.73	UP	87.11	0.013452	*
Solyc03g093610	ERF1	T1	T1_C	T1_P	4.72	UP	47.87	0.013452	*
TCONS_00070216	Solyc10g008400.1	T1	T1_C	T1_P	4.66	UP	88.06	0.013452	*
Solyc06g074030	Solyc06g074030.1	T1	T1_C	T1_P	4.64	UP	346.34	0.013452	*

Table A.5 continued.

Gene ID	**Gene Name**	**Time**	**Group 1**	**Group 2**	**Fold Change**	**Direction**	**Total Fpkm**	**q-value**	**Sig. Lvl**
Solyc08g083050	Solyc08g083050.1	T1	T1_C	T1_P	4.6	UP	104.05	0.013452	*
Solyc07g040960	SLSRG2	T1	T1_C	T1_P	4.43	UP	311.92	0.0316739	*
Solyc06g049020	Solyc06g049020.1	T1	T1_C	T1_P	4.31	UP	134.04	0.013452	*
Solyc07g062490	Solyc07g062490.1	T1	T1_C	T1_P	4.31	UP	50.63	0.013452	*
Solyc09g082230	Solyc09g082230.1	T1	T1_C	T1_P	4.31	UP	53.63	0.0471539	*
Solyc01g066430	Solyc01g066430.2	T1	T1_C	T1_P	4.17	UP	149.26	0.013452	*
Solyc12g057150	Solyc12g057150.1	T1	T1_C	T1_P	4.16	UP	143.31	0.013452	*
Solyc01g080870	Solyc01g080870.2	T1	T1_C	T1_P	4.13	UP	10.69	0.023556	*
Solyc02g093230	Solyc02g093230.2	T1	T1_C	T1_P	4.07	UP	30.04	0.013452	*
Solyc01g065530	Solyc01g065530.2	T1	T1_C	T1_P	4	UP	59.06	0.013452	*
Solyc07g053740	Solyc07g053740.1	T1	T1_C	T1_P	3.83	UP	576.23	0.013452	*
Solyc04g077620	Solyc04g077620.1	T1	T1_C	T1_P	3.82	UP	126.06	0.0316739	*
Solyc07g045100	Solyc07g045100.1	T1	T1_C	T1_P	3.8	UP	19.94	0.013452	*
Solyc11g068710	Solyc11g068710.1	T1	T1_C	T1_P	3.77	UP	113.74	0.013452	*
Solyc01g100010	Solyc01g100010.2	T1	T1_C	T1_P	3.76	UP	20.22	0.0471539	*
Solyc08g068600	Solyc08g068600.2	T1	T1_C	T1_P	3.75	UP	20.77	0.013452	*
Solyc03g083470	Solyc03g083470.2	T1	T1_C	T1_P	3.65	UP	16.92	0.013452	*
Solyc01g100200	GRAS4	T1	T1_C	T1_P	3.59	UP	53.39	0.013452	*
Solyc05g005260	Solyc05g005260.1	T1	T1_C	T1_P	3.57	UP	194.74	0.013452	*
Solyc04g071030	Solyc04g071030.1	T1	T1_C	T1_P	3.56	UP	28.77	0.013452	*
TCONS_00070312	ERF3	T1	T1_C	T1_P	3.56	UP	90.79	0.013452	*
Solyc05g052040	DDTFR10/A	T1	T1_C	T1_P	3.55	UP	231.75	0.013452	*
Solyc04g077270	Solyc04g077270.2	T1	T1_C	T1_P	3.46	UP	16.52	0.013452	*
Solyc01g095630	WRKY3	T1	T1_C	T1_P	3.41	UP	128.22	0.013452	*
Solyc08g080670	Solyc08g080670.1	T1	T1_C	T1_P	3.36	UP	65.27	0.0316739	*

Table A.5 continued.

Gene ID	**Gene Name**	**Time**	**Group 1**	**Group 2**	**Fold Change**	**Direction**	**Total Fpkm**	**q-value**	**Sig. Lvl**
Solyc10g081040	Solyc10g081040.1	T1	T1_C	T1_P	3.35	UP	241.18	0.013452	*
Solyc01g099370	Solyc01g099370.2	T1	T1_C	T1_P	3.32	UP	121.11	0.0316739	*
Solyc03g112340	Solyc03g112340.1	T1	T1_C	T1_P	3.29	UP	39.31	0.013452	*
Solyc04g025650	Solyc04g025650.2	T1	T1_C	T1_P	3.28	UP	97.2	0.0403049	*
Solyc06g060690	Solyc06g060690.2	T1	T1_C	T1_P	3.26	UP	34.14	0.013452	*
Solyc06g068460	Solyc06g068460.2	T1	T1_C	T1_P	3.25	UP	244.96	0.0316739	*
Solyc06g005650	Solyc06g005650.2	T1	T1_C	T1_P	3.2	UP	94.39	0.013452	*
Solyc08g008100	LE-ACS6	T1	T1_C	T1_P	3.05	UP	45.98	0.0316739	*
Solyc11g020230	Solyc11g020230.1	T1	T1_C	T1_P	3.05	UP	20.54	0.013452	*
Solyc06g009140	Solyc06g009140.2	T1	T1_C	T1_P	3.04	UP	337.73	0.013452	*
Solyc10g079420	Solyc10g079420.1	T1	T1_C	T1_P	3.02	UP	571.67	0.013452	*
Solyc00g206460	Solyc00g206460.1	T1	T1_C	T1_P	3.01	UP	121.71	0.013452	*
Solyc10g074440	Solyc10g074440.1	T1	T1_C	T1_P	3.01	UP	56.28	0.013452	*
TCONS_00073043	Solyc10g006130.1	T1	T1_C	T1_P	3.01	UP	118.46	0.013452	*
Solyc04g005050	Solyc04g005050.1	T1	T1_C	T1_P	2.96	UP	32.34	0.013452	*
Solyc04g018110	Solyc04g018110.1	T1	T1_C	T1_P	2.94	UP	380.29	0.013452	*
Solyc06g066370	Solyc06g066370.2	T1	T1_C	T1_P	2.88	UP	152.52	0.023556	*
Solyc03g007870	Solyc03g007870.2	T1	T1_C	T1_P	2.86	UP	151.12	0.013452	*
Solyc03g095770	Solyc03g095770.2	T1	T1_C	T1_P	2.8	UP	64.65	0.0316739	*
Solyc03g098730	Solyc03g098730.1	T1	T1_C	T1_P	2.78	UP	103.94	0.0316739	*
Solyc04g077230	Solyc04g077230.1	T1	T1_C	T1_P	2.77	UP	1154.6	0.0471539	*
Solyc05g009790	Solyc05g009790.1	T1	T1_C	T1_P	2.77	UP	244.81	0.013452	*
Solyc06g076020	HSC70.1	T1	T1_C	T1_P	2.7	UP	17.03	0.0316739	*
Solyc10g080370	Solyc10g080370.1	T1	T1_C	T1_P	2.68	UP	9260.61	0.0403049	*
Solyc08g006320	Solyc08g006320.2	T1	T1_C	T1_P	2.64	UP	149.16	0.013452	*

Table A.5 continued.

Gene ID	**Gene Name**	**Time**	**Group 1**	**Group 2**	**Fold Change**	**Direction**	**Total Fpkm**	**q-value**	**Sig. Lvl**
Solyc08g081230	Solyc08g081230.1	T1	T1_C	T1_P	2.56	UP	37.71	0.0471539	*
Solyc11g010500	Solyc11g010500.1	T1	T1_C	T1_P	2.49	UP	208.81	0.023556	*
Solyc01g005470	Solyc01g005470.2	T1	T1_C	T1_P	2.36	UP	123.33	0.0471539	*
Solyc05g052050	Solyc05g052050.1	T1	T1_C	T1_P	2.35	UP	160.37	0.023556	*
Solyc07g054310	Solyc07g054310.1	T1	T1_C	T1_P	8.8	DOWN	70.3	0.013452	*
Solyc09g091110	Solyc09g091110.2	T1	T1_C	T1_P	7.04	DOWN	38.3	0.023556	*
Solyc12g039030	Solyc12g039030.1	T1	T1_C	T1_P	6.98	DOWN	33123.89	0.013452	*
Solyc09g055950	Solyc09g055950.1	T1	T1_C	T1_P	6.31	DOWN	98.32	0.013452	*
Solyc10g079350	Solyc10g079350.1	T1	T1_C	T1_P	3.46	DOWN	27.03	0.0471539	*
Solyc05g043330	Solyc05g043330.2	T1	T1_C	T1_P	3.02	DOWN	31.32	0.0316739	*
Solyc01g095140	ER5	T2	T2_C	T2_P	37.35	UP	72.5	0.0130452	*
Solyc11g018800	Solyc11g018800.1	T2	T2_C	T2_P	28.36	UP	12.44	0.0130452	*
XLOC_011927	-	T2	T2_C	T2_P	18.87	UP	7.74	0.0130452	*
Solyc01g087590	Solyc01g087590.2	T2	T2_C	T2_P	18.54	UP	6.75	0.0130452	*
Solyc06g007190	Solyc06g007190.2	T2	T2_C	T2_P	11.55	UP	9.03	0.0220602	*
Solyc07g006560	Solyc07g006560.2	T2	T2_C	T2_P	7.86	UP	24.6	0.0304876	*
Solyc03g120990	Solyc03g120990.2	T2	T2_C	T2_P	6.59	UP	44.46	0.0130452	*
Solyc09g011860	Solyc09g011860.2	T2	T2_C	T2_P	5.99	UP	4.13	0.0304876	*
Solyc01g095150	LEMMI9	T2	T2_C	T2_P	4.63	UP	119.41	0.0130452	*
Solyc06g076020	HSC70.1	T2	T2_C	T2_P	3.98	UP	32.62	0.0130452	*
Solyc01g057770	Solyc01g057770.2	T2	T2_C	T2_P	3.95	UP	30.82	0.0130452	*
Solyc07g006570	Solyc07g006570.2	T2	T2_C	T2_P	3.59	UP	79.33	0.0130452	*
XLOC_030414	-	T2	T2_C	T2_P	3.56	UP	57.9	0.0378174	*
Solyc04g025650	Solyc04g025650.2	T2	T2_C	T2_P	3.23	UP	29.64	0.0130452	*
Solyc01g005590	Solyc01g005590.2	T2	T2_C	T2_P	3.03	UP	232.61	0.0130452	*

Table A.5 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc04g005480	Solyc04g005480.1	T2	T2_C	T2_P	3	UP	96.89	0.0130452	*
Solyc10g080370	Solyc10g080370.1	T2	T2_C	T2_P	2.69	UP	3520.64	0.0220602	*
Solyc02g090360	Solyc02g090360.2	T2	T2_C	T2_P	2.67	UP	18.14	0.0378174	*
Solyc06g068960	Solyc06g068960.1	T2	T2_C	T2_P	2.64	UP	206.27	0.0220602	*
XLOC_022709	-	T2	T2_C	T2_P	18.32	DOWN	35.99	0.0130452	*
Solyc09g089540	Solyc09g089540.2	T2	T2_C	T2_P	13.83	DOWN	47.83	0.0304876	*
Solyc09g007010	Solyc09g007010.1	T2	T2_C	T2_P	4.8	DOWN	272.09	0.0220602	*
TCONS_00056275	Solyc07g056640.1	T2	T2_C	T2_P	4.55	DOWN	80.32	0.0130452	*
Solyc12g098900	Solyc12g098900.1	T2	T2_C	T2_P	4.38	DOWN	47.2	0.0130452	*
Solyc10g079860	TOMQ`B	T2	T2_C	T2_P	3.11	DOWN	65.51	0.0130452	*
Solyc02g082920	CHI3	T2	T2_C	T2_P	2.8	DOWN	414.22	0.0130452	*
Solyc01g097240	Solyc01g097240.2	T2	T2_C	T2_P	2.64	DOWN	119.79	0.0220602	*
Solyc03g025670	Solyc03g025670.2	T2	T2_C	T2_P	2.62	DOWN	175.61	0.0304876	*
Solyc01g091170	ARG2	T2	T2_C	T2_P	2.34	DOWN	43.45	0.0220602	*
XLOC_011946	-	T3	T3_C	T3_P	111.2	UP	58.89	0.0278285	*
Solyc03g097170	Solyc03g097170.2	T3	T3_C	T3_P	13.18	UP	31.77	0.00782778	**
Solyc03g093110	Solyc03g093110.2	T3	T3_C	T3_P	12.79	UP	26.6	0.00782778	**
Solyc03g093120	Solyc03g093120.2	T3	T3_C	T3_P	10.7	UP	26.41	0.00782778	**
Solyc12g011030	Solyc12g011030.1	T3	T3_C	T3_P	9	UP	20.45	0.00782778	**
Solyc06g065820	ERF1	T3	T3_C	T3_P	8.96	UP	7.26	0.0487551	*
Solyc12g057160	Solyc12g057160.1	T3	T3_C	T3_P	8.8	UP	136.48	0.00782778	**
Solyc01g087590	Solyc01g087590.2	T3	T3_C	T3_P	8.34	UP	5.61	0.00782778	**
Solyc07g054470	Solyc07g054470.1	T3	T3_C	T3_P	7.96	UP	669.14	0.00782778	**
Solyc03g097050	Solyc03g097050.2	T3	T3_C	T3_P	7.68	UP	10.4	0.00782778	**
Solyc09g011860	Solyc09g011860.2	T3	T3_C	T3_P	7.27	UP	8.32	0.014053	*

Table A.5 continued.

Gene ID	**Gene Name**	**Time**	**Group 1**	**Group 2**	**Fold Change**	**Direction**	**Total Fpkm**	**q-value**	**Sig. Lvl**
Solyc09g092520	BR1	T3	T3_C	T3_P	6.71	UP	184.18	0.00782778	**
Solyc12g057150	Solyc12g057150.1	T3	T3_C	T3_P	6.46	UP	139.19	0.00782778	**
XLOC_011927	-	T3	T3_C	T3_P	5.96	UP	3.7	0.0487551	*
Solyc06g007180	AS1	T3	T3_C	T3_P	5.43	UP	17.14	0.00782778	**
Solyc04g078340	Solyc04g078340.2	T3	T3_C	T3_P	5.34	UP	5.7	0.014053	*
Solyc01g095140	ER5	T3	T3_C	T3_P	4.87	UP	57.52	0.00782778	**
Solyc02g090360	Solyc02g090360.2	T3	T3_C	T3_P	4.81	UP	33.72	0.00782778	**
Solyc02g092790	AGP-1C	T3	T3_C	T3_P	4.61	UP	212.32	0.00782778	**
XLOC_030520	CYP97C11	T3	T3_C	T3_P	4.55	UP	19.91	0.0190315	*
Solyc01g079580	Solyc01g079580.2	T3	T3_C	T3_P	4.49	UP	75.03	0.00782778	**
Solyc01g057770	Solyc01g057770.2	T3	T3_C	T3_P	4.46	UP	73.02	0.00782778	**
Solyc01g086640	Solyc01g086640.2	T3	T3_C	T3_P	4.43	UP	9.08	0.00782778	**
Solyc04g074310	Solyc04g074310.2	T3	T3_C	T3_P	4.43	UP	11.41	0.00782778	**
Solyc06g030470	Solyc06g030470.2	T3	T3_C	T3_P	4.32	UP	15.43	0.00782778	**
TCONS_00083749	Solyc12g006980.1	T3	T3_C	T3_P	4.07	UP	93.02	0.00782778	**
Solyc02g064680	Solyc02g064680.2	T3	T3_C	T3_P	4.05	UP	71.95	0.00782778	**
Solyc00g206460	Solyc00g206460.1	T3	T3_C	T3_P	4.03	UP	83.19	0.00782778	**
Solyc05g006510	Solyc05g006510.1	T3	T3_C	T3_P	4	UP	26.32	0.00782778	**
Solyc07g062490	Solyc07g062490.1	T3	T3_C	T3_P	3.86	UP	37.81	0.00782778	**
Solyc10g074540	Solyc10g074540.1	T3	T3_C	T3_P	3.74	UP	88.1	0.00782778	**
Solyc01g079940	Solyc01g079940.2	T3	T3_C	T3_P	3.63	UP	15.42	0.00782778	**
Solyc04g077140	Solyc04g077140.2	T3	T3_C	T3_P	3.57	UP	16.91	0.00782778	**
Solyc08g079090	Solyc08g079090.2	T3	T3_C	T3_P	3.42	UP	48.5	0.00782778	**
Solyc09g097960	Solyc09g097960.2	T3	T3_C	T3_P	3.32	UP	52.3	0.00782778	**
Solyc10g078580	Solyc10g078580.1	T3	T3_C	T3_P	3.32	UP	4112.15	0.00782778	**

Table A.5 continued.

Gene ID	**Gene Name**	**Time**	**Group 1**	**Group 2**	**Fold Change**	**Direction**	**Total Fpkm**	**q-value**	**Sig. Lvl**
Solyc03g117860	Solyc03g117860.2	T3	T3_C	T3_P	3.21	UP	25.41	0.0237964	*
Solyc01g065530	Solyc01g065530.2	T3	T3_C	T3_P	3.18	UP	56.3	0.00782778	**
Solyc07g056000	TXET-B2	T3	T3_C	T3_P	3.14	UP	99.34	0.0487551	*
Solyc02g092580	Solyc02g092580.2	T3	T3_C	T3_P	3.09	UP	17.77	0.0190315	*
Solyc11g005150	TEGII	T3	T3_C	T3_P	3.09	UP	11.06	0.0190315	*
Solyc11g010390	Solyc11g010390.1	T3	T3_C	T3_P	3.04	UP	320.52	0.00782778	**
Solyc04g025650	Solyc04g025650.2	T3	T3_C	T3_P	2.93	UP	66.34	0.00782778	**
Solyc08g077210	5PT1	T3	T3_C	T3_P	2.93	UP	194.56	0.00782778	**
Solyc02g079520	Solyc02g079520.1	T3	T3_C	T3_P	2.9	UP	179.46	0.042196	*
Solyc03g005320	Solyc03g005320.2	T3	T3_C	T3_P	2.85	UP	12.38	0.014053	*
Solyc06g074670	Solyc06g074670.2	T3	T3_C	T3_P	2.85	UP	59.28	0.00782778	**
Solyc09g082870	Solyc09g082870.1	T3	T3_C	T3_P	2.83	UP	6.25	0.0454516	*
Solyc01g112000	EXLA1	T3	T3_C	T3_P	2.82	UP	310.99	0.0190315	*
XLOC_005181	-	T3	T3_C	T3_P	2.79	UP	5.76	0.0358998	*
Solyc08g068770	Solyc08g068770.1	T3	T3_C	T3_P	2.74	UP	140.37	0.014053	*
Solyc01g097240	Solyc01g097240.2	T3	T3_C	T3_P	2.73	UP	63.64	0.0278285	*
Solyc04g082140	Solyc04g082140.2	T3	T3_C	T3_P	2.63	UP	106.57	0.00782778	**
Solyc07g065120	Solyc07g065120.2	T3	T3_C	T3_P	2.61	UP	111.85	0.014053	*
Solyc07g009380	LEXET2	T3	T3_C	T3_P	2.6	UP	129.39	0.00782778	**
Solyc01g087020	Solyc01g087020.2	T3	T3_C	T3_P	2.53	UP	83.32	0.0237964	*
Solyc01g102310	Solyc01g102310.2	T3	T3_C	T3_P	2.51	UP	87.62	0.0278285	*
TCONS_00032262	Solyc04g071110.1	T3	T3_C	T3_P	2.44	UP	104.74	0.0392249	*
Solyc07g063240	Solyc07g063240.2	T3	T3_C	T3_P	2.42	UP	28.27	0.042196	*
Solyc02g079590	Solyc02g079590.2	T3	T3_C	T3_P	2.4	UP	14.86	0.042196	*
Solyc03g083560	Solyc03g083560.1	T3	T3_C	T3_P	2.32	UP	61.8	0.0237964	*

Table A.5 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc03g114320	Solyc03g114320.2	T3	T3_C	T3_P	2.22	UP	61.59	0.0358998	*
Solyc08g065850	Solyc08g065850.1	T3	T3_C	T3_P	2.19	UP	9318.75	0.0454516	*
Solyc01g112260	Solyc01g112260.2	T3	T3_C	T3_P	2.17	UP	86.87	0.0454516	*
Solyc06g048820	Solyc06g048820.1	T3	T3_C	T3_P	2.11	UP	992.66	0.0454516	*
Solyc03g098790	CATHDINH	T3	T3_C	T3_P	36.08	DOWN	708.5	0.00782778	**
XLOC_020087	-	T3	T3_C	T3_P	25.13	DOWN	4249.3	0.00782778	**
Solyc11g021060	ARPI	T3	T3_C	T3_P	8.13	DOWN	1012.52	0.00782778	**
Solyc07g008380	Solyc07g008380.1	T3	T3_C	T3_P	7.71	DOWN	4.82	0.0237964	*
XLOC_011836	-	T3	T3_C	T3_P	6.4	DOWN	7445.92	0.042196	*
XLOC_027820	-	T3	T3_C	T3_P	5.36	DOWN	4967.06	0.014053	*
Solyc07g061800	Solyc07g061800.2	T3	T3_C	T3_P	5.34	DOWN	22.74	0.00782778	**
XLOC_027800	-	T3	T3_C	T3_P	5.34	DOWN	3.4	0.0278285	*
Solyc07g007240	Solyc07g007240.2	T3	T3_C	T3_P	4.22	DOWN	87.43	0.00782778	**
Solyc09g008670	TD	T3	T3_C	T3_P	3.95	DOWN	29.74	0.00782778	**
TCONS_00071198	XLOC_028464	T3	T3_C	T3_P	3.68	DOWN	52.16	0.0190315	*
Solyc06g066420	Solyc06g066420.2	T3	T3_C	T3_P	3.23	DOWN	108.57	0.00782778	**
Solyc06g051940	Solyc06g051940.2	T3	T3_C	T3_P	3.18	DOWN	31.87	0.00782778	**
TCONS_00071197	XLOC_028463	T3	T3_C	T3_P	3.01	DOWN	146.54	0.0190315	*
XLOC_017278	-	T3	T3_C	T3_P	2.96	DOWN	116.48	0.00782778	**
Solyc10g008350	Solyc10g008350.2	T3	T3_C	T3_P	2.9	DOWN	72.52	0.0237964	*
Solyc12g088840	Solyc12g088840.1	T3	T3_C	T3_P	2.79	DOWN	632.8	0.0319336	*
TCONS_00042960	XLOC_017075	T3	T3_C	T3_P	2.65	DOWN	77.08	0.0487551	*
Solyc09g009130	PSK1	T3	T3_C	T3_P	2.6	DOWN	183.4	0.00782778	**
Solyc01g006400	Solyc01g006400.2	T3	T3_C	T3_P	2.57	DOWN	547.74	0.0237964	*
Solyc01g067460	Solyc01g067460.1	T3	T3_C	T3_P	2.51	DOWN	363.62	0.0392249	*

Table A.5 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc04g078200	Solyc04g078200.2	T3	T3_C	T3_P	2.47	DOWN	551.76	0.014053	*
Solyc10g009150	Solyc10g009150.2	T3	T3_C	T3_P	2.45	DOWN	158.78	0.014053	*
Solyc01g091320	Solyc01g091320.2	T3	T3_C	T3_P	2.42	DOWN	74.57	0.00782778	**
Solyc01g090340	Solyc01g090340.2	T3	T3_C	T3_P	2.41	DOWN	56.7	0.014053	*
Solyc02g072540	Solyc02g072540.2	T3	T3_C	T3_P	2.29	DOWN	21.22	0.0487551	*
Solyc04g082710	Solyc04g082710.2	T3	T3_C	T3_P	2.28	DOWN	47.46	0.0358998	*
Solyc01g006290	Solyc01g006290.2	T3	T3_C	T3_P	2.27	DOWN	58.38	0.014053	*

Time represents time point as indicated in methods. Group represents the specified group of plants according to their insect treatment. Direction represents the up- or down-regulation of the expressed gene. Total FPKM (Fragments Per Kilobase of transcript per Million) mapped reads represent the sum of all expression of genes among the compared groups. q-value indicates the adjusted p-value after the Benjamini-Hochberg correction for multiple comparison. * q-value < 0.05. ** q-value < 0.01.

Table A.6 List of significantly differentially expressed genes (DEGs) in C vs L comparison

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
XLOC_022709	-	T1	T1_C	T1_L	40.77	UP	212.33	0.013452	*
TCONS_00056275	Solyc07g056640.1	T1	T1_C	T1_L	29.37	UP	139.42	0.013452	*
Solyc06g049020	Solyc06g049020.1	T1	T1_C	T1_L	3.46	UP	112.63	0.0316739	*
Solyc05g006420	Solyc05g006420.2	T1	T1_C	T1_L	3.35	UP	88.2	0.013452	*
Solyc10g005400	Solyc10g005400.2	T1	T1_C	T1_L	3.17	UP	91.72	0.013452	*
Solyc01g107370	Solyc01g107370.2	T1	T1_C	T1_L	1.08	UP	1.3	0.0403049	*
Solyc07g007250	Solyc07g007250.2	T1	T1_C	T1_L	69.03	DOWN	1284.72	0.013452	*
Solyc09g089510	Solyc09g089510.2	T1	T1_C	T1_L	17.55	DOWN	1379.3	0.013452	*

Table A.6 continued.

Gene ID	**Gene Name**	**Time**	**Group 1**	**Group 2**	**Fold Change**	**Direction**	**Total Fpkm**	**q-value**	**Sig. Lvl**
Solyc09g008670	TD	T1	T1_C	T1_L	14.36	DOWN	44.03	0.013452	*
Solyc12g039030	Solyc12g039030.1	T1	T1_C	T1_L	11.62	DOWN	31465.61	0.013452	*
Solyc09g055950	Solyc09g055950.1	T1	T1_C	T1_L	10.51	DOWN	92.94	0.0316739	*
Solyc06g007180	AS1	T1	T1_C	T1_L	9.78	DOWN	14.56	0.013452	*
Solyc03g026280	CBF1	T1	T1_C	T1_L	9.7	DOWN	16.77	0.0471539	*
Solyc01g091170	ARG2	T1	T1_C	T1_L	7.99	DOWN	30.04	0.013452	*
XLOC_000904	-	T1	T1_C	T1_L	6	DOWN	84484.9	0.013452	*
XLOC_027806	-	T1	T1_C	T1_L	5.99	DOWN	11581.1	0.013452	*
Solyc07g006570	Solyc07g006570.2	T1	T1_C	T1_L	5.85	DOWN	51.79	0.013452	*
XLOC_027820	-	T1	T1_C	T1_L	5.59	DOWN	6673.07	0.0403049	*
Solyc03g006360	Solyc03g006360.2	T1	T1_C	T1_L	5.3	DOWN	113.51	0.013452	*
Solyc02g067050	Solyc02g067050.2	T1	T1_C	T1_L	4.97	DOWN	101.86	0.013452	*
XLOC_032854	-	T1	T1_C	T1_L	4.59	DOWN	191.92	0.013452	*
XLOC_030463	-	T1	T1_C	T1_L	3.9	DOWN	266.53	0.0403049	*
Solyc01g095150	LEMMI9	T1	T1_C	T1_L	3.31	DOWN	65.18	0.0316739	*
Solyc08g076730	Solyc08g076730.2	T1	T1_C	T1_L	3.16	DOWN	71.04	0.0316739	*
Solyc08g080670	Solyc08g080670.1	T2	T2_C	T2_L	31.41	UP	98.01	0.0130452	*
Solyc02g078650	Solyc02g078650.2	T2	T2_C	T2_L	23.83	UP	5.23	0.0304876	*
Solyc06g007180	AS1	T2	T2_C	T2_L	23.42	UP	76.94	0.0130452	*
Solyc02g062390	Solyc02g062390.2	T2	T2_C	T2_L	19.44	UP	21.65	0.0130452	*
Solyc02g070110	Solyc02g070110.1	T2	T2_C	T2_L	17.06	UP	11.35	0.0130452	*
Solyc08g029000	Solyc08g029000.2	T2	T2_C	T2_L	15.61	UP	5.54	0.0130452	*
Solyc04g007000	Solyc04g007000.1	T2	T2_C	T2_L	15.61	UP	65.33	0.0130452	*
Solyc09g097760	Solyc09g097760.2	T2	T2_C	T2_L	13.5	UP	85.76	0.0130452	*
Solyc08g077330	Solyc08g077330.2	T2	T2_C	T2_L	12	UP	142.61	0.0130452	*

Table A.6 continued.

Gene ID	**Gene Name**	**Time**	**Group 1**	**Group 2**	**Fold Change**	**Direction**	**Total Fpkm**	**q-value**	**Sig. Lvl**
Solyc05g052680	Solyc05g052680.1	T2	T2_C	T2_L	11.51	UP	10.21	0.0130452	*
Solyc08g080660	PR-5	T2	T2_C	T2_L	11.27	UP	36.83	0.0130452	*
Solyc03g006360	Solyc03g006360.2	T2	T2_C	T2_L	11.04	UP	213.89	0.0130452	*
Solyc06g062460	Solyc06g062460.2	T2	T2_C	T2_L	10.99	UP	54.71	0.0130452	*
Solyc02g078150	Solyc02g078150.2	T2	T2_C	T2_L	10.09	UP	30.77	0.0130452	*
Solyc07g006560	Solyc07g006560.2	T2	T2_C	T2_L	10.05	UP	30.68	0.0130452	*
Solyc08g021820	Solyc08g021820.2	T2	T2_C	T2_L	9.67	UP	57.44	0.0130452	*
Solyc01g080010	ACI25	T2	T2_C	T2_L	9.01	UP	39.28	0.0130452	*
Solyc02g071470	Solyc02g071470.2	T2	T2_C	T2_L	7.33	UP	7.23	0.0220602	*
Solyc07g054720	Solyc07g054720.1	T2	T2_C	T2_L	7.31	UP	624.71	0.0220602	*
Solyc03g020010	Solyc03g020010.1	T2	T2_C	T2_L	7.18	UP	47.39	0.0130452	*
Solyc05g041540	Solyc05g041540.2	T2	T2_C	T2_L	7.17	UP	9.39	0.0130452	*
Solyc08g079230	Solyc08g079230.1	T2	T2_C	T2_L	6.92	UP	109.15	0.0447756	*
Solyc05g052670	Solyc05g052670.1	T2	T2_C	T2_L	6.81	UP	13.46	0.0130452	*
Solyc09g092520	BR1	T2	T2_C	T2_L	6.78	UP	54.96	0.0130452	*
Solyc01g060020	Solyc01g060020.2	T2	T2_C	T2_L	6.65	UP	81.36	0.0130452	*
Solyc10g017960	Solyc10g017960.1	T2	T2_C	T2_L	6.55	UP	15.38	0.0220602	*
Solyc04g064880	Solyc04g064880.2	T2	T2_C	T2_L	6.53	UP	10.88	0.0378174	*
TCONS_00032661	Solyc04g074410.1	T2	T2_C	T2_L	6.39	UP	32.65	0.0130452	*
Solyc03g025380	Solyc03g025380.2	T2	T2_C	T2_L	6.18	UP	10.17	0.0447756	*
Solyc02g092580	Solyc02g092580.2	T2	T2_C	T2_L	5.72	UP	35.57	0.0130452	*
Solyc04g011770	Solyc04g011770.2	T2	T2_C	T2_L	5.68	UP	17.61	0.0378174	*
Solyc03g098740	Solyc03g098740.1	T2	T2_C	T2_L	5.67	UP	83.65	0.0130452	*
Solyc04g078340	Solyc04g078340.2	T2	T2_C	T2_L	5.65	UP	9.08	0.0130452	*
Solyc08g062180	Solyc08g062180.1	T2	T2_C	T2_L	5.53	UP	21.38	0.0130452	*

Table A.6 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc02g077590	Solyc02g077590.1	T2	T2_C	T2_L	5.4	UP	93.47	0.0130452	*
Solyc06g067910	Solyc06g067910.2	T2	T2_C	T2_L	5.27	UP	31.12	0.0130452	*
Solyc08g074680	PPO	T2	T2_C	T2_L	5.24	UP	2.86	0.0220602	*
Solyc04g076220	Solyc04g076220.2	T2	T2_C	T2_L	5.2	UP	27.48	0.0130452	*
Solyc05g007950	RNALE	T2	T2_C	T2_L	5.04	UP	36.7	0.0378174	*
Solyc06g060830	Solyc06g060830.2	T2	T2_C	T2_L	4.69	UP	50.48	0.0130452	*
Solyc08g079900	Solyc08g079900.1	T2	T2_C	T2_L	4.66	UP	30.56	0.0130452	*
Solyc10g083690	Solyc10g083690.2	T2	T2_C	T2_L	4.61	UP	11.52	0.0130452	*
Solyc06g009140	Solyc06g009140.2	T2	T2_C	T2_L	4.6	UP	152.64	0.0130452	*
Solyc03g031890	Solyc03g031890.2	T2	T2_C	T2_L	4.56	UP	20.46	0.0220602	*
Solyc07g062490	Solyc07g062490.1	T2	T2_C	T2_L	4.53	UP	43.15	0.0130452	*
Solyc04g071890	Solyc04g071890.2	T2	T2_C	T2_L	4.5	UP	184.59	0.0130452	*
Solyc04g005610	Solyc04g005610.2	T2	T2_C	T2_L	4.39	UP	21.36	0.0220602	*
Solyc08g068730	THT1-3	T2	T2_C	T2_L	4.37	UP	76.34	0.0130452	*
Solyc09g090970	Solyc09g090970.2	T2	T2_C	T2_L	4.34	UP	28.36	0.0130452	*
Solyc03g098730	Solyc03g098730.1	T2	T2_C	T2_L	4.3	UP	33.78	0.0130452	*
Solyc08g077900	Solyc08g077900.2	T2	T2_C	T2_L	4.21	UP	25.14	0.0447756	*
Solyc01g079940	Solyc01g079940.2	T2	T2_C	T2_L	4.17	UP	10.92	0.0220602	*
Solyc03g078490	Solyc03g078490.2	T2	T2_C	T2_L	4.01	UP	74.41	0.0130452	*
Solyc09g098510	Solyc09g098510.2	T2	T2_C	T2_L	3.97	UP	88.2	0.0130452	*
Solyc09g065780	Solyc09g065780.2	T2	T2_C	T2_L	3.87	UP	14.56	0.0304876	*
Solyc08g078870	Solyc08g078870.1	T2	T2_C	T2_L	3.78	UP	926.47	0.0220602	*
TCONS_00070216	Solyc10g008400.1	T2	T2_C	T2_L	3.62	UP	26.37	0.0447756	*
Solyc05g009790	Solyc05g009790.1	T2	T2_C	T2_L	3.49	UP	63.72	0.0130452	*
Solyc06g011350	Solyc06g011350.2	T2	T2_C	T2_L	3.46	UP	25.2	0.0220602	*

Table A.6 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc04g080820	Solyc04g080820.2	T2	T2_C	T2_L	3.41	UP	14.66	0.0378174	*
Solyc02g082900	Solyc02g082900.2	T2	T2_C	T2_L	3.4	UP	43.73	0.0130452	*
Solyc04g079860	Solyc04g079860.1	T2	T2_C	T2_L	3.26	UP	21.24	0.0447756	*
Solyc07g005100	Solyc07g005100.2	T2	T2_C	T2_L	3.26	UP	54.04	0.0447756	*
Solyc01g005470	Solyc01g005470.2	T2	T2_C	T2_L	2.98	UP	123.73	0.0130452	*
Solyc03g044790	Solyc03g044790.2	T2	T2_C	T2_L	2.96	UP	35.03	0.0220602	*
Solyc04g040180	Solyc04g040180.2	T2	T2_C	T2_L	2.92	UP	48.21	0.0130452	*
Solyc12g045030	Solyc12g045030.1	T2	T2_C	T2_L	2.91	UP	260.77	0.0220602	*
Solyc07g063410	Solyc07g063410.2	T2	T2_C	T2_L	2.88	UP	23.18	0.0447756	*
Solyc06g068500	Solyc06g068500.2	T2	T2_C	T2_L	2.81	UP	283.51	0.0130452	*
Solyc09g065540	Solyc09g065540.2	T2	T2_C	T2_L	2.8	UP	34.96	0.0130452	*
Solyc05g007770	Solyc05g007770.2	T2	T2_C	T2_L	2.72	UP	29.27	0.0304876	*
TCONS_00056024	Solyc07g054730.1	T2	T2_C	T2_L	2.7	UP	459.05	0.0220602	*
Solyc02g064690	Solyc02g064690.2	T2	T2_C	T2_L	2.61	UP	31.62	0.0304876	*
TCONS_00040539	Solyc05g008110.2	T2	T2_C	T2_L	2.38	UP	186.03	0.0220602	*
Solyc03g119520	Solyc03g119520.2	T2	T2_C	T2_L	2.32	UP	58.33	0.0378174	*
XLOC_022709	-	T2	T2_C	T2_L	24.48	DOWN	35.52	0.0130452	*
Solyc09g011080	Solyc09g011080.2	T2	T2_C	T2_L	13.49	DOWN	18.73	0.0130452	*
XLOC_020087	-	T2	T2_C	T2_L	7.36	DOWN	1363.12	0.0220602	*
Solyc06g069730	Solyc06g069730.2	T2	T2_C	T2_L	6.44	DOWN	778.78	0.0130452	*
Solyc01g095320	Solyc01g095320.2	T2	T2_C	T2_L	5.79	DOWN	14.53	0.0130452	*
Solyc02g070980	Solyc02g070980.1	T2	T2_C	T2_L	5.7	DOWN	2447.66	0.0378174	*
Solyc07g042520	Solyc07g042520.2	T2	T2_C	T2_L	5.61	DOWN	7.17	0.0130452	*
TCONS_00056275	Solyc07g056640.1	T2	T2_C	T2_L	5.49	DOWN	77.82	0.0130452	*
Solyc02g070990	Solyc02g070990.1	T2	T2_C	T2_L	5.33	DOWN	1220.34	0.0130452	*

Table A.6 continued.

Gene ID	**Gene Name**	**Time**	**Group 1**	**Group 2**	**Fold Change**	**Direction**	**Total Fpkm**	**q-value**	**Sig. Lvl**
TCONS_00087655	XLOC_034361	T2	T2_C	T2_L	4.79	DOWN	160.52	0.0130452	*
Solyc02g080210	Solyc02g080210.2	T2	T2_C	T2_L	4.28	DOWN	90.37	0.0378174	*
Solyc06g072710	Solyc06g072710.2	T2	T2_C	T2_L	4.26	DOWN	118.96	0.0130452	*
Solyc12g098900	Solyc12g098900.1	T2	T2_C	T2_L	3.93	DOWN	48.21	0.0130452	*
Solyc05g043330	Solyc05g043330.2	T2	T2_C	T2_L	3.63	DOWN	25.36	0.0130452	*
XLOC_020108	-	T2	T2_C	T2_L	3.62	DOWN	119.86	0.0130452	*
Solyc03g005790	Solyc03g005790.2	T2	T2_C	T2_L	3.44	DOWN	155.81	0.0130452	*
Solyc06g060310	Solyc06g060310.2	T2	T2_C	T2_L	3.43	DOWN	49.2	0.0130452	*
Solyc06g060340	PSBS	T2	T2_C	T2_L	3.26	DOWN	614.17	0.0130452	*
Solyc06g068950	Solyc06g068950.2	T2	T2_C	T2_L	3.21	DOWN	39.21	0.0130452	*
Solyc07g055260	Solyc07g055260.2	T2	T2_C	T2_L	3.21	DOWN	107.79	0.0130452	*
Solyc04g007780	Solyc04g007780.2	T2	T2_C	T2_L	3.14	DOWN	25.6	0.0378174	*
Solyc05g047680	Solyc05g047680.2	T2	T2_C	T2_L	3.04	DOWN	15.05	0.0220602	*
Solyc01g102610	Solyc01g102610.2	T2	T2_C	T2_L	3.03	DOWN	64	0.0130452	*
XLOC_000904	-	T2	T2_C	T2_L	2.97	DOWN	49067	0.0130452	*
Solyc05g050770	Solyc05g050770.2	T2	T2_C	T2_L	2.9	DOWN	38.47	0.0130452	*
Solyc09g008320	Solyc09g008320.2	T2	T2_C	T2_L	2.86	DOWN	77.96	0.0130452	*
TCONS_00042960	XLOC_017075	T2	T2_C	T2_L	2.64	DOWN	85.52	0.0220602	*
Solyc03g114130	Solyc03g114130.1	T2	T2_C	T2_L	2.58	DOWN	213.41	0.0304876	*
Solyc01g006330	Solyc01g006330.2	T2	T2_C	T2_L	2.55	DOWN	108.99	0.0220602	*
Solyc01g087710	Solyc01g087710.2	T2	T2_C	T2_L	2.44	DOWN	71.92	0.0304876	*
Solyc01g005520	Solyc01g005520.2	T2	T2_C	T2_L	2.38	DOWN	234.35	0.0220602	*
Solyc07g009500	Solyc07g009500.1	T3	T3_C	T3_L	31	UP	519.1	0.00782778	**
Solyc09g097810	Solyc09g097810.2	T3	T3_C	T3_L	27.76	UP	32.05	0.0454516	*
Solyc03g093120	Solyc03g093120.2	T3	T3_C	T3_L	23.3	UP	54.88	0.00782778	**

Table A.6 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc03g093110	Solyc03g093110.2	T3	T3_C	T3_L	22.17	UP	44.7	0.00782778	**
Solyc03g119590	Solyc03g119590.1	T3	T3_C	T3_L	20.29	UP	138.36	0.00782778	**
Solyc03g097170	Solyc03g097170.2	T3	T3_C	T3_L	18.57	UP	43.85	0.00782778	**
Solyc12g100270	Solyc12g100270.1	T3	T3_C	T3_L	18.28	UP	4.19	0.0392249	*
Solyc04g007140	Solyc04g007140.1	T3	T3_C	T3_L	17.64	UP	127.17	0.00782778	**
Solyc06g065820	ERF1	T3	T3_C	T3_L	16.37	UP	12.66	0.0190315	*
Solyc11g018800	Solyc11g018800.1	T3	T3_C	T3_L	16.32	UP	8.92	0.0319336	*
Solyc09g092520	BR1	T3	T3_C	T3_L	14.29	UP	365.43	0.00782778	**
Solyc09g090990	Solyc09g090990.2	T3	T3_C	T3_L	14.26	UP	19.43	0.00782778	**
Solyc03g097050	Solyc03g097050.2	T3	T3_C	T3_L	12.79	UP	16.54	0.00782778	**
Solyc11g030730	Solyc11g030730.1	T3	T3_C	T3_L	12.74	UP	8.3	0.00782778	**
Solyc12g011030	Solyc12g011030.1	T3	T3_C	T3_L	12.14	UP	26.89	0.00782778	**
Solyc09g011860	Solyc09g011860.2	T3	T3_C	T3_L	11.86	UP	12.95	0.00782778	**
Solyc06g062920	Solyc06g062920.2	T3	T3_C	T3_L	11.68	UP	3.39	0.00782778	**
Solyc08g067360	Solyc08g067360.2	T3	T3_C	T3_L	10.96	UP	14.3	0.00782778	**
Solyc12g057160	Solyc12g057160.1	T3	T3_C	T3_L	10.92	UP	165.98	0.00782778	**
Solyc12g049030	Solyc12g049030.1	T3	T3_C	T3_L	10.82	UP	18.42	0.00782778	**
Solyc03g005980	Solyc03g005980.2	T3	T3_C	T3_L	10.72	UP	9.05	0.00782778	**
Solyc02g093580	Solyc02g093580.2	T3	T3_C	T3_L	10.04	UP	8.01	0.00782778	**
Solyc04g074680	Solyc04g074680.1	T3	T3_C	T3_L	9.84	UP	39.34	0.0190315	*
Solyc08g068710	Solyc08g068710.1	T3	T3_C	T3_L	9.47	UP	29.33	0.00782778	**
Solyc08g067340	Solyc08g067340.2	T3	T3_C	T3_L	9.25	UP	40.58	0.00782778	**
Solyc11g011240	GGPS1	T3	T3_C	T3_L	9.14	UP	8.02	0.0319336	*
Solyc08g067310	Solyc08g067310.1	T3	T3_C	T3_L	8.74	UP	7.36	0.00782778	**
Solyc12g057150	Solyc12g057150.1	T3	T3_C	T3_L	8.57	UP	178.54	0.00782778	**

Table A.6 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc04g072070	Solyc04g072070.2	T3	T3_C	T3_L	8.49	UP	19.34	0.00782778	**
XLOC_022709	-	T3	T3_C	T3_L	8.21	UP	11.35	0.0190315	*
Solyc06g030470	Solyc06g030470.2	T3	T3_C	T3_L	7.99	UP	26.06	0.00782778	**
Solyc03g026230	Solyc03g026230.1	T3	T3_C	T3_L	7.93	UP	4.82	0.0278285	*
Solyc03g122350	Solyc03g122350.2	T3	T3_C	T3_L	7.75	UP	68.96	0.00782778	**
Solyc08g068680	AADC1A	T3	T3_C	T3_L	7.39	UP	12.4	0.00782778	**
Solyc07g054470	Solyc07g054470.1	T3	T3_C	T3_L	7.36	UP	623.68	0.00782778	**
Solyc04g051690	Solyc04g051690.2	T3	T3_C	T3_L	7.31	UP	58.41	0.00782778	**
Solyc10g005320	Solyc10g005320.2	T3	T3_C	T3_L	7.17	UP	6.43	0.014053	*
Solyc03g033790	Solyc03g033790.2	T3	T3_C	T3_L	7.1	UP	6.44	0.00782778	**
Solyc06g062420	Solyc06g062420.2	T3	T3_C	T3_L	6.92	UP	17.08	0.042196	*
Solyc10g055740	Solyc10g055740.1	T3	T3_C	T3_L	6.7	UP	5.8	0.00782778	**
Solyc07g009230	Solyc07g009230.2	T3	T3_C	T3_L	6.37	UP	19.61	0.0392249	*
Solyc02g077370	PTI5	T3	T3_C	T3_L	6.33	UP	24.68	0.0190315	*
Solyc12g096960	Solyc12g096960.1	T3	T3_C	T3_L	6.33	UP	36.4	0.0319336	*
Solyc01g008620	Solyc01g008620.2	T3	T3_C	T3_L	6.28	UP	59.93	0.00782778	**
Solyc10g076480	Solyc10g076480.1	T3	T3_C	T3_L	6.18	UP	8.26	0.042196	*
Solyc04g078340	Solyc04g078340.2	T3	T3_C	T3_L	6.02	UP	6.31	0.00782778	**
Solyc09g082870	Solyc09g082870.1	T3	T3_C	T3_L	6.01	UP	11.42	0.00782778	**
Solyc03g115930	Solyc03g115930.1	T3	T3_C	T3_L	5.9	UP	36.78	0.00782778	**
Solyc05g006510	Solyc05g006510.1	T3	T3_C	T3_L	5.79	UP	35.73	0.00782778	**
Solyc05g051530	Solyc05g051530.2	T3	T3_C	T3_L	5.65	UP	22.17	0.00782778	**
Solyc09g091000	Solyc09g091000.2	T3	T3_C	T3_L	5.64	UP	40.5	0.00782778	**
Solyc08g079900	Solyc08g079900.1	T3	T3_C	T3_L	5.62	UP	15.95	0.00782778	**
Solyc11g069940	Solyc11g069940.1	T3	T3_C	T3_L	5.45	UP	212.88	0.00782778	**

Table A.6 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc12g036390	Solyc12g036390.1	T3	T3_C	T3_L	5.42	UP	7.61	0.014053	*
Solyc02g092580	Solyc02g092580.2	T3	T3_C	T3_L	5.38	UP	27.75	0.00782778	**
Solyc07g045530	Solyc07g045530.1	T3	T3_C	T3_L	5.36	UP	25.82	0.0237964	*
Solyc07g056000	TXET-B2	T3	T3_C	T3_L	5.23	UP	149.3	0.00782778	**
Solyc07g008140	Solyc07g008140.2	T3	T3_C	T3_L	5.17	UP	52.14	0.00782778	**
Solyc08g077110	Solyc08g077110.2	T3	T3_C	T3_L	5.12	UP	7.84	0.00782778	**
Solyc02g092790	AGP-1C	T3	T3_C	T3_L	5.12	UP	231.71	0.00782778	**
Solyc09g097760	Solyc09g097760.2	T3	T3_C	T3_L	5.01	UP	26.53	0.042196	*
Solyc05g053550	CHS2	T3	T3_C	T3_L	4.99	UP	34.31	0.00782778	**
Solyc02g082740	Solyc02g082740.1	T3	T3_C	T3_L	4.96	UP	56.74	0.00782778	**
Solyc01g079580	Solyc01g079580.2	T3	T3_C	T3_L	4.89	UP	80.48	0.00782778	**
Solyc08g007460	Solyc08g007460.2	T3	T3_C	T3_L	4.88	UP	83.53	0.00782778	**
Solyc04g077270	Solyc04g077270.2	T3	T3_C	T3_L	4.86	UP	44.2	0.00782778	**
Solyc02g090360	Solyc02g090360.2	T3	T3_C	T3_L	4.83	UP	33.84	0.00782778	**
Solyc04g005100	Solyc04g005100.2	T3	T3_C	T3_L	4.83	UP	48.26	0.00782778	**
Solyc09g007010	Solyc09g007010.1	T3	T3_C	T3_L	4.81	UP	126.03	0.00782778	**
Solyc10g076500	Solyc10g076500.1	T3	T3_C	T3_L	4.8	UP	3.67	0.0190315	*
Solyc06g069040	Solyc06g069040.2	T3	T3_C	T3_L	4.78	UP	14.23	0.0454516	*
Solyc05g009420	Solyc05g009420.1	T3	T3_C	T3_L	4.75	UP	33.34	0.00782778	**
Solyc00g206460	Solyc00g206460.1	T3	T3_C	T3_L	4.75	UP	95.11	0.014053	*
Solyc02g062550	Solyc02g062550.2	T3	T3_C	T3_L	4.73	UP	4.7	0.0392249	*
Solyc01g086640	Solyc01g086640.2	T3	T3_C	T3_L	4.72	UP	9.57	0.00782778	**
Solyc10g075150	Solyc10g075150.1	T3	T3_C	T3_L	4.69	UP	2155.67	0.0278285	*
Solyc12g042480	Solyc12g042480.1	T3	T3_C	T3_L	4.66	UP	29.96	0.00782778	**
Solyc10g007280	Solyc10g007280.2	T3	T3_C	T3_L	4.56	UP	18.7	0.00782778	**

Table A.6 continued.

Gene ID	**Gene Name**	**Time**	**Group 1**	**Group 2**	**Fold Change**	**Direction**	**Total Fpkm**	**q-value**	**Sig. Lvl**
Solyc02g078400	Solyc02g078400.2	T3	T3_C	T3_L	4.55	UP	29.89	0.00782778	**
Solyc04g071780	Solyc04g071780.2	T3	T3_C	T3_L	4.55	UP	73.2	0.00782778	**
Solyc04g054690	AO	T3	T3_C	T3_L	4.53	UP	18.44	0.00782778	**
Solyc04g009640	Solyc04g009640.2	T3	T3_C	T3_L	4.52	UP	2.33	0.0392249	*
XLOC_025270	-	T3	T3_C	T3_L	4.5	UP	57.91	0.00782778	**
Solyc05g050130	Solyc05g050130.2	T3	T3_C	T3_L	4.46	UP	284.29	0.00782778	**
Solyc10g085010	Solyc10g085010.1	T3	T3_C	T3_L	4.41	UP	62.13	0.00782778	**
Solyc10g055200	Solyc10g055200.1	T3	T3_C	T3_L	4.37	UP	111.38	0.00782778	**
Solyc01g010060	Solyc01g010060.2	T3	T3_C	T3_L	4.37	UP	35.64	0.0358998	*
Solyc09g005730	Solyc09g005730.2	T3	T3_C	T3_L	4.31	UP	35.21	0.00782778	**
Solyc12g056360	Solyc12g056360.1	T3	T3_C	T3_L	4.31	UP	26.58	0.0237964	*
Solyc04g007380	Solyc04g007380.1	T3	T3_C	T3_L	4.29	UP	12.33	0.0454516	*
Solyc04g054760	Solyc04g054760.2	T3	T3_C	T3_L	4.26	UP	83.06	0.00782778	**
Solyc11g010390	Solyc11g010390.1	T3	T3_C	T3_L	4.18	UP	411.23	0.00782778	**
Solyc07g042490	Solyc07g042490.1	T3	T3_C	T3_L	4.16	UP	48.98	0.0237964	*
Solyc03g013160	Solyc03g013160.2	T3	T3_C	T3_L	4.08	UP	22.12	0.00782778	**
Solyc02g064680	Solyc02g064680.2	T3	T3_C	T3_L	3.99	UP	71.18	0.00782778	**
Solyc10g083290	WIV-1	T3	T3_C	T3_L	3.95	UP	12.67	0.00782778	**
Solyc07g009380	LEXET2	T3	T3_C	T3_L	3.91	UP	176.11	0.00782778	**
Solyc02g090820	Solyc02g090820.2	T3	T3_C	T3_L	3.87	UP	32.59	0.00782778	**
Solyc09g011560	Solyc09g011560.2	T3	T3_C	T3_L	3.82	UP	41.81	0.00782778	**
Solyc02g077040	PIP1	T3	T3_C	T3_L	3.81	UP	266.38	0.00782778	**
Solyc02g093230	Solyc02g093230.2	T3	T3_C	T3_L	3.79	UP	62.5	0.0190315	*
Solyc09g097960	Solyc09g097960.2	T3	T3_C	T3_L	3.74	UP	57.45	0.00782778	**
Solyc09g014990	Solyc09g014990.2	T3	T3_C	T3_L	3.67	UP	27.29	0.00782778	**

Table A.6 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc03g083460	Solyc03g083460.2	T3	T3_C	T3_L	3.65	UP	13.64	0.0190315	*
Solyc06g048820	Solyc06g048820.1	T3	T3_C	T3_L	3.62	UP	1473.62	0.00782778	**
Solyc03g094160	Solyc03g094160.2	T3	T3_C	T3_L	3.59	UP	33.7	0.00782778	**
Solyc09g015770	Solyc09g015770.2	T3	T3_C	T3_L	3.58	UP	312.99	0.00782778	**
Solyc07g056190	Solyc07g056190.2	T3	T3_C	T3_L	3.55	UP	51.9	0.0319336	*
Solyc03g025670	Solyc03g025670.2	T3	T3_C	T3_L	3.54	UP	244.42	0.00782778	**
Solyc02g063440	Solyc02g063440.2	T3	T3_C	T3_L	3.53	UP	237.4	0.00782778	**
Solyc04g077140	Solyc04g077140.2	T3	T3_C	T3_L	3.51	UP	16.69	0.00782778	**
Solyc01g100010	Solyc01g100010.2	T3	T3_C	T3_L	3.51	UP	34.05	0.00782778	**
Solyc05g051460	Solyc05g051460.2	T3	T3_C	T3_L	3.47	UP	34.34	0.00782778	**
Solyc11g005150	TEGII	T3	T3_C	T3_L	3.46	UP	12.03	0.0319336	*
Solyc07g056200	Solyc07g056200.2	T3	T3_C	T3_L	3.43	UP	86.24	0.00782778	**
Solyc02g036480	Solyc02g036480.1	T3	T3_C	T3_L	3.42	UP	39.55	0.00782778	**
Solyc01g097240	Solyc01g097240.2	T3	T3_C	T3_L	3.37	UP	74.57	0.00782778	**
Solyc03g097610	Solyc03g097610.2	T3	T3_C	T3_L	3.34	UP	34.8	0.00782778	**
Solyc06g007620	Solyc06g007620.2	T3	T3_C	T3_L	3.34	UP	136.68	0.0237964	*
Solyc09g011490	Solyc09g011490.2	T3	T3_C	T3_L	3.32	UP	41.08	0.014053	*
Solyc03g082370	Solyc03g082370.1	T3	T3_C	T3_L	3.32	UP	595.23	0.0237964	*
Solyc01g089880	Solyc01g089880.2	T3	T3_C	T3_L	3.28	UP	83.27	0.00782778	**
Solyc08g068770	Solyc08g068770.1	T3	T3_C	T3_L	3.28	UP	160.78	0.0319336	*
Solyc02g090490	Solyc02g090490.2	T3	T3_C	T3_L	3.26	UP	15.6	0.0278285	*
Solyc03g083400	Solyc03g083400.2	T3	T3_C	T3_L	3.22	UP	65.15	0.00782778	**
Solyc08g060920	AIL	T3	T3_C	T3_L	3.21	UP	36.5	0.0190315	*
Solyc02g091380	Solyc02g091380.1	T3	T3_C	T3_L	3.2	UP	183.47	0.0190315	*
Solyc03g095770	Solyc03g095770.2	T3	T3_C	T3_L	3.19	UP	174.18	0.00782778	**

Table A.6 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc01g006300	CEVI-1	T3	T3_C	T3_L	3.18	UP	202.1	0.00782778	**
Solyc03g006700	Solyc03g006700.2	T3	T3_C	T3_L	3.15	UP	11.36	0.0392249	*
Solyc09g075910	Solyc09g075910.1	T3	T3_C	T3_L	3.13	UP	8.91	0.0392249	*
Solyc10g079860	TOMQ`B	T3	T3_C	T3_L	3.1	UP	67.47	0.00782778	**
Solyc02g032950	Solyc02g032950.2	T3	T3_C	T3_L	3.09	UP	29.32	0.00782778	**
Solyc06g061230	Solyc06g061230.2	T3	T3_C	T3_L	3.09	UP	55.92	0.014053	*
Solyc06g050440	Solyc06g050440.2	T3	T3_C	T3_L	3.09	UP	23.45	0.042196	*
Solyc07g062490	Solyc07g062490.1	T3	T3_C	T3_L	3.08	UP	31.71	0.00782778	**
Solyc03g122120	Solyc03g122120.2	T3	T3_C	T3_L	3.07	UP	19.87	0.00782778	**
Solyc01g109880	ZIP	T3	T3_C	T3_L	3.07	UP	101.79	0.00782778	**
Solyc03g121660	Solyc03g121660.2	T3	T3_C	T3_L	3.05	UP	70.97	0.014053	*
Solyc03g114600	ASC-1	T3	T3_C	T3_L	3.05	UP	17.8	0.0392249	*
Solyc02g082920	CHI3	T3	T3_C	T3_L	3.04	UP	470.29	0.0278285	*
Solyc03g117860	Solyc03g117860.2	T3	T3_C	T3_L	3.03	UP	24.34	0.0319336	*
Solyc04g080820	Solyc04g080820.2	T3	T3_C	T3_L	3.03	UP	12.89	0.042196	*
Solyc04g078290	Solyc04g078290.2	T3	T3_C	T3_L	3.01	UP	85.14	0.00782778	**
Solyc03g083560	Solyc03g083560.1	T3	T3_C	T3_L	2.98	UP	74.11	0.00782778	**
Solyc04g079110	Solyc04g079110.1	T3	T3_C	T3_L	2.98	UP	25.86	0.0278285	*
Solyc05g009040	Solyc05g009040.2	T3	T3_C	T3_L	2.96	UP	28.99	0.0319336	*
Solyc08g068730	THT1-3	T3	T3_C	T3_L	2.91	UP	44.95	0.0358998	*
Solyc04g011440	HSC70.3	T3	T3_C	T3_L	2.88	UP	13.33	0.00782778	**
Solyc03g121620	Solyc03g121620.1	T3	T3_C	T3_L	2.86	UP	76.77	0.0237964	*
XLOC_005215	Solyc01g108050.2	T3	T3_C	T3_L	2.83	UP	2.03	0.0278285	*
Solyc07g049550	ACO4	T3	T3_C	T3_L	2.82	UP	26.81	0.0190315	*
Solyc06g074530	Solyc06g074530.1	T3	T3_C	T3_L	2.78	UP	31.85	0.0190315	*

Table A.6 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc03g113520	Solyc03g113520.2	T3	T3_C	T3_L	2.76	UP	9.27	0.0358998	*
Solyc05g007890	Solyc05g007890.2	T3	T3_C	T3_L	2.75	UP	25.6	0.00782778	**
Solyc09g065890	Solyc09g065890.2	T3	T3_C	T3_L	2.75	UP	38.72	0.0190315	*
Solyc09g090980	Solyc09g090980.2	T3	T3_C	T3_L	2.73	UP	369.03	0.014053	*
Solyc01g087020	Solyc01g087020.2	T3	T3_C	T3_L	2.65	UP	86.2	0.0278285	*
Solyc01g088660	Solyc01g088660.2	T3	T3_C	T3_L	2.64	UP	156.35	0.00782778	**
Solyc05g005200	Solyc05g005200.2	T3	T3_C	T3_L	2.64	UP	44.18	0.014053	*
Solyc01g102310	Solyc01g102310.2	T3	T3_C	T3_L	2.61	UP	90.31	0.0392249	*
Solyc07g008590	Solyc07g008590.1	T3	T3_C	T3_L	2.58	UP	8.69	0.0392249	*
Solyc03g034370	Solyc03g034370.1	T3	T3_C	T3_L	2.55	UP	4195.51	0.00782778	**
Solyc04g076060	TFT10	T3	T3_C	T3_L	2.55	UP	116.14	0.0237964	*
Solyc02g093860	Solyc02g093860.2	T3	T3_C	T3_L	2.53	UP	33.93	0.0278285	*
Solyc03g078490	Solyc03g078490.2	T3	T3_C	T3_L	2.5	UP	28.35	0.0358998	*
TCONS_00051896	Solyc07g041620.1	T3	T3_C	T3_L	2.49	UP	18.13	0.00782778	**
Solyc08g077480	Solyc08g077480.2	T3	T3_C	T3_L	2.48	UP	251.46	0.0190315	*
XLOC_017161	-	T3	T3_C	T3_L	2.47	UP	117.37	0.0278285	*
Solyc09g011590	Solyc09g011590.2	T3	T3_C	T3_L	2.45	UP	70.18	0.0237964	*
Solyc03g114100	Solyc03g114100.1	T3	T3_C	T3_L	2.44	UP	354.84	0.00782778	**
Solyc02g069800	Solyc02g069800.1	T3	T3_C	T3_L	2.42	UP	102.47	0.00782778	**
Solyc04g079940	Solyc04g079940.2	T3	T3_C	T3_L	2.41	UP	72.19	0.0392249	*
Solyc07g054850	Solyc07g054850.2	T3	T3_C	T3_L	2.4	UP	41.11	0.00782778	**
Solyc01g010230	Solyc01g010230.2	T3	T3_C	T3_L	2.39	UP	98.08	0.0237964	*
Solyc07g005100	Solyc07g005100.2	T3	T3_C	T3_L	2.39	UP	29.99	0.042196	*
Solyc10g009410	Solyc10g009410.1	T3	T3_C	T3_L	2.37	UP	39.03	0.0358998	*
TCONS_00048992	Solyc06g065560.1	T3	T3_C	T3_L	2.36	UP	23.67	0.0237964	*

Table A.6 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc09g005260	Solyc09g005260.2	T3	T3_C	T3_L	2.36	UP	241.15	0.0278285	*
Solyc04g077230	Solyc04g077230.1	T3	T3_C	T3_L	2.36	UP	1564.32	0.0319336	*
Solyc03g116700	Solyc03g116700.2	T3	T3_C	T3_L	2.35	UP	123.73	0.014053	*
Solyc03g031420	Solyc03g031420.1	T3	T3_C	T3_L	2.35	UP	19.35	0.0392249	*
Solyc03g119600	Solyc03g119600.1	T3	T3_C	T3_L	2.32	UP	917.77	0.0392249	*
Solyc05g041910	Solyc05g041910.2	T3	T3_C	T3_L	2.26	UP	116.55	0.0487551	*
Solyc07g014670	Solyc07g014670.2	T3	T3_C	T3_L	2.23	UP	40.35	0.0278285	*
Solyc09g075820	HT2	T3	T3_C	T3_L	2.23	UP	46.04	0.0358998	*
Solyc06g008870	Solyc06g008870.2	T3	T3_C	T3_L	2.23	UP	25.73	0.0454516	*
Solyc04g054500	Solyc04g054500.2	T3	T3_C	T3_L	2.14	UP	81.48	0.0278285	*
Solyc02g092800	Solyc02g092800.2	T3	T3_C	T3_L	2.06	UP	50.38	0.0487551	*
Solyc03g098790	CATHDINH	T3	T3_C	T3_L	37.09	DOWN	707.98	0.00782778	**
Solyc08g081620	CEL1	T3	T3_C	T3_L	28.47	DOWN	7.19	0.00782778	**
Solyc01g017600	Solyc01g017600.2	T3	T3_C	T3_L	27.6	DOWN	11.63	0.0190315	*
Solyc06g072350	Solyc06g072350.2	T3	T3_C	T3_L	23.9	DOWN	93.78	0.00782778	**
Solyc12g011010	Solyc12g011010.1	T3	T3_C	T3_L	21.11	DOWN	30.1	0.00782778	**
Solyc03g121900	Solyc03g121900.1	T3	T3_C	T3_L	14.16	DOWN	218.95	0.00782778	**
Solyc02g063000	Solyc02g063000.2	T3	T3_C	T3_L	13.04	DOWN	3.3	0.042196	*
Solyc02g070980	Solyc02g070980.1	T3	T3_C	T3_L	11.33	DOWN	3250.73	0.00782778	**
XLOC_020087	-	T3	T3_C	T3_L	10.96	DOWN	4459.55	0.00782778	**
Solyc12g006140	CAB5	T3	T3_C	T3_L	10.89	DOWN	3514.79	0.0190315	*
Solyc03g005790	Solyc03g005790.2	T3	T3_C	T3_L	9.87	DOWN	155.84	0.00782778	**
Solyc07g055950	Solyc07g055950.2	T3	T3_C	T3_L	8.48	DOWN	23.97	0.00782778	**
Solyc02g070990	Solyc02g070990.1	T3	T3_C	T3_L	8.43	DOWN	2004.72	0.00782778	**
Solyc02g071000	CAB1D	T3	T3_C	T3_L	8.42	DOWN	7585.59	0.00782778	**

Table A.6 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc02g070970	CAB1B	T3	T3_C	T3_L	8.42	DOWN	10247.16	0.042196	*
Solyc06g069730	Solyc06g069730.2	T3	T3_C	T3_L	8.36	DOWN	872.37	0.00782778	**
Solyc02g070950	CAB1B	T3	T3_C	T3_L	8.12	DOWN	6846.87	0.014053	*
Solyc10g008440	Solyc10g008440.2	T3	T3_C	T3_L	7.6	DOWN	17.04	0.00782778	**
TCONS_00081745	XLOC_032292	T3	T3_C	T3_L	7.33	DOWN	10.05	0.00782778	**
Solyc06g062370	Solyc06g062370.2	T3	T3_C	T3_L	7.21	DOWN	39.3	0.0237964	*
Solyc11g006250	Solyc11g006250.1	T3	T3_C	T3_L	6.63	DOWN	14.14	0.00782778	**
Solyc08g067530	Solyc08g067530.1	T3	T3_C	T3_L	6.25	DOWN	61.25	0.0237964	*
Solyc05g043330	Solyc05g043330.2	T3	T3_C	T3_L	6.07	DOWN	25.05	0.00782778	**
Solyc10g005400	Solyc10g005400.2	T3	T3_C	T3_L	5.93	DOWN	7.62	0.0278285	*
Solyc11g021060	ARPI	T3	T3_C	T3_L	5.87	DOWN	1055.21	0.014053	*
Solyc04g015620	Solyc04g015620.2	T3	T3_C	T3_L	5.74	DOWN	49.45	0.00782778	**
Solyc06g083470	Solyc06g083470.2	T3	T3_C	T3_L	5.71	DOWN	11.94	0.014053	*
Solyc05g005230	Solyc05g005230.2	T3	T3_C	T3_L	5.69	DOWN	135.91	0.00782778	**
Solyc06g069790	Solyc06g069790.2	T3	T3_C	T3_L	5.67	DOWN	22.29	0.014053	*
Solyc02g081980	Solyc02g081980.2	T3	T3_C	T3_L	5.48	DOWN	31.58	0.00782778	**
Solyc10g005030	Solyc10g005030.2	T3	T3_C	T3_L	5.23	DOWN	23.32	0.00782778	**
Solyc05g051580	Solyc05g051580.2	T3	T3_C	T3_L	5.05	DOWN	13.94	0.0392249	*
Solyc07g014730	Solyc07g014730.2	T3	T3_C	T3_L	4.85	DOWN	20.51	0.00782778	**
Solyc05g024260	Solyc05g024260.2	T3	T3_C	T3_L	4.85	DOWN	21.05	0.042196	*
Solyc09g008320	Solyc09g008320.2	T3	T3_C	T3_L	4.71	DOWN	48.14	0.00782778	**
Solyc04g014510	GTS1	T3	T3_C	T3_L	4.64	DOWN	12.75	0.00782778	**
Solyc05g009270	Solyc05g009270.2	T3	T3_C	T3_L	4.57	DOWN	33.76	0.00782778	**
Solyc07g006630	Solyc07g006630.2	T3	T3_C	T3_L	4.56	DOWN	108.69	0.00782778	**
Solyc06g066420	Solyc06g066420.2	T3	T3_C	T3_L	4.55	DOWN	101.1	0.00782778	**

Table A.6 continued.

Gene ID	**Gene Name**	**Time**	**Group 1**	**Group 2**	**Fold Change**	**Direction**	**Total Fpkm**	**q-value**	**Sig. Lvl**
Solyc07g049440	Solyc07g049440.2	T3	T3_C	T3_L	4.54	DOWN	8.55	0.00782778	**
Solyc01g110340	Solyc01g110340.2	T3	T3_C	T3_L	4.44	DOWN	9.17	0.00782778	**
Solyc03g006490	Solyc03g006490.2	T3	T3_C	T3_L	4.44	DOWN	87.03	0.00782778	**
Solyc09g010220	Solyc09g010220.2	T3	T3_C	T3_L	4.41	DOWN	19.81	0.00782778	**
Solyc04g015750	Solyc04g015750.2	T3	T3_C	T3_L	4.4	DOWN	286.51	0.00782778	**
Solyc06g084140	Solyc06g084140.2	T3	T3_C	T3_L	4.22	DOWN	33.24	0.00782778	**
Solyc06g069150	Solyc06g069150.1	T3	T3_C	T3_L	4.2	DOWN	35	0.014053	*
Solyc03g118310	Solyc03g118310.2	T3	T3_C	T3_L	4.12	DOWN	30.96	0.00782778	**
Solyc06g072710	Solyc06g072710.2	T3	T3_C	T3_L	4.12	DOWN	104.89	0.00782778	**
Solyc08g067330	Solyc08g067330.1	T3	T3_C	T3_L	4.09	DOWN	2417.66	0.00782778	**
Solyc06g064550	Solyc06g064550.2	T3	T3_C	T3_L	4.06	DOWN	61.93	0.014053	*
Solyc09g009420	Solyc09g009420.1	T3	T3_C	T3_L	4.02	DOWN	145.38	0.00782778	**
Solyc07g005390	Solyc07g005390.2	T3	T3_C	T3_L	4	DOWN	107.14	0.00782778	**
Solyc06g071320	Solyc06g071320.2	T3	T3_C	T3_L	3.96	DOWN	31	0.00782778	**
Solyc08g078870	Solyc08g078870.1	T3	T3_C	T3_L	3.96	DOWN	422.4	0.00782778	**
Solyc06g005750	Solyc06g005750.2	T3	T3_C	T3_L	3.92	DOWN	84.98	0.042196	*
Solyc07g007240	Solyc07g007240.2	T3	T3_C	T3_L	3.91	DOWN	88.76	0.00782778	**
Solyc11g010410	Solyc11g010410.1	T3	T3_C	T3_L	3.88	DOWN	37	0.014053	*
Solyc05g005540	GP3	T3	T3_C	T3_L	3.87	DOWN	19.21	0.00782778	**
Solyc08g061970	SPE4	T3	T3_C	T3_L	3.87	DOWN	17.79	0.0278285	*
Solyc07g063600	Solyc07g063600.2	T3	T3_C	T3_L	3.87	DOWN	3665.2	0.0358998	*
Solyc03g116730	Solyc03g116730.2	T3	T3_C	T3_L	3.86	DOWN	114.37	0.00782778	**
Solyc04g015030	Solyc04g015030.2	T3	T3_C	T3_L	3.84	DOWN	19.79	0.00782778	**
Solyc08g075490	Solyc08g075490.2	T3	T3_C	T3_L	3.79	DOWN	220.45	0.00782778	**
Solyc12g096490	Solyc12g096490.1	T3	T3_C	T3_L	3.78	DOWN	32.76	0.042196	*

Table A.6 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc01g095530	Solyc01g095530.2	T3	T3_C	T3_L	3.77	DOWN	885.87	0.00782778	**
Solyc09g075750	Solyc09g075750.1	T3	T3_C	T3_L	3.73	DOWN	74.46	0.00782778	**
Solyc07g006570	Solyc07g006570.2	T3	T3_C	T3_L	3.71	DOWN	61.21	0.00782778	**
Solyc08g076820	Solyc08g076820.2	T3	T3_C	T3_L	3.69	DOWN	31.45	0.00782778	**
Solyc01g090970	Solyc01g090970.2	T3	T3_C	T3_L	3.67	DOWN	227.28	0.00782778	**
Solyc09g010860	EXPA4	T3	T3_C	T3_L	3.62	DOWN	68.73	0.00782778	**
Solyc08g067320	Solyc08g067320.1	T3	T3_C	T3_L	3.58	DOWN	2643.64	0.00782778	**
Solyc05g056050	Solyc05g056050.2	T3	T3_C	T3_L	3.53	DOWN	2799.02	0.0454516	*
Solyc06g053260	Solyc06g053260.1	T3	T3_C	T3_L	3.49	DOWN	105.13	0.0392249	*
Solyc01g087710	Solyc01g087710.2	T3	T3_C	T3_L	3.44	DOWN	68.67	0.00782778	**
Solyc03g006880	GA20OX1	T3	T3_C	T3_L	3.43	DOWN	17.54	0.00782778	**
Solyc04g008260	Solyc04g008260.2	T3	T3_C	T3_L	3.4	DOWN	26.7	0.014053	*
Solyc12g019550	Solyc12g019550.1	T3	T3_C	T3_L	3.38	DOWN	1669.64	0.0190315	*
Solyc07g061800	Solyc07g061800.2	T3	T3_C	T3_L	3.33	DOWN	24.9	0.0454516	*
Solyc04g008040	Solyc04g008040.2	T3	T3_C	T3_L	3.32	DOWN	98.13	0.00782778	**
Solyc03g111550	Solyc03g111550.2	T3	T3_C	T3_L	3.31	DOWN	11.46	0.0392249	*
Solyc09g075360	Solyc09g075360.2	T3	T3_C	T3_L	3.28	DOWN	27.09	0.00782778	**
Solyc03g111100	Solyc03g111100.1	T3	T3_C	T3_L	3.27	DOWN	21.79	0.0278285	*
Solyc06g051940	Solyc06g051940.2	T3	T3_C	T3_L	3.26	DOWN	31.69	0.00782778	**
TCONS_00011478	Solyc01g106960.2	T3	T3_C	T3_L	3.17	DOWN	1.74	0.0358998	*
Solyc12g009200	Solyc12g009200.1	T3	T3_C	T3_L	3.16	DOWN	383.38	0.042196	*
TCONS_00048557	Solyc06g060640.1	T3	T3_C	T3_L	3.15	DOWN	142.53	0.0392249	*
Solyc01g073680	Solyc01g073680.2	T3	T3_C	T3_L	3.14	DOWN	24.26	0.0319336	*
Solyc06g007440	Solyc06g007440.2	T3	T3_C	T3_L	3.12	DOWN	43.98	0.00782778	**
Solyc09g007150	Solyc09g007150.2	T3	T3_C	T3_L	3.12	DOWN	51.49	0.0487551	*

Table A.6 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc11g056680	Solyc11g056680.1	T3	T3_C	T3_L	3.05	DOWN	155.16	0.00782778	**
Solyc09g008670	TD	T3	T3_C	T3_L	3.05	DOWN	31.51	0.0454516	*
Solyc08g006160	Solyc08g006160.2	T3	T3_C	T3_L	2.98	DOWN	205.4	0.00782778	**
Solyc06g075170	Solyc06g075170.1	T3	T3_C	T3_L	2.96	DOWN	80.29	0.0319336	*
Solyc07g045080	Solyc07g045080.2	T3	T3_C	T3_L	2.95	DOWN	65.91	0.0190315	*
Solyc07g007150	Solyc07g007150.1	T3	T3_C	T3_L	2.93	DOWN	166.6	0.00782778	**
Solyc06g069760	Solyc06g069760.2	T3	T3_C	T3_L	2.91	DOWN	74.92	0.00782778	**
Solyc04g054370	Solyc04g054370.1	T3	T3_C	T3_L	2.9	DOWN	342.94	0.00782778	**
Solyc06g073290	Solyc06g073290.1	T3	T3_C	T3_L	2.88	DOWN	480.37	0.00782778	**
Solyc06g053830	IAA7	T3	T3_C	T3_L	2.87	DOWN	45.16	0.00782778	**
TCONS_00055327	Solyc07g042390.1	T3	T3_C	T3_L	2.87	DOWN	25.95	0.0190315	*
Solyc01g086920	Solyc01g086920.2	T3	T3_C	T3_L	2.85	DOWN	209.49	0.00782778	**
TCONS_00087655	XLOC_034361	T3	T3_C	T3_L	2.83	DOWN	218.49	0.00782778	**
Solyc05g012110	Solyc05g012110.2	T3	T3_C	T3_L	2.83	DOWN	233.34	0.00782778	**
Solyc05g014000	Solyc05g014000.2	T3	T3_C	T3_L	2.81	DOWN	84.84	0.00782778	**
XLOC_005223	-	T3	T3_C	T3_L	2.8	DOWN	0.97	0.00782778	**
Solyc12g087940	Solyc12g087940.1	T3	T3_C	T3_L	2.79	DOWN	32.84	0.042196	*
Solyc03g019790	LEAGAL	T3	T3_C	T3_L	2.77	DOWN	20.96	0.014053	*
Solyc07g052950	Solyc07g052950.2	T3	T3_C	T3_L	2.73	DOWN	167.97	0.00782778	**
Solyc02g071380	Solyc02g071380.2	T3	T3_C	T3_L	2.72	DOWN	71.91	0.00782778	**
Solyc06g049050	LEEXP2	T3	T3_C	T3_L	2.72	DOWN	136.52	0.00782778	**
Solyc10g008710	Solyc10g008710.2	T3	T3_C	T3_L	2.72	DOWN	54.45	0.042196	*
Solyc07g055260	Solyc07g055260.2	T3	T3_C	T3_L	2.69	DOWN	61.84	0.00782778	**
Solyc01g007810	Solyc01g007810.1	T3	T3_C	T3_L	2.66	DOWN	36.97	0.0358998	*
Solyc05g053760	Solyc05g053760.2	T3	T3_C	T3_L	2.65	DOWN	86.08	0.00782778	**

Table A.6 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc05g056300	Solyc05g056300.2	T3	T3_C	T3_L	2.65	DOWN	497.32	0.00782778	**
Solyc01g091320	Solyc01g091320.2	T3	T3_C	T3_L	2.64	DOWN	72.7	0.00782778	**
Solyc04g071960	Solyc04g071960.2	T3	T3_C	T3_L	2.63	DOWN	75.04	0.00782778	**
Solyc02g077330	Solyc02g077330.2	T3	T3_C	T3_L	2.62	DOWN	26.78	0.00782778	**
Solyc01g099020	CGT	T3	T3_C	T3_L	2.61	DOWN	115.3	0.0278285	*
Solyc07g043130	Solyc07g043130.2	T3	T3_C	T3_L	2.57	DOWN	188.57	0.00782778	**
Solyc07g054210	Solyc07g054210.2	T3	T3_C	T3_L	2.57	DOWN	807.52	0.0487551	*
TCONS_00033897	Solyc04g007500.1	T3	T3_C	T3_L	2.56	DOWN	65.34	0.00782778	**
Solyc05g054320	Solyc05g054320.2	T3	T3_C	T3_L	2.55	DOWN	41.95	0.00782778	**
Solyc03g043740	Solyc03g043740.2	T3	T3_C	T3_L	2.52	DOWN	49.05	0.042196	*
Solyc11g010960	Solyc11g010960.1	T3	T3_C	T3_L	2.51	DOWN	75.93	0.014053	*
Solyc01g009080	Solyc01g009080.2	T3	T3_C	T3_L	2.45	DOWN	110.97	0.00782778	**
Solyc11g072110	Solyc11g072110.1	T3	T3_C	T3_L	2.45	DOWN	43.34	0.014053	*
Solyc02g072540	Solyc02g072540.2	T3	T3_C	T3_L	2.43	DOWN	20.86	0.0319336	*
TCONS_00036271	XLOC_014347	T3	T3_C	T3_L	2.42	DOWN	184.3	0.0190315	*
Solyc03g119860	Solyc03g119860.2	T3	T3_C	T3_L	2.4	DOWN	192.31	0.0319336	*
Solyc03g097380	Solyc03g097380.2	T3	T3_C	T3_L	2.37	DOWN	115.48	0.00782778	**
Solyc05g052030	ERF4	T3	T3_C	T3_L	2.36	DOWN	363.11	0.00782778	**
Solyc12g044330	Solyc12g044330.1	T3	T3_C	T3_L	2.35	DOWN	213.07	0.0190315	*
Solyc07g007260	Solyc07g007260.2	T3	T3_C	T3_L	2.33	DOWN	309.24	0.0319336	*
Solyc01g111570	Solyc01g111570.2	T3	T3_C	T3_L	2.32	DOWN	25.22	0.0278285	*
Solyc10g009150	Solyc10g009150.2	T3	T3_C	T3_L	2.31	DOWN	161.52	0.0358998	*
Solyc09g014350	Solyc09g014350.2	T3	T3_C	T3_L	2.31	DOWN	19.68	0.0454516	*
Solyc05g055400	Solyc05g055400.2	T3	T3_C	T3_L	2.3	DOWN	43.31	0.014053	*
Solyc01g112060	Solyc01g112060.2	T3	T3_C	T3_L	2.29	DOWN	186.3	0.0278285	*

Table A.6 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc06g053840	IAA1	T3	T3_C	T3_L	2.29	DOWN	109.55	0.0319336	*
Solyc12g056980	Solyc12g056980.1	T3	T3_C	T3_L	2.28	DOWN	60.87	0.042196	*
Solyc08g079280	Solyc08g079280.2	T3	T3_C	T3_L	2.26	DOWN	141.66	0.0237964	*
Solyc04g081300	Solyc04g081300.2	T3	T3_C	T3_L	2.24	DOWN	26.38	0.0487551	*
Solyc03g110860	Solyc03g110860.2	T3	T3_C	T3_L	2.22	DOWN	165.47	0.042196	*
Solyc01g087040	Solyc01g087040.2	T3	T3_C	T3_L	2.2	DOWN	282.68	0.0487551	*
Solyc01g102610	Solyc01g102610.2	T3	T3_C	T3_L	2.19	DOWN	39.73	0.0454516	*
Solyc02g080210	Solyc02g080210.2	T3	T3_C	T3_L	4.55	DOWN	181.7	0.0190315	*
Solyc03g025410	Solyc03g025410.2	T3	T3_C	T3_L	2.19	DOWN	186.2	0.0454516	*
Solyc04g078900	CYP707A1	T3	T3_C	T3_L	2.18	DOWN	44.44	0.0278285	*
TCONS_00054779	Solyc07g021530.2	T3	T3_C	T3_L	2.17	DOWN	178.37	0.0358998	*
TCONS_00042840	XLOC_017029	T3	T3_C	T3_L	2.16	DOWN	75.29	0.042196	*
XLOC_005221	-	T3	T3_C	T3_L	1.27	DOWN	2.84	0.0190315	*

Time represents time point as indicated in the method. Group represents the specified group of plants according to their insect treatment. Direction represents the up- or down-regulation of the expressed gene. Total FPKM (Fragments Per Kilobase of transcript per Million) mapped reads represent the sum of all expression of genes among the compared groups. q-value indicates the adjusted p-value after the Benjamini-Hochberg correction for multiple comparison. * q-value < 0.05. ** q-value < 0.01.

Table A.7 List of significantly differentially expressed genes (DEGs) in P vs L comparison

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
XLOC_022709	-	T1	T1_P	T1_L	25.88	UP	215.26	0.013452	*
TCONS_00056275	Solyc07g056640.1	T1	T1_P	T1_L	17.72	UP	142.44	0.0403049	*
Solyc01g097240	Solyc01g097240.2	T1	T1_P	T1_L	5.65	UP	37.34	0.0471539	*
Solyc10g005400	Solyc10g005400.2	T1	T1_P	T1_L	4.81	UP	84.19	0.013452	*
Solyc03g078490	Solyc03g078490.2	T1	T1_P	T1_L	4.6	UP	15.88	0.0471539	*
Solyc06g049050	LEEXP2	T1	T1_P	T1_L	2.99	UP	246.11	0.0403049	*
Solyc07g053640	Solyc07g053640.1	T1	T1_P	T1_L	2.83	UP	77.32	0.023556	*
Solyc07g007250	Solyc07g007250.2	T1	T1_P	T1_L	76.25	DOWN	1417.25	0.013452	*
Solyc03g026280	CBF1	T1	T1_P	T1_L	45.87	DOWN	73.48	0.013452	*
Solyc03g093110	Solyc03g093110.2	T1	T1_P	T1_L	40.97	DOWN	26.54	0.013452	*
Solyc07g056000	TXET-B2	T1	T1_P	T1_L	38.77	DOWN	131.95	0.013452	*
Solyc01g091590	Solyc01g091590.2	T1	T1_P	T1_L	29	DOWN	97.86	0.013452	*
Solyc12g009000	Solyc12g009000.1	T1	T1_P	T1_L	24.74	DOWN	19.98	0.013452	*
Solyc09g008670	TD	T1	T1_P	T1_L	24.55	DOWN	73.25	0.013452	*
Solyc02g091180	Solyc02g091180.1	T1	T1_P	T1_L	24.29	DOWN	63.48	0.0316739	*
Solyc09g089510	Solyc09g089510.2	T1	T1_P	T1_L	24.12	DOWN	1867.68	0.013452	*
Solyc08g083050	Solyc08g083050.1	T1	T1_P	T1_L	21.36	DOWN	89.47	0.013452	*
Solyc07g040960	SLSRG2	T1	T1_P	T1_L	20.53	DOWN	266.86	0.013452	*
Solyc03g082370	Solyc03g082370.1	T1	T1_P	T1_L	19.68	DOWN	465.02	0.013452	*
Solyc10g006700	Solyc10g006700.1	T1	T1_P	T1_L	15.94	DOWN	510.62	0.013452	*
Solyc12g017240	TXET-B1	T1	T1_P	T1_L	15.64	DOWN	129.14	0.023556	*
Solyc01g091170	ARG2	T1	T1_P	T1_L	14.96	DOWN	53.33	0.013452	*
Solyc03g083480	Solyc03g083480.2	T1	T1_P	T1_L	14.7	DOWN	41.22	0.013452	*
Solyc08g078190	Solyc08g078190.1	T1	T1_P	T1_L	13.11	DOWN	63.2	0.013452	*
Solyc08g077020	Solyc08g077020.1	T1	T1_P	T1_L	12.63	DOWN	125.32	0.013452	*
Solyc04g077980	CZFP1	T1	T1_P	T1_L	12.58	DOWN	200.93	0.013452	*

Table A.7 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc10g084880	Solyc10g084880.2	T1	T1_P	T1_L	12.29	DOWN	20.18	0.013452	*
Solyc01g087580	Solyc01g087580.2	T1	T1_P	T1_L	12.04	DOWN	119.01	0.013452	*
Solyc06g074030	Solyc06g074030.1	T1	T1_P	T1_L	10.42	DOWN	312.25	0.013452	*
Solyc03g093550	Solyc03g093550.1	T1	T1_P	T1_L	9.71	DOWN	234.87	0.0471539	*
Solyc06g007190	Solyc06g007190.2	T1	T1_P	T1_L	9.44	DOWN	10.86	0.0316739	*
Solyc07g006560	Solyc07g006560.2	T1	T1_P	T1_L	9.12	DOWN	35.75	0.0316739	*
Solyc06g060690	Solyc06g060690.2	T1	T1_P	T1_L	8.64	DOWN	29.15	0.013452	*
TCONS_00061631	Solyc08g062680.1	T1	T1_P	T1_L	8.55	DOWN	64.23	0.023556	*
Solyc12g011030	Solyc12g011030.1	T1	T1_P	T1_L	8.48	DOWN	41.59	0.013452	*
Solyc01g099370	Solyc01g099370.2	T1	T1_P	T1_L	8.29	DOWN	104.28	0.013452	*
Solyc08g068770	Solyc08g068770.1	T1	T1_P	T1_L	8.12	DOWN	131.6	0.013452	*
Solyc01g066430	Solyc01g066430.2	T1	T1_P	T1_L	7.66	DOWN	136.11	0.013452	*
Solyc01g112000	EXLA1	T1	T1_P	T1_L	7.64	DOWN	243.13	0.013452	*
Solyc03g093610	ERF1	T1	T1_P	T1_L	7.54	DOWN	44.74	0.013452	*
Solyc12g005340	Solyc12g005340.1	T1	T1_P	T1_L	7.54	DOWN	46.91	0.013452	*
Solyc06g007180	AS1	T1	T1_P	T1_L	7.2	DOWN	11.08	0.013452	*
Solyc03g118810	Solyc03g118810.1	T1	T1_P	T1_L	7.18	DOWN	431.06	0.0471539	*
TCONS_00024947	Solyc03g118810.1	T1	T1_P	T1_L	7.16	DOWN	319.67	0.013452	*
Solyc03g097170	Solyc03g097170.2	T1	T1_P	T1_L	7.11	DOWN	39.59	0.023556	*
Solyc06g051680	Solyc06g051680.1	T1	T1_P	T1_L	7.11	DOWN	285.03	0.013452	*
Solyc08g008370	Solyc08g008370.2	T1	T1_P	T1_L	7.11	DOWN	68.62	0.013452	*
Solyc09g082870	Solyc09g082870.1	T1	T1_P	T1_L	6.98	DOWN	4.45	0.023556	*
Solyc08g079700	SAP6	T1	T1_P	T1_L	6.95	DOWN	368.08	0.013452	*
Solyc06g068460	Solyc06g068460.2	T1	T1_P	T1_L	6.86	DOWN	214.66	0.013452	*
Solyc10g009550	Solyc10g009550.2	T1	T1_P	T1_L	6.82	DOWN	14.46	0.013452	*
Solyc01g100010	Solyc01g100010.2	T1	T1_P	T1_L	6.75	DOWN	18.34	0.0316739	*

Table A.7 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc01g080870	Solyc01g080870.2	T1	T1_P	T1_L	6.74	DOWN	9.89	0.023556	*
Solyc01g100200	GRAS4	T1	T1_P	T1_L	6.64	DOWN	48.03	0.013452	*
Solyc09g014990	Solyc09g014990.2	T1	T1_P	T1_L	6.61	DOWN	26.87	0.013452	*
Solyc08g068600	Solyc08g068600.2	T1	T1_P	T1_L	6.53	DOWN	18.91	0.013452	*
Solyc11g068710	Solyc11g068710.1	T1	T1_P	T1_L	6.48	DOWN	103.75	0.013452	*
Solyc12g057150	Solyc12g057150.1	T1	T1_P	T1_L	6.46	DOWN	133.4	0.023556	*
TCONS_00070312	ERF3	T1	T1_P	T1_L	6.43	DOWN	81.91	0.013452	*
Solyc04g005040	Solyc04g005040.1	T1	T1_P	T1_L	6.33	DOWN	15.22	0.0403049	*
Solyc07g053740	Solyc07g053740.1	T1	T1_P	T1_L	6.33	DOWN	529.06	0.013452	*
Solyc01g065530	Solyc01g065530.2	T1	T1_P	T1_L	6.32	DOWN	54.73	0.013452	*
Solyc01g111980	Solyc01g111980.2	T1	T1_P	T1_L	6.24	DOWN	148.52	0.013452	*
Solyc02g064680	Solyc02g064680.2	T1	T1_P	T1_L	6.04	DOWN	59.14	0.013452	*
Solyc00g206460	Solyc00g206460.1	T1	T1_P	T1_L	6	DOWN	106.58	0.013452	*
Solyc05g052040	DDTFR10/A	T1	T1_P	T1_L	5.94	DOWN	211.23	0.013452	*
Solyc03g006360	Solyc03g006360.2	T1	T1_P	T1_L	5.78	DOWN	122.07	0.013452	*
Solyc06g009140	Solyc06g009140.2	T1	T1_P	T1_L	5.78	DOWN	298.1	0.013452	*
TCONS_00070216	Solyc10g008400.1	T1	T1_P	T1_L	5.75	DOWN	85.11	0.013452	*
Solyc01g079600	Solyc01g079600.2	T1	T1_P	T1_L	5.74	DOWN	21.15	0.023556	*
Solyc03g083470	Solyc03g083470.2	T1	T1_P	T1_L	5.72	DOWN	15.61	0.023556	*
TCONS_00016221	Solyc02g091500.1	T1	T1_P	T1_L	5.72	DOWN	27.2	0.013452	*
Solyc10g081040	Solyc10g081040.1	T1	T1_P	T1_L	5.66	DOWN	218.49	0.013452	*
Solyc02g067050	Solyc02g067050.2	T1	T1_P	T1_L	5.46	DOWN	110.3	0.013452	*
Solyc03g112340	Solyc03g112340.1	T1	T1_P	T1_L	5.37	DOWN	35.76	0.013452	*
Solyc01g102840	Solyc01g102840.2	T1	T1_P	T1_L	5.34	DOWN	17.46	0.013452	*
Solyc12g006260	Solyc12g006260.1	T1	T1_P	T1_L	5.34	DOWN	223.62	0.013452	*
Solyc07g006570	Solyc07g006570.2	T1	T1_P	T1_L	5.32	DOWN	47.84	0.013452	*

Table A.7 continued.

Gene ID	**Gene Name**	**Time**	**Group 1**	**Group 2**	**Fold Change**	**Direction**	**Total Fpkm**	**q-value**	**Sig. Lvl**
Solyc10g079420	Solyc10g079420.1	T1	T1_P	T1_L	5.25	DOWN	511.34	0.013452	*
TCONS_00014057	Solyc02g073580.1	T1	T1_P	T1_L	5.22	DOWN	21.69	0.013452	*
Solyc03g114100	Solyc03g114100.1	T1	T1_P	T1_L	5.19	DOWN	283.41	0.013452	*
Solyc04g025650	Solyc04g025650.2	T1	T1_P	T1_L	5.19	DOWN	88.84	0.013452	*
Solyc02g093230	Solyc02g093230.2	T1	T1_P	T1_L	5.13	DOWN	28.82	0.013452	*
Solyc11g020230	Solyc11g020230.1	T1	T1_P	T1_L	5.12	DOWN	18.49	0.013452	*
TCONS_00073043	Solyc10g006130.1	T1	T1_P	T1_L	5.1	DOWN	106.32	0.013452	*
Solyc03g119250	Solyc03g119250.2	T1	T1_P	T1_L	5.02	DOWN	45.53	0.0316739	*
Solyc04g077620	Solyc04g077620.1	T1	T1_P	T1_L	4.98	DOWN	119.99	0.0471539	*
Solyc11g010500	Solyc11g010500.1	T1	T1_P	T1_L	4.89	DOWN	179.5	0.013452	*
Solyc01g095150	LEMMI9	T1	T1_P	T1_L	4.84	DOWN	88.31	0.013452	*
Solyc07g007130	Solyc07g007130.1	T1	T1_P	T1_L	4.82	DOWN	254.31	0.013452	*
Solyc03g098730	Solyc03g098730.1	T1	T1_P	T1_L	4.8	DOWN	92.41	0.013452	*
Solyc05g051400	Solyc05g051400.2	T1	T1_P	T1_L	4.79	DOWN	48.13	0.023556	*
Solyc05g005260	Solyc05g005260.1	T1	T1_P	T1_L	4.76	DOWN	184.05	0.013452	*
Solyc03g097050	Solyc03g097050.2	T1	T1_P	T1_L	4.62	DOWN	11.57	0.023556	*
Solyc04g018110	Solyc04g018110.1	T1	T1_P	T1_L	4.58	DOWN	345.63	0.013452	*
Solyc07g045100	Solyc07g045100.1	T1	T1_P	T1_L	4.53	DOWN	19.27	0.013452	*
Solyc06g005650	Solyc06g005650.2	T1	T1_P	T1_L	4.51	DOWN	87.86	0.013452	*
Solyc10g009340	Solyc10g009340.1	T1	T1_P	T1_L	4.35	DOWN	296.09	0.013452	*
Solyc04g005480	Solyc04g005480.1	T1	T1_P	T1_L	4.33	DOWN	139.02	0.013452	*
Solyc08g008100	LE-ACS6	T1	T1_P	T1_L	4.33	DOWN	42.61	0.013452	*
Solyc11g010250	Solyc11g010250.1	T1	T1_P	T1_L	4.29	DOWN	134	0.0403049	*
Solyc01g057770	Solyc01g057770.2	T1	T1_P	T1_L	4.27	DOWN	65.51	0.023556	*
Solyc05g009790	Solyc05g009790.1	T1	T1_P	T1_L	4.27	DOWN	222.09	0.013452	*
Solyc08g077480	Solyc08g077480.2	T1	T1_P	T1_L	4.21	DOWN	94.29	0.013452	*

Table A.7 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc01g079940	Solyc01g079940.2	T1	T1_P	T1_L	4.17	DOWN	35.56	0.013452	*
Solyc08g078670	Solyc08g078670.2	T1	T1_P	T1_L	3.98	DOWN	51.43	0.013452	*
Solyc09g015770	Solyc09g015770.2	T1	T1_P	T1_L	3.95	DOWN	97.56	0.0471539	*
Solyc11g010390	Solyc11g010390.1	T1	T1_P	T1_L	3.92	DOWN	171.93	0.023556	*
Solyc06g059870	Solyc06g059870.1	T1	T1_P	T1_L	3.91	DOWN	2943.06	0.013452	*
Solyc06g036310	Solyc06g036310.2	T1	T1_P	T1_L	3.88	DOWN	171.31	0.013452	*
Solyc10g074740	Solyc10g074740.1	T1	T1_P	T1_L	3.87	DOWN	210.81	0.013452	*
Solyc01g095630	WRKY3	T1	T1_P	T1_L	3.82	DOWN	125.06	0.013452	*
Solyc05g051750	Solyc05g051750.2	T1	T1_P	T1_L	3.77	DOWN	224.84	0.0471539	*
Solyc06g060680	Solyc06g060680.1	T1	T1_P	T1_L	3.77	DOWN	57.58	0.013452	*
Solyc10g080370	Solyc10g080370.1	T1	T1_P	T1_L	3.7	DOWN	8569.21	0.013452	*
Solyc03g007870	Solyc03g007870.2	T1	T1_P	T1_L	3.68	DOWN	142.33	0.013452	*
Solyc02g094400	Solyc02g094400.2	T1	T1_P	T1_L	3.65	DOWN	25.8	0.023556	*
Solyc06g061230	Solyc06g061230.2	T1	T1_P	T1_L	3.65	DOWN	115.14	0.013452	*
Solyc04g071030	Solyc04g071030.1	T1	T1_P	T1_L	3.59	DOWN	28.71	0.0316739	*
Solyc06g066370	Solyc06g066370.2	T1	T1_P	T1_L	3.55	DOWN	145.08	0.0316739	*
Solyc12g010540	Solyc12g010540.1	T1	T1_P	T1_L	3.52	DOWN	94.66	0.013452	*
Solyc04g007000	Solyc04g007000.1	T1	T1_P	T1_L	3.42	DOWN	65.2	0.013452	*
Solyc10g077130	Solyc10g077130.1	T1	T1_P	T1_L	3.31	DOWN	128.28	0.013452	*
Solyc07g042170	Solyc07g042170.2	T1	T1_P	T1_L	3.18	DOWN	84.03	0.023556	*
Solyc01g079580	Solyc01g079580.2	T1	T1_P	T1_L	3.15	DOWN	69.44	0.023556	*
Solyc03g005570	Solyc03g005570.2	T1	T1_P	T1_L	3.13	DOWN	45.29	0.0316739	*
TCONS_00036424	Solyc04g078420.1	T1	T1_P	T1_L	3.13	DOWN	76.44	0.0316739	*
Solyc06g067910	Solyc06g067910.2	T1	T1_P	T1_L	3.1	DOWN	44.78	0.013452	*
Solyc03g121660	Solyc03g121660.2	T1	T1_P	T1_L	3.05	DOWN	33.26	0.013452	*
Solyc08g081230	Solyc08g081230.1	T1	T1_P	T1_L	3.05	DOWN	36.03	0.0471539	*

Table A.7 continued.

Gene ID	**Gene Name**	**Time**	**Group 1**	**Group 2**	**Fold Change**	**Direction**	**Total Fpkm**	**q-value**	**Sig. Lvl**
Solyc01g086960	Solyc01g086960.2	T1	T1_P	T1_L	3.01	DOWN	423.08	0.0316739	*
Solyc06g048820	Solyc06g048820.1	T1	T1_P	T1_L	2.95	DOWN	514.75	0.023556	*
Solyc09g015040	Solyc09g015040.1	T1	T1_P	T1_L	2.85	DOWN	64.17	0.013452	*
TCONS_00082183	Solyc11g051180.1	T1	T1_P	T1_L	2.8	DOWN	608440	0.013452	*
Solyc05g006030	Solyc05g006030.2	T1	T1_P	T1_L	2.72	DOWN	148.74	0.013452	*
Solyc06g075610	Solyc06g075610.1	T1	T1_P	T1_L	2.7	DOWN	41.26	0.0471539	*
Solyc04g071890	Solyc04g071890.2	T1	T1_P	T1_L	2.65	DOWN	88.37	0.023556	*
TCONS_00023686	LEMKK4	T1	T1_P	T1_L	2.64	DOWN	62.82	0.0471539	*
Solyc08g006320	Solyc08g006320.2	T1	T1_P	T1_L	2.59	DOWN	149.87	0.023556	*
Solyc05g007950	RNALE	T2	T2_P	T2_L	53.51	UP	31.19	0.0220602	*
Solyc09g007010	Solyc09g007010.1	T2	T2_P	T2_L	45.86	UP	2197.18	0.0130452	*
Solyc09g089540	Solyc09g089540.2	T2	T2_P	T2_L	42.95	UP	141.73	0.0130452	*
Solyc06g007180	AS1	T2	T2_P	T2_L	41.61	UP	75.57	0.0130452	*
Solyc07g054720	Solyc07g054720.1	T2	T2_P	T2_L	30.54	UP	567.57	0.0220602	*
Solyc09g097760	Solyc09g097760.2	T2	T2_P	T2_L	28.98	UP	82.6	0.0130452	*
Solyc00g187050	Solyc00g187050.2	T2	T2_P	T2_L	28.69	UP	9.01	0.0304876	*
Solyc02g078650	Solyc02g078650.2	T2	T2_P	T2_L	23.67	UP	5.23	0.0130452	*
Solyc08g029000	Solyc08g029000.2	T2	T2_P	T2_L	23.67	UP	5.43	0.0130452	*
Solyc01g059980	Solyc01g059980.2	T2	T2_P	T2_L	19.19	UP	23.53	0.0378174	*
Solyc03g006210	Solyc03g006210.1	T2	T2_P	T2_L	19.03	UP	12.13	0.0130452	*
Solyc08g021820	Solyc08g021820.2	T2	T2_P	T2_L	15.17	UP	55.49	0.0130452	*
Solyc02g070110	Solyc02g070110.1	T2	T2_P	T2_L	15.05	UP	11.43	0.0130452	*
Solyc02g093580	Solyc02g093580.2	T2	T2_P	T2_L	13.05	UP	14.04	0.0130452	*
Solyc08g080670	Solyc08g080670.1	T2	T2_P	T2_L	13	UP	102.3	0.0130452	*
Solyc05g052680	Solyc05g052680.1	T2	T2_P	T2_L	12.81	UP	10.13	0.0220602	*
Solyc06g062460	Solyc06g062460.2	T2	T2_P	T2_L	12.35	UP	54.21	0.0130452	*

Table A.7 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc10g055820	Solyc10g055820.1	T2	T2_P	T2_L	12.04	UP	20.08	0.0130452	*
Solyc02g092580	Solyc02g092580.2	T2	T2_P	T2_L	11.95	UP	32.81	0.0130452	*
Solyc04g007000	Solyc04g007000.1	T2	T2_P	T2_L	11.65	UP	66.67	0.0130452	*
Solyc01g060020	Solyc01g060020.2	T2	T2_P	T2_L	11.29	UP	76.98	0.0130452	*
Solyc02g091990	ACS3	T2	T2_P	T2_L	11.21	UP	7.35	0.0130452	*
Solyc01g110180	Solyc01g110180.2	T2	T2_P	T2_L	10.89	UP	9.33	0.0378174	*
Solyc02g062390	Solyc02g062390.2	T2	T2_P	T2_L	10.32	UP	22.59	0.0130452	*
Solyc04g078340	Solyc04g078340.2	T2	T2_P	T2_L	9.81	UP	8.5	0.0130452	*
Solyc01g097240	Solyc01g097240.2	T2	T2_P	T2_L	9.79	UP	354.82	0.0130452	*
Solyc08g077900	Solyc08g077900.2	T2	T2_P	T2_L	9.6	UP	22.43	0.0130452	*
Solyc03g114890	Solyc03g114890.2	T2	T2_P	T2_L	9.43	UP	8.1	0.0220602	*
Solyc08g077330	Solyc08g077330.2	T2	T2_P	T2_L	9.16	UP	146.02	0.0130452	*
Solyc03g025670	Solyc03g025670.2	T2	T2_P	T2_L	8.49	UP	460.95	0.0130452	*
Solyc06g011350	Solyc06g011350.2	T2	T2_P	T2_L	8.12	UP	21.95	0.0130452	*
Solyc03g078490	Solyc03g078490.2	T2	T2_P	T2_L	7.95	UP	67.05	0.0130452	*
Solyc01g080010	ACI25	T2	T2_P	T2_L	7.82	UP	39.88	0.0130452	*
Solyc10g017960	Solyc10g017960.1	T2	T2_P	T2_L	7.61	UP	15.09	0.0130452	*
Solyc03g025380	Solyc03g025380.2	T2	T2_P	T2_L	7.57	UP	9.91	0.0130452	*
Solyc03g098740	Solyc03g098740.1	T2	T2_P	T2_L	7.47	UP	80.64	0.0130452	*
Solyc12g049030	Solyc12g049030.1	T2	T2_P	T2_L	7.32	UP	9.34	0.0378174	*
Solyc09g090970	Solyc09g090970.2	T2	T2_P	T2_L	7.21	UP	26.24	0.0378174	*
Solyc08g079900	Solyc08g079900.1	T2	T2_P	T2_L	6.92	UP	28.79	0.0130452	*
Solyc10g083690	Solyc10g083690.2	T2	T2_P	T2_L	6.79	UP	10.86	0.0130452	*
Solyc02g078150	Solyc02g078150.2	T2	T2_P	T2_L	6.65	UP	32.21	0.0130452	*
Solyc05g052670	Solyc05g052670.1	T2	T2_P	T2_L	6.53	UP	13.54	0.0130452	*
Solyc10g079860	TOMQ`B	T2	T2_P	T2_L	6.51	UP	119.86	0.0130452	*

Table A.7 continued.

Gene ID	**Gene Name**	**Time**	**Group 1**	**Group 2**	**Fold Change**	**Direction**	**Total Fpkm**	**q-value**	**Sig. Lvl**
Solyc09g090980	Solyc09g090980.2	T2	T2_P	T2_L	6.46	UP	523.51	0.0130452	*
Solyc03g020010	Solyc03g020010.1	T2	T2_P	T2_L	6.41	UP	48.09	0.0130452	*
Solyc09g091000	Solyc09g091000.2	T2	T2_P	T2_L	6.4	UP	68.76	0.0130452	*
Solyc07g005100	Solyc07g005100.2	T2	T2_P	T2_L	6.32	UP	47.9	0.0130452	*
Solyc08g080660	PR-5	T2	T2_P	T2_L	6.15	UP	39.33	0.0130452	*
Solyc10g083290	WIV-1	T2	T2_P	T2_L	5.83	UP	13.35	0.0130452	*
Solyc05g041540	Solyc05g041540.2	T2	T2_P	T2_L	5.77	UP	9.68	0.0130452	*
Solyc08g007460	Solyc08g007460.2	T2	T2_P	T2_L	5.6	UP	103.37	0.0130452	*
Solyc08g068730	THT1-3	T2	T2_P	T2_L	5.43	UP	73.56	0.0130452	*
Solyc02g077590	Solyc02g077590.1	T2	T2_P	T2_L	5.42	UP	93.42	0.0130452	*
Solyc04g005610	Solyc04g005610.2	T2	T2_P	T2_L	5.2	UP	20.74	0.0130452	*
Solyc12g045020	Solyc12g045020.1	T2	T2_P	T2_L	5.12	UP	9.18	0.0304876	*
Solyc03g006360	Solyc03g006360.2	T2	T2_P	T2_L	4.82	UP	236.85	0.0130452	*
Solyc03g044790	Solyc03g044790.2	T2	T2_P	T2_L	4.67	UP	31.79	0.0130452	*
Solyc06g060830	Solyc06g060830.2	T2	T2_P	T2_L	4.66	UP	50.54	0.0130452	*
Solyc08g062180	Solyc08g062180.1	T2	T2_P	T2_L	4.36	UP	22.26	0.0130452	*
Solyc03g006700	Solyc03g006700.2	T2	T2_P	T2_L	4.34	UP	17.69	0.0220602	*
Solyc01g091170	ARG2	T2	T2_P	T2_L	4.1	UP	66.28	0.0130452	*
Solyc09g092520	BR1	T2	T2_P	T2_L	4.01	UP	59.84	0.0130452	*
Solyc07g006370	Solyc07g006370.1	T2	T2_P	T2_L	3.9	UP	14.55	0.0130452	*
Solyc04g076220	Solyc04g076220.2	T2	T2_P	T2_L	3.42	UP	29.79	0.0130452	*
Solyc02g082900	Solyc02g082900.2	T2	T2_P	T2_L	3.38	UP	43.78	0.0130452	*
Solyc01g008620	Solyc01g008620.2	T2	T2_P	T2_L	3.36	UP	43.03	0.0130452	*
Solyc09g097960	Solyc09g097960.2	T2	T2_P	T2_L	3.35	UP	55.41	0.0130452	*
Solyc04g040180	Solyc04g040180.2	T2	T2_P	T2_L	3.31	UP	46.78	0.0130452	*
Solyc05g007770	Solyc05g007770.2	T2	T2_P	T2_L	3.27	UP	27.94	0.0304876	*

Table A.7 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
TCONS_00032262	Solyc04g071110.1	T2	T2_P	T2_L	3.19	UP	168.63	0.0447756	*
Solyc12g042480	Solyc12g042480.1	T2	T2_P	T2_L	3.12	UP	23.83	0.0130452	*
Solyc09g098510	Solyc09g098510.2	T2	T2_P	T2_L	3.11	UP	93.15	0.0130452	*
Solyc07g056200	Solyc07g056200.2	T2	T2_P	T2_L	2.89	UP	77.92	0.0130452	*
Solyc05g050130	Solyc05g050130.2	T2	T2_P	T2_L	2.87	UP	233.39	0.0304876	*
Solyc06g068500	Solyc06g068500.2	T2	T2_P	T2_L	2.83	UP	283.06	0.0130452	*
Solyc08g078670	Solyc08g078670.2	T2	T2_P	T2_L	2.75	UP	56.24	0.0130452	*
Solyc04g077860	Solyc04g077860.2	T2	T2_P	T2_L	2.6	UP	101.53	0.0378174	*
Solyc11g020670	TCP12	T2	T2_P	T2_L	2.42	UP	152.68	0.0304876	*
Solyc11g071740	Solyc11g071740.1	T2	T2_P	T2_L	23.59	DOWN	22.57	0.0220602	*
Solyc01g087590	Solyc01g087590.2	T2	T2_P	T2_L	15.74	DOWN	6.81	0.0220602	*
Solyc01g095140	ER5	T2	T2_P	T2_L	11.25	DOWN	76.89	0.0130452	*
Solyc03g025710	Solyc03g025710.2	T2	T2_P	T2_L	10.33	DOWN	17.32	0.0447756	*
Solyc02g070980	Solyc02g070980.1	T2	T2_P	T2_L	8.61	DOWN	3511.91	0.0220602	*
Solyc02g070990	Solyc02g070990.1	T2	T2_P	T2_L	8.36	DOWN	1804.7	0.0130452	*
Solyc06g069730	Solyc06g069730.2	T2	T2_P	T2_L	7.52	DOWN	891.75	0.0130452	*
Solyc03g120990	Solyc03g120990.2	T2	T2_P	T2_L	7.36	DOWN	43.84	0.0130452	*
TCONS_00087655	XLOC_034361	T2	T2_P	T2_L	7.26	DOWN	228.98	0.0130452	*
Solyc02g063000	Solyc02g063000.2	T2	T2_P	T2_L	6.63	DOWN	7.87	0.0304876	*
Solyc06g007190	Solyc06g007190.2	T2	T2_P	T2_L	5.96	DOWN	9.71	0.0130452	*
Solyc02g080210	Solyc02g080210.2	T2	T2_P	T2_L	5.94	DOWN	118.9	0.0130452	*
Solyc03g005790	Solyc03g005790.2	T2	T2_P	T2_L	5.41	DOWN	224.95	0.0130452	*
Solyc10g009150	Solyc10g009150.2	T2	T2_P	T2_L	5.07	DOWN	190.69	0.0130452	*
Solyc07g042520	Solyc07g042520.2	T2	T2_P	T2_L	4.71	DOWN	6.19	0.0220602	*
Solyc02g081980	Solyc02g081980.2	T2	T2_P	T2_L	4.54	DOWN	28	0.0304876	*
Solyc06g076020	HSC70.1	T2	T2_P	T2_L	4.53	DOWN	31.82	0.0130452	*

Table A.7 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc11g018800	Solyc11g018800.1	T2	T2_P	T2_L	4.48	DOWN	14.69	0.0447756	*
Solyc10g078580	Solyc10g078580.1	T2	T2_P	T2_L	4.42	DOWN	2748.99	0.0378174	*
Solyc03g116730	Solyc03g116730.2	T2	T2_P	T2_L	4.4	DOWN	147.14	0.0130452	*
XLOC_005181	-	T2	T2_P	T2_L	4.33	DOWN	2.33	0.0304876	*
Solyc06g060340	PSBS	T2	T2_P	T2_L	4.26	DOWN	757.66	0.0220602	*
Solyc01g073640	YFE37	T2	T2_P	T2_L	4.23	DOWN	1184.09	0.0130452	*
Solyc09g008320	Solyc09g008320.2	T2	T2_P	T2_L	4.09	DOWN	102.8	0.0130452	*
TCONS_00045527	Solyc06g066800.1	T2	T2_P	T2_L	4.05	DOWN	26.86	0.0220602	*
Solyc01g087710	Solyc01g087710.2	T2	T2_P	T2_L	4.03	DOWN	105.33	0.0130452	*
XLOC_025212	-	T2	T2_P	T2_L	4.03	DOWN	167.78	0.0130452	*
Solyc05g043330	Solyc05g043330.2	T2	T2_P	T2_L	3.88	DOWN	26.72	0.0130452	*
Solyc11g010410	Solyc11g010410.1	T2	T2_P	T2_L	3.62	DOWN	39.29	0.0130452	*
XLOC_020108	-	T2	T2_P	T2_L	3.62	DOWN	119.76	0.0130452	*
Solyc12g009200	Solyc12g009200.1	T2	T2_P	T2_L	3.54	DOWN	375.37	0.0447756	*
Solyc06g068950	Solyc06g068950.2	T2	T2_P	T2_L	3.49	DOWN	41.87	0.0130452	*
Solyc03g007030	Solyc03g007030.2	T2	T2_P	T2_L	3.44	DOWN	228.84	0.0220602	*
Solyc01g009080	Solyc01g009080.2	T2	T2_P	T2_L	3.33	DOWN	161.42	0.0130452	*
Solyc06g072710	Solyc06g072710.2	T2	T2_P	T2_L	3.26	DOWN	96.19	0.0130452	*
Solyc12g096770	Solyc12g096770.1	T2	T2_P	T2_L	3.21	DOWN	23.29	0.0304876	*
Solyc03g034070	Solyc03g034070.1	T2	T2_P	T2_L	3.18	DOWN	222.45	0.0130452	*
Solyc01g099020	CGT	T2	T2_P	T2_L	3.15	DOWN	167.51	0.0378174	*
Solyc01g103100	Solyc01g103100.2	T2	T2_P	T2_L	3.13	DOWN	117.19	0.0130452	*
Solyc01g005590	Solyc01g005590.2	T2	T2_P	T2_L	3.1	DOWN	231.35	0.0130452	*
Solyc07g007260	Solyc07g007260.2	T2	T2_P	T2_L	3.1	DOWN	398.51	0.0130452	*
Solyc07g052610	Solyc07g052610.2	T2	T2_P	T2_L	2.78	DOWN	87.18	0.0130452	*
Solyc08g079090	Solyc08g079090.2	T2	T2_P	T2_L	2.77	DOWN	28.55	0.0220602	*

Table A.7 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc07g055740	Solyc07g055740.1	T2	T2_P	T2_L	2.71	DOWN	155.7	0.0130452	*
Solyc07g042440	Solyc07g042440.2	T2	T2_P	T2_L	2.7	DOWN	237.6	0.0378174	*
Solyc07g045080	Solyc07g045080.2	T2	T2_P	T2_L	2.69	DOWN	84.25	0.0304876	*
Solyc05g050770	Solyc05g050770.2	T2	T2_P	T2_L	2.61	DOWN	35.62	0.0378174	*
Solyc04g071960	Solyc04g071960.2	T2	T2_P	T2_L	2.49	DOWN	82.1	0.0378174	*
Solyc07g055260	Solyc07g055260.2	T2	T2_P	T2_L	2.48	DOWN	88.96	0.0304876	*
Solyc07g009500	Solyc07g009500.1	T3	T3_P	T3_L	25.33	UP	522.73	0.00782778	**
Solyc10g084960	Solyc10g084960.1	T3	T3_P	T3_L	19.16	UP	15.44	0.0278285	*
Solyc09g090990	Solyc09g090990.2	T3	T3_P	T3_L	15.8	UP	19.3	0.00782778	**
Solyc09g097810	Solyc09g097810.2	T3	T3_P	T3_L	15.15	UP	32.98	0.00782778	**
Solyc12g096960	Solyc12g096960.1	T3	T3_P	T3_L	10.57	UP	34.41	0.00782778	**
Solyc03g119590	Solyc03g119590.1	T3	T3_P	T3_L	10.38	UP	144.56	0.00782778	**
Solyc07g045530	Solyc07g045530.1	T3	T3_P	T3_L	9.99	UP	23.94	0.00782778	**
Solyc05g053550	CHS2	T3	T3_P	T3_L	9.76	UP	31.52	0.00782778	**
Solyc07g009230	Solyc07g009230.2	T3	T3_P	T3_L	8.79	UP	18.88	0.00782778	**
Solyc08g067360	Solyc08g067360.2	T3	T3_P	T3_L	8.76	UP	14.6	0.00782778	**
Solyc11g011240	GGPS1	T3	T3_P	T3_L	8.32	UP	8.1	0.0190315	*
Solyc10g055740	Solyc10g055740.1	T3	T3_P	T3_L	7.15	UP	5.75	0.0319336	*
Solyc12g049030	Solyc12g049030.1	T3	T3_P	T3_L	6.6	UP	19.41	0.00782778	**
Solyc08g067340	Solyc08g067340.2	T3	T3_P	T3_L	6.25	UP	42.48	0.00782778	**
Solyc08g068710	Solyc08g068710.1	T3	T3_P	T3_L	6.23	UP	30.78	0.00782778	**
Solyc10g055200	Solyc10g055200.1	T3	T3_P	T3_L	6.21	UP	105.25	0.00782778	**
Solyc10g075150	Solyc10g075150.1	T3	T3_P	T3_L	6.12	UP	2067.21	0.00782778	**
Solyc03g005980	Solyc03g005980.2	T3	T3_P	T3_L	6.09	UP	9.63	0.0237964	*
TCONS_00087919	Solyc12g011150.1	T3	T3_P	T3_L	5.8	UP	25.21	0.00782778	**
Solyc07g008210	Solyc07g008210.2	T3	T3_P	T3_L	5.71	UP	38.74	0.00782778	**

Table A.7 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc02g061780	Solyc02g061780.2	T3	T3_P	T3_L	5.69	UP	12.09	0.0278285	*
Solyc03g033790	Solyc03g033790.2	T3	T3_P	T3_L	5.59	UP	6.65	0.00782778	**
Solyc04g051690	Solyc04g051690.2	T3	T3_P	T3_L	5.56	UP	60.61	0.00782778	**
Solyc01g006300	CEVI-1	T3	T3_P	T3_L	5.44	UP	181.98	0.00782778	**
Solyc09g063150	Solyc09g063150.2	T3	T3_P	T3_L	5.32	UP	8.73	0.0319336	*
TCONS_00071198	XLOC_028464	T3	T3_P	T3_L	5.15	UP	68.51	0.00782778	**
XLOC_027754	-	T3	T3_P	T3_L	5.09	UP	35.39	0.0278285	*
Solyc04g054760	Solyc04g054760.2	T3	T3_P	T3_L	4.83	UP	81.2	0.00782778	**
Solyc12g100270	Solyc12g100270.1	T3	T3_P	T3_L	4.72	UP	4.81	0.0358998	*
Solyc09g097760	Solyc09g097760.2	T3	T3_P	T3_L	4.51	UP	27.02	0.0190315	*
Solyc05g006870	Solyc05g006870.2	T3	T3_P	T3_L	4.49	UP	17.59	0.0319336	*
Solyc04g072070	Solyc04g072070.2	T3	T3_P	T3_L	4.48	UP	21.16	0.0237964	*
Solyc11g066270	XTH6	T3	T3_P	T3_L	4.45	UP	21.84	0.0454516	*
XLOC_025270	-	T3	T3_P	T3_L	4.45	UP	58.03	0.00782778	**
TCONS_00071197	XLOC_028463	T3	T3_P	T3_L	4.43	UP	198.2	0.00782778	**
Solyc08g079900	Solyc08g079900.1	T3	T3_P	T3_L	4.39	UP	16.63	0.00782778	**
Solyc11g069940	Solyc11g069940.1	T3	T3_P	T3_L	4.39	UP	220.86	0.00782778	**
Solyc07g008140	Solyc07g008140.2	T3	T3_P	T3_L	4.35	UP	53.73	0.00782778	**
XLOC_025245	-	T3	T3_P	T3_L	4.34	UP	15.23	0.0392249	*
Solyc06g069040	Solyc06g069040.2	T3	T3_P	T3_L	4.28	UP	14.52	0.00782778	**
Solyc11g030730	Solyc11g030730.1	T3	T3_P	T3_L	4.18	UP	9.53	0.00782778	**
Solyc05g009040	Solyc05g009040.2	T3	T3_P	T3_L	4.13	UP	26.91	0.00782778	**
Solyc04g007380	Solyc04g007380.1	T3	T3_P	T3_L	4.07	UP	12.45	0.0319336	*
Solyc04g040130	Solyc04g040130.1	T3	T3_P	T3_L	3.95	UP	27.07	0.00782778	**
Solyc03g122350	Solyc03g122350.2	T3	T3_P	T3_L	3.69	UP	77.62	0.00782778	**
TCONS_00026519	Solyc03g033800.1	T3	T3_P	T3_L	3.65	UP	15.38	0.0237964	*

Table A.7 continued.

Gene ID	**Gene Name**	**Time**	**Group 1**	**Group 2**	**Fold Change**	**Direction**	**Total Fpkm**	**q-value**	**Sig. Lvl**
Solyc02g093580	Solyc02g093580.2	T3	T3_P	T3_L	3.64	UP	9.28	0.0278285	*
Solyc02g082740	Solyc02g082740.1	T3	T3_P	T3_L	3.61	UP	60.31	0.00782778	**
Solyc05g050130	Solyc05g050130.2	T3	T3_P	T3_L	3.59	UP	296.85	0.00782778	**
Solyc01g086670	Solyc01g086670.2	T3	T3_P	T3_L	3.52	UP	68.39	0.042196	*
Solyc02g080510	Solyc02g080510.1	T3	T3_P	T3_L	3.49	UP	81.51	0.00782778	**
Solyc12g087870	Solyc12g087870.1	T3	T3_P	T3_L	3.49	UP	23.21	0.00782778	**
Solyc08g060920	AIL	T3	T3_P	T3_L	3.48	UP	35.85	0.00782778	**
Solyc03g025670	Solyc03g025670.2	T3	T3_P	T3_L	3.44	UP	245.92	0.00782778	**
Solyc09g090080	PT3	T3	T3_P	T3_L	3.31	UP	24.12	0.00782778	**
Solyc01g008620	Solyc01g008620.2	T3	T3_P	T3_L	3.28	UP	67.46	0.00782778	**
Solyc04g076010	Solyc04g076010.2	T3	T3_P	T3_L	3.27	UP	76.5	0.00782778	**
Solyc02g077040	PIP1	T3	T3_P	T3_L	3.26	UP	275.71	0.00782778	**
Solyc08g007460	Solyc08g007460.2	T3	T3_P	T3_L	3.25	UP	90.63	0.00782778	**
Solyc10g083290	WIV-1	T3	T3_P	T3_L	3.23	UP	13.24	0.0190315	*
Solyc12g042480	Solyc12g042480.1	T3	T3_P	T3_L	3.18	UP	32.42	0.00782778	**
Solyc01g089880	Solyc01g089880.2	T3	T3_P	T3_L	3.17	UP	83.95	0.00782778	**
Solyc09g009130	PSK1	T3	T3_P	T3_L	3.17	UP	212.23	0.00782778	**
Solyc10g079860	TOMQ`B	T3	T3_P	T3_L	3.12	UP	67.38	0.00782778	**
Solyc09g011560	Solyc09g011560.2	T3	T3_P	T3_L	3.09	UP	43.89	0.00782778	**
Solyc05g051530	Solyc05g051530.2	T3	T3_P	T3_L	3.04	UP	25.04	0.00782778	**
Solyc01g088660	Solyc01g088660.2	T3	T3_P	T3_L	3.03	UP	150.85	0.00782778	**
Solyc03g013160	Solyc03g013160.2	T3	T3_P	T3_L	2.98	UP	23.74	0.0358998	*
Solyc09g091000	Solyc09g091000.2	T3	T3_P	T3_L	2.98	UP	45.94	0.014053	*
Solyc02g014030	Solyc02g014030.1	T3	T3_P	T3_L	2.96	UP	7.1	0.0358998	*
Solyc02g082920	CHI3	T3	T3_P	T3_L	2.92	UP	474.89	0.042196	*
Solyc06g050440	Solyc06g050440.2	T3	T3_P	T3_L	2.86	UP	23.91	0.0237964	*

Table A.7 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc05g006850	Solyc05g006850.2	T3	T3_P	T3_L	2.83	UP	298.19	0.00782778	**
Solyc01g109880	ZIP	T3	T3_P	T3_L	2.81	UP	104.11	0.00782778	**
Solyc02g076980	RCR3	T3	T3_P	T3_L	2.79	UP	59.99	0.00782778	**
Solyc05g051460	Solyc05g051460.2	T3	T3_P	T3_L	2.79	UP	36.2	0.0454516	*
Solyc08g074490	Solyc08g074490.2	T3	T3_P	T3_L	2.78	UP	65.49	0.00782778	**
Solyc09g011600	Solyc09g011600.2	T3	T3_P	T3_L	2.78	UP	90.97	0.014053	*
Solyc01g010230	Solyc01g010230.2	T3	T3_P	T3_L	2.77	UP	94.04	0.00782778	**
XLOC_017277	-	T3	T3_P	T3_L	2.77	UP	71.21	0.0487551	*
Solyc08g077480	Solyc08g077480.2	T3	T3_P	T3_L	2.72	UP	244.96	0.014053	*
TCONS_00030967	Solyc04g016040.1	T3	T3_P	T3_L	2.72	UP	16.77	0.00782778	**
Solyc04g005100	Solyc04g005100.2	T3	T3_P	T3_L	2.66	UP	54.97	0.0190315	*
Solyc03g097610	Solyc03g097610.2	T3	T3_P	T3_L	2.63	UP	36.96	0.0237964	*
Solyc07g049550	ACO4	T3	T3_P	T3_L	2.63	UP	27.3	0.0190315	*
Solyc03g095770	Solyc03g095770.2	T3	T3_P	T3_L	2.56	UP	184.3	0.0190315	*
Solyc05g009520	Solyc05g009520.1	T3	T3_P	T3_L	2.54	UP	94.16	0.0454516	*
Solyc03g034370	Solyc03g034370.1	T3	T3_P	T3_L	2.52	UP	4209.97	0.0190315	*
Solyc02g063440	Solyc02g063440.2	T3	T3_P	T3_L	2.44	UP	260.95	0.0319336	*
Solyc03g114100	Solyc03g114100.1	T3	T3_P	T3_L	2.37	UP	357.57	0.00782778	**
Solyc07g056200	Solyc07g056200.2	T3	T3_P	T3_L	2.34	UP	95.24	0.0190315	*
Solyc09g011590	Solyc09g011590.2	T3	T3_P	T3_L	2.33	UP	71.26	0.0392249	*
XLOC_017161	-	T3	T3_P	T3_L	2.3	UP	119.88	0.0487551	*
Solyc03g119600	Solyc03g119600.1	T3	T3_P	T3_L	2.29	UP	921.34	0.042196	*
Solyc04g078290	Solyc04g078290.2	T3	T3_P	T3_L	2.28	UP	91.87	0.0237964	*
Solyc08g076730	Solyc08g076730.2	T3	T3_P	T3_L	2.18	UP	84.91	0.0358998	*
Solyc01g098590	Solyc01g098590.2	T3	T3_P	T3_L	2.11	UP	100.1	0.0392249	*
XLOC_011946	-	T3	T3_P	T3_L	19.48	DOWN	61.37	0.00782778	**

Table A.7 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc08g081620	CEL1	T3	T3_P	T3_L	14.75	DOWN	3.84	0.014053	*
Solyc06g072350	Solyc06g072350.2	T3	T3_P	T3_L	12.22	DOWN	49.8	0.00782778	**
Solyc10g080690	Solyc10g080690.1	T3	T3_P	T3_L	11.84	DOWN	10.31	0.0454516	*
Solyc03g121900	Solyc03g121900.1	T3	T3_P	T3_L	10.02	DOWN	159.13	0.0278285	*
Solyc10g076940	Solyc10g076940.1	T3	T3_P	T3_L	9.55	DOWN	3.42	0.0392249	*
Solyc12g011010	Solyc12g011010.1	T3	T3_P	T3_L	9.45	DOWN	14.22	0.00782778	**
Solyc07g055950	Solyc07g055950.2	T3	T3_P	T3_L	6.57	DOWN	19.14	0.00782778	**
Solyc06g069790	Solyc06g069790.2	T3	T3_P	T3_L	6.38	DOWN	24.67	0.00782778	**
Solyc11g006250	Solyc11g006250.1	T3	T3_P	T3_L	6	DOWN	12.98	0.00782778	**
Solyc02g070990	Solyc02g070990.1	T3	T3_P	T3_L	5.81	DOWN	1448.06	0.0278285	*
Solyc06g069730	Solyc06g069730.2	T3	T3_P	T3_L	5.51	DOWN	606.34	0.00782778	**
Solyc01g079830	Solyc01g079830.2	T3	T3_P	T3_L	5.24	DOWN	19.76	0.0190315	*
Solyc03g005790	Solyc03g005790.2	T3	T3_P	T3_L	4.99	DOWN	85.88	0.00782778	**
Solyc01g008420	Solyc01g008420.2	T3	T3_P	T3_L	4.97	DOWN	9.23	0.00782778	**
Solyc01g095140	ER5	T3	T3_P	T3_L	4.77	DOWN	57.74	0.00782778	**
Solyc10g005030	Solyc10g005030.2	T3	T3_P	T3_L	3.64	DOWN	17.36	0.0319336	*
Solyc03g111550	Solyc03g111550.2	T3	T3_P	T3_L	3.54	DOWN	12.08	0.0237964	*
Solyc09g075750	Solyc09g075750.1	T3	T3_P	T3_L	3.51	DOWN	70.94	0.00782778	**
Solyc05g051850	INS-1P	T3	T3_P	T3_L	3.44	DOWN	166.32	0.00782778	**
Solyc03g005900	Solyc03g005900.2	T3	T3_P	T3_L	3.42	DOWN	50.02	0.00782778	**
Solyc08g078870	Solyc08g078870.1	T3	T3_P	T3_L	3.35	DOWN	370.89	0.00782778	**
Solyc04g014510	GTS1	T3	T3_P	T3_L	3.31	DOWN	9.75	0.0392249	*
Solyc02g077330	Solyc02g077330.2	T3	T3_P	T3_L	3.3	DOWN	31.8	0.00782778	**
Solyc07g007550	Solyc07g007550.2	T3	T3_P	T3_L	3.24	DOWN	10	0.0237964	*
Solyc06g060310	Solyc06g060310.2	T3	T3_P	T3_L	3.19	DOWN	37.02	0.0392249	*
Solyc06g071320	Solyc06g071320.2	T3	T3_P	T3_L	3.07	DOWN	25.46	0.0487551	*

Table A.7 continued.

Gene ID	Gene Name	Time	Group 1	Group 2	Fold Change	Direction	Total Fpkm	q-value	Sig. Lvl
Solyc04g015620	Solyc04g015620.2	T3	T3_P	T3_L	2.98	DOWN	29.21	0.0278285	*
Solyc04g008040	Solyc04g008040.2	T3	T3_P	T3_L	2.95	DOWN	89.64	0.00782778	**
Solyc07g006630	Solyc07g006630.2	T3	T3_P	T3_L	2.95	DOWN	77.27	0.00782778	**
Solyc04g076880	Solyc04g076880.2	T3	T3_P	T3_L	2.94	DOWN	84.11	0.0190315	*
Solyc03g006490	Solyc03g006490.2	T3	T3_P	T3_L	2.88	DOWN	62.1	0.00782778	**
Solyc06g084140	Solyc06g084140.2	T3	T3_P	T3_L	2.86	DOWN	24.57	0.00782778	**
Solyc03g118310	Solyc03g118310.2	T3	T3_P	T3_L	2.76	DOWN	22.77	0.00782778	**
Solyc08g075490	Solyc08g075490.2	T3	T3_P	T3_L	2.74	DOWN	172.4	0.014053	*
Solyc01g087710	Solyc01g087710.2	T3	T3_P	T3_L	2.73	DOWN	57.7	0.00782778	**
Solyc06g072710	Solyc06g072710.2	T3	T3_P	T3_L	2.69	DOWN	75.52	0.014053	*
Solyc01g090970	Solyc01g090970.2	T3	T3_P	T3_L	2.62	DOWN	175.93	0.00782778	**
Solyc09g009420	Solyc09g009420.1	T3	T3_P	T3_L	2.52	DOWN	101.75	0.0487551	*
Solyc01g086920	Solyc01g086920.2	T3	T3_P	T3_L	2.51	DOWN	191.07	0.014053	*
Solyc08g067330	Solyc08g067330.1	T3	T3_P	T3_L	2.42	DOWN	1623.43	0.014053	*

Time represents time point as indicated in the method. Group represents the specified group of plants according to their insect treatment. Direction represents the up- or down-regulation of the expressed gene. Total FPKM (Fragments Per Kilobase of transcript per Million) mapped reads represent the sum of all expression of genes among the compared groups. q-value indicates the adjusted p-value after the Benjamini-Hochberg correction for multiple comparison. * q-value < 0.05. Double ** q-value < 0.01.

Table A.8 List of DEGs with their associated GO terms resulted from the C vs P comparison

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T1	Up	AADC1A	Q1KSC6_SOLLC	GO:0016831; GO:0019752; GO:0030170	Aromatic amino acid decarboxylase 1A (Uncharacterized protein)
T1	Up	CBF1	Q8S9N5_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	CBF1 (Putative transcriptional activator CBF1) (Uncharacterized protein)
T1	Up	CZFP1	A6ZIC0_SOLLC	GO:0046872	C2H2-type zinc finger protein (Cold zinc finger protein 1)
T1	Up	GRAS4	Q00LP5_SOLLC	GO:0006355; GO:0006351	GRAS4 (Uncharacterized protein)
T1	Up	hsc70	K4C9W3_SOLLC	GO:0005524	Uncharacterized protein
T1	Up	Solyc06g068460.2	K4C821_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T1	Up	Solyc08g080670.1	K4CP65_SOLLC		Uncharacterized protein
T1	Up	Solyc04g005050.1	I7JCM3_SOLLC	GO:0031012; GO:0004222; GO:0008270	Matrix metalloproteinase (Uncharacterized protein)
T1	Up	Solyc00g206460.1	K4ARX5_SOLLC		Uncharacterized protein
T1	Up	Solyc01g005470.2	K4ASB4_SOLLC		Uncharacterized protein
T1	Up	Solyc01g065530.2	K4AWF7_SOLLC	GO:0031225; GO:0016049; GO:0010215	Uncharacterized protein
T1	Up	Solyc01g066430.2	K4AWP6_SOLLC	GO:0008270	Uncharacterized protein
T1	Up	Solyc01g080870.2	K4AXY0_SOLLC	GO:0016020; GO:0005215	Uncharacterized protein
T1	Up	Solyc01g087580.2	K4AYE8_SOLLC		Uncharacterized protein
T1	Up	Solyc01g091590.2	K4AZ99_SOLLC		Uncharacterized protein
T1	Up	Solyc01g096510.2	K4B039_SOLLC		Uncharacterized protein
T1	Up	Solyc01g099370.2	K4B0X4_SOLLC		Uncharacterized protein
T1	Up	Solyc01g100010.2	K4B135_SOLLC		Uncharacterized protein
T1	Up	Solyc02g091180.1	K4BCR7_SOLLC		Uncharacterized protein
T1	Up	Solyc02g093230.2	K4BDB9_SOLLC	GO:0008171	Uncharacterized protein
T1	Up	Solyc03g007870.2	K4BEK9_SOLLC	GO:0046872; GO:0030001	Uncharacterized protein
T1	Up	Solyc03g082370.1	K4BI14_SOLLC		Uncharacterized protein
T1	Up	Solyc03g083470.2	K4BIC3_SOLLC	GO:0005524; GO:0004674	Uncharacterized protein
T1	Up	Solyc03g083480.2	K4BIC4_SOLLC	GO:0030247	Uncharacterized protein
T1	Up	Solyc03g093110.2	K4BII8_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)

Table A.8 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T1	Up	Solyc03g093120.2	K4BII9_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T1	Up	Solyc03g093610.1	K4BIN7_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	Uncharacterized protein
T1	Up	Solyc03g095770.2	K4BIZ9_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T1	Up	Solyc03g098730.1	K4BJT6_SOLLC	GO:0004866	Uncharacterized protein
T1	Up	Solyc03g112340.1	K4BK88_SOLLC	GO:0008270	Uncharacterized protein
T1	Up	Solyc04g018110.1	K4BQL0_SOLLC	GO:0005509	Uncharacterized protein
T1	Up	Solyc04g025650.2	K4BR09_SOLLC	GO:0016491	Uncharacterized protein
T1	Up	Solyc04g071030.1	K4BT95_SOLLC	GO:0016874; GO:0004842	Uncharacterized protein
T1	Up	Solyc04g077230.1	K4BUG0_SOLLC		Uncharacterized protein
T1	Up	Solyc04g077270.2	K4BUG4_SOLLC	GO:0005524; GO:0004674; GO:0048544	Serine/threonine-protein kinase (EC 2.7.11.1)
T1	Up	Solyc04g077620.1	K4BUJ9_SOLLC		Uncharacterized protein
T1	Up	Solyc05g005260.1	K4BW57_SOLLC		Uncharacterized protein
T1	Up	Solyc05g009790.1	K4BXF3_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	Uncharacterized protein
T1	Up	Solyc05g047680.2	K4C100_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T1	Up	Solyc05g052040.1	K4C1N5_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	Uncharacterized protein
T1	Up	Solyc05g052050.1	K4C1N6_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	Uncharacterized protein
T1	Up	Solyc06g005650.2	K4C347_SOLLC		Uncharacterized protein
T1	Up	Solyc06g009140.2	K4C3U4_SOLLC	GO:0006950	Uncharacterized protein
T1	Up	Solyc06g049020.1	K4C5E8_SOLLC		Uncharacterized protein
T1	Up	Solyc06g050500.2	K4C5J4_SOLLC		Uncharacterized protein
T1	Up	Solyc06g060690.2	K4C6P9_SOLLC	GO:0005524; GO:0004672	Uncharacterized protein
T1	Up	Solyc06g066370.2	K4C7R3_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T1	Up	Solyc06g074030.1	K4C9C1_SOLLC	GO:0003676; GO:0005634	Uncharacterized protein
T1	Up	Solyc07g045100.1	K4CER8_SOLLC	GO:0004190	Uncharacterized protein
T1	Up	Solyc07g053740.1	K4CFR9_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	Uncharacterized protein

Table A.8 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T1	Up	Solyc07g055710.2	K4CGA4_SOLLC	GO:0005634; GO:0009408; GO:0043565; GO:0003700	Uncharacterized protein
T1	Up	Solyc07g062490.1	K4CGT2_SOLLC		Uncharacterized protein
T1	Up	Solyc08g006320.2	K4CIC1_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T1	Up	Solyc08g008100.2	K4CIU4_SOLLC	GO:0009058; GO:0003824; GO:0030170	Uncharacterized protein
T1	Up	Solyc08g068600.2	K4CM83_SOLLC	GO:0016831; GO:0019752; GO:0030170	Uncharacterized protein
T1	Up	Solyc08g068770.1	K4CM99_SOLLC	GO:0008080	Uncharacterized protein
T1	Up	Solyc08g077020.1	K4CN62_SOLLC	GO:0009741	Uncharacterized protein
T1	Up	Solyc08g078190.1	K4CNH8_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	Uncharacterized protein
T1	Up	Solyc08g079700.1	K4CNX0_SOLLC	GO:0003677; GO:0008270	Uncharacterized protein
T1	Up	Solyc08g081230.1	K4CPC0_SOLLC	GO:0051260	Uncharacterized protein
T1	Up	Solyc08g083050.1	K4CPV1_SOLLC		Uncharacterized protein
T1	Up	Solyc09g014990.2	K4CRX3_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T1	Up	Solyc09g082230.1	K4CVK0_SOLLC	GO:0008080	Uncharacterized protein
T1	Up	Solyc10g006130.1	K4CXE5_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	Uncharacterized protein
T1	Up	Solyc10g006700.1	K4CXK1_SOLLC	GO:0005509	Uncharacterized protein
T1	Up	Solyc10g008400.1	K4CY17_SOLLC	GO:0008270	Uncharacterized protein
T1	Up	Solyc10g074440.1	K4D1N6_SOLLC	GO:0005975; GO:0016998; GO:0008061; GO:0006032; GO:0004568	Uncharacterized protein
T1	Up	Solyc10g079420.1	K4D2I3_SOLLC	GO:0005509	Uncharacterized protein
T1	Up	Solyc10g080370.1	K4D2S7_SOLLC		Uncharacterized protein
T1	Up	Solyc10g081040.1	K4D2Z1_SOLLC		Uncharacterized protein
T1	Up	Solyc11g010500.1	K4D5L1_SOLLC	GO:0016021; GO:0031966; GO:0006839	Uncharacterized protein
T1	Up	Solyc11g020230.1	K4D6X5_SOLLC	GO:0005524; GO:0009693; GO:0016021; GO:0004674; GO:0010200	Uncharacterized protein

Table A.8 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T1	Up	Solyc11g068710.1	K4DA28_SOLLC	GO:0009738; GO:0009693; GO:0009873; GO:0010286; GO:0042538; GO:0002679; GO:0010200; GO:0009414	Uncharacterized protein
T1	Up	Solyc12g009000.1	K4DBY8_SOLLC		Uncharacterized protein
T1	Up	Solyc12g057150.1	K4DG45_SOLLC		Uncharacterized protein
T1	Up	SRG2	K4CDX3_SOLLC		Uncharacterized protein
T1	Up	tXET-B2	Q43528_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T1	Up	WRKY3	D3YEX5_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein (WRKY transcription factor)
T1	Down	Solyc05g043330.2	K4C0L5_SOLLC	GO:0016788; GO:0006629	Uncharacterized protein
T1	Down	Solyc09g055950.1	K4CT90_SOLLC	GO:0045156; GO:0009772	Uncharacterized protein
T1	Down	Solyc07g054310.1	K4CFX6_SOLLC		Uncharacterized protein
T1	Down	Solyc09g091110.2	K4CWD7_SOLLC		Uncharacterized protein
T1	Down	Solyc10g079350.1	K4D2H6_SOLLC	GO:0016758	Uncharacterized protein
T1	Down	Solyc12g039030.1	K4DEP9_SOLLC	GO:0045156; GO:0009772	Uncharacterized protein
T2	Up	ER5	P93220_SOLLC	GO:0009269	Ethylene-responsive late embryogenesis-like protein (Uncharacterized protein)
T2	Up	hsc70.1	H1ZXA7_SOLLC	GO:0005524	Heat shock protein 70 isoform 1
T2	Up	Lemmi9	Q40155_SOLLC		Lemmi9 protein (Fragment)
T2	Up	Solyc03g120990.2	K4BMP8_SOLLC	GO:0051287; GO:0004471; GO:0006108; GO:0046872	Malic enzyme
T2	Up	Solyc06g007190.2	K4C3A2_SOLLC	GO:0046872; GO:0006470; GO:0004722	Uncharacterized protein
T2	Up	Solyc01g087590.2	K4AYE9_SOLLC	GO:0052895; GO:0050660; GO:0052894; GO:0046592; GO:0046208; GO:0052901	Uncharacterized protein
T2	Up	Solyc01g057770.2	K4AVY8_SOLLC	GO:0005452; GO:0016021; GO:0005886	Uncharacterized protein
T2	Up	Solyc04g025650.2	K4BR09_SOLLC	GO:0016491	Uncharacterized protein
T2	Up	Solyc07g006570.2	K4CBC8_SOLLC	GO:0003723; GO:0033897	Uncharacterized protein
T2	Up	Solyc04g005480.1	K4BNF4_SOLLC		Uncharacterized protein

Table A.8 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T2	Up	Solyc02g090360.2	K4BCI5_SOLLC	GO:0005507; GO:0016491	Uncharacterized protein
T2	Up	Solyc06g068960.1	K4C869_SOLLC	GO:0005509	Uncharacterized protein
T2	Up	Solyc09g011860.2	K4CRL2_SOLLC		Uncharacterized protein
T2	Up	Solyc01g005590.2	K4ASC5_SOLLC		Uncharacterized protein
T2	Up	Solyc11g018800.1	K4D6T3_SOLLC	GO:0020037; GO:0004601; GO:0006979	Uncharacterized protein
T2	Up	Solyc07g006560.2	K4CBC7_SOLLC	GO:0003723; GO:0033897	Uncharacterized protein
T2	Up	Solyc10g080370.1	K4D2S7_SOLLC		Uncharacterized protein
T2	Down	CHI3	CHIA_SOLLC	GO:0016998; GO:0006032; GO:0004568; GO:0006952; GO:0005615; GO:0000272; GO:0009607	Acidic 26 kDa endochitinase (EC 3.2.1.14)
T2	Down	Solyc09g007010.1	PR04_SOLLC	GO:0006952; GO:0005576; GO:0009607	Pathogenesis-related leaf protein 4 (P4)
T2	Down	Solyc01g097240.2	PRP2_SOLLC	GO:0005618; GO:0042742; GO:0050832; GO:0005576	Pathogenesis-related protein P2
T2	Down	ARG2	Q5UNS1_SOLLC	GO:0016813; GO:0046872	Arginase 2 (Uncharacterized protein)
T2	Down	Solyc03g025670.2	K4BF40_SOLLC		Uncharacterized protein
T2	Down	Solyc09g089540.2	K4CVY1_SOLLC	GO:0009611; GO:0004867	Uncharacterized protein
T2	Down	Solyc12g098900.1	K4DHR3_SOLLC		Uncharacterized protein
T2	Down	Solyc07g056640.1	K4CGJ6_SOLLC		Uncharacterized protein
T2	Down	tomQ`b	Q42890_SOLLC	GO:0005975; GO:0042973	Glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39)
T3	Up	Solyc03g005320.2	K4BDV6_SOLLC	GO:0006633; GO:0016020; GO:0016747	3-ketoacyl-CoA synthase (EC 2.3.1.-)
T3	Up	AGP-1C	Q43719_SOLLC		Arabinogalactan (Putative arabinogalactan-protein)
T3	Up	Solyc06g007180.2	K4C3A1_SOLLC	GO:0005524; GO:0070981; GO:0004066; GO:0009063; GO:0006541; GO:0009646	Asparagine synthetase (EC 6.3.5.4)
T3	Up	Solyc09g082870.1	K4CVR3_SOLLC	GO:0005524; GO:0005388; GO:0016021; GO:0046872	Calcium-transporting ATPase (EC 3.6.3.8)
T3	Up	Solyc02g064680.2	K4B6Q4_SOLLC	GO:0005524; GO:0005388; GO:0016021; GO:0046872	Calcium-transporting ATPase (EC 3.6.3.8)

Table A.8 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Up	ERF1	Q8S9H4_SOLLC	GO:0003677; GO:0009873; GO:0009740; GO:0005634; GO:0010162; GO:0003700; GO:0006351	Ethylene response factor 1 (Ethylene-responsive transcription factor 1)
T3	Up	ER5	P93220_SOLLC	GO:0009269	Ethylene-responsive late embryogenesis-like protein
T3	Up	EXLA1	A7X331_SOLLC	GO:0005576; GO:0019953	Expansin-like protein (Uncharacterized protein)
T3	Up	5PT1	A8IDV8_SOLLC	GO:0046856	Inositol-1,4,5-triphosphate-5-phosphatase (Uncharacterized protein)
T3	Up	Solyc01g097240.2	PRP2_SOLLC	GO:0005618; GO:0042742; GO:0050832; GO:0005576	Pathogenesis-related protein P2
T3	Up	Solyc02g092580.2	K4BD54_SOLLC	GO:0005576; GO:0020037; GO:0046872; GO:0004601; GO:0006979	Peroxidase (EC 1.11.1.7)
T3	Up	Solyc02g079590.2	K4B9I0_SOLLC	GO:0005524; GO:0004674; GO:0048544	Serine/threonine-protein kinase (EC 2.7.11.1)
T3	Up	Solyc06g074670.2	K4C9I5_SOLLC	GO:0003824; GO:0050662	Uncharacterized protein
T3	Up	Solyc06g030470.2	K4C4H1_SOLLC	GO:0005886	Auxin-regulated protein
T3	Up	Solyc03g097170.2	K4BJD4_SOLLC	GO:0003854; GO:0006694	Uncharacterized protein
T3	Up	Solyc01g087590.2	K4AYE9_SOLLC	GO:0052895; GO:0050660; GO:0052894; GO:0046592; GO:0046208; GO:0052901	Uncharacterized protein
T3	Up	Solyc12g057160.1	K4DG46_SOLLC		Uncharacterized protein
T3	Up	Solyc03g114320.2	K4BKT4_SOLLC		Uncharacterized protein
T3	Up	Solyc11g010390.1	K4D5K0_SOLLC		Uncharacterized protein
T3	Up	Solyc07g063240.2	K4CH07_SOLLC	GO:0010267	Uncharacterized protein
T3	Up	Solyc03g117860.2	K4BLT7_SOLLC	GO:0003676; GO:0008270	Uncharacterized protein
T3	Up	Solyc03g097050.2	K4BJC2_SOLLC	GO:0030244; GO:0016760; GO:0016021	Uncharacterized protein
T3	Up	Solyc07g065120.2	K4CHJ1_SOLLC	GO:0006071; GO:0008889; GO:0006629	Uncharacterized protein
T3	Up	Solyc01g057770.2	K4AVY8_SOLLC	GO:0005452; GO:0016021; GO:0005886	Uncharacterized protein

Table A.8 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Up	Solyc09g097960.2	K4CWW8_SOLLC		Uncharacterized protein
T3	Up	Solyc04g025650.2	K4BR09_SOLLC	GO:0016491	Uncharacterized protein
T3	Up	Solyc01g079940.2	K4AXN9_SOLLC	GO:0004190	Uncharacterized protein
T3	Up	Solyc03g083560.1	K4BID2_SOLLC		Uncharacterized protein
T3	Up	Solyc10g078580.1	K4D2A0_SOLLC		Uncharacterized protein
T3	Up	Solyc01g102310.2	K4B1F9_SOLLC		Uncharacterized protein
T3	Up	Solyc02g090360.2	K4BCI5_SOLLC	GO:0005507; GO:0016491	Uncharacterized protein
T3	Up	Solyc04g082140.2	K4BVU1_SOLLC	GO:0005507; GO:0016491	Uncharacterized protein
T3	Up	Solyc01g079580.2	K4AXK3_SOLLC		Uncharacterized protein
T3	Up	Solyc09g011860.2	K4CRL2_SOLLC		Uncharacterized protein
T3	Up	Solyc12g006980.1	K4DBN5_SOLLC		Uncharacterized protein
T3	Up	Solyc02g079520.1	K4B9H3_SOLLC	GO:0005509	Uncharacterized protein
T3	Up	Solyc04g074310.2	K4BTW9_SOLLC	GO:0003676; GO:0000166	Uncharacterized protein
T3	Up	Solyc10g074540.1	K4D1P6_SOLLC		Uncharacterized protein
T3	Up	Solyc08g079090.2	K4CNR8_SOLLC	GO:0046658; GO:0043481; GO:0048046; GO:0009932; GO:0071555; GO:0030243; GO:0005507; GO:0009825; GO:0016491; GO:0009505; GO:0009506; GO:0000271; GO:0010817; GO:0048767; GO:0005774	Uncharacterized protein
T3	Up	Solyc01g087020.2	K4AY95_SOLLC		Uncharacterized protein
T3	Up	Solyc01g112260.2	K4B487_SOLLC		Uncharacterized protein
T3	Up	Solyc00g206460.1	K4ARX5_SOLLC		Uncharacterized protein
T3	Up	Solyc12g057150.1	K4DG45_SOLLC		Uncharacterized protein
T3	Up	Solyc04g078340.2	K4BUS0_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T3	Up	Solyc11g005150.1	K4D4C8_SOLLC		Uncharacterized protein
T3	Up	Solyc07g062490.1	K4CGT2_SOLLC		Uncharacterized protein
T3	Up	Solyc08g068770.1	K4CM99_SOLLC	GO:0008080	Uncharacterized protein
T3	Up	Solyc04g077140.2	K4BUF1_SOLLC		Uncharacterized protein
T3	Up	Solyc05g006510.1	K4BWH7_SOLLC	GO:0016757	Uncharacterized protein
T3	Up	Solyc01g086640.2	K4AY57_SOLLC		Uncharacterized protein

Table A.8 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Up	Solyc01g065530.2	K4AWF7_SOLLC	GO:0031225; GO:0016049; GO:0010215	Uncharacterized protein
T3	Up	Solyc06g048820.1	K4C5C8_SOLLC		Uncharacterized protein
T3	Up	Solyc07g054470.1	K4CFZ2_SOLLC		Uncharacterized protein
T3	Up	Solyc08g065850.1	K4CLG4_SOLLC		Uncharacterized protein
T3	Up	Solyc04g071110.1	K4BTA3_SOLLC		Uncharacterized protein
T3	Up	tXET-B2	Q43528_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T3	Up	LeXET2 XET2	Q9FZ05_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T3	Up	Solyc03g093120.2	K4BII9_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T3	Up	Solyc09g092520.2	K4CWS8_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T3	Up	Solyc03g093110.2	K4BII8_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T3	Up	Solyc12g011030.1	K4DCI9_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T3	Down	CATHDINH	Q9LEG1_SOLLC	GO:0004866	Cathepsin D Inhibitor (Uncharacterized protein)
T3	Down	Solyc01g006400.2	G8Z274_SOLLC		Hop-interacting protein THI101 (Uncharacterized protein)
T3	Down	Solyc02g072540.2	K4B8M8_SOLLC	GO:0005524; GO:0004674; GO:0007165	Non-specific serine/threonine protein kinase (EC 2.7.11.1)
T3	Down	Solyc01g006290.2	K4ASJ5_SOLLC	GO:0005576; GO:0020037; GO:0046872; GO:0004601; GO:0006979	Peroxidase (EC 1.11.1.7)

Table A.8 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Down	ARPI	IP22_SOLLC	GO:0004867	Proteinase inhibitor type-2 TR8 (Proteinase inhibitor type II TR8)
T3	Down	PSK1	Q7PCA9_SOLLC	GO:0008283; GO:0005576	Putative phytosulfokine peptide (Uncharacterized protein)
T3	Down	TD	THD1_SOLLC	GO:0004794; GO:0009507; GO:0009097; GO:0030170	Threonine dehydratase biosynthetic, chloroplastic (EC 4.3.1.19) (Threonine deaminase) (TD)
T3	Down	Solyc06g051940.2	K4C5Y0_SOLLC	GO:0046872; GO:0006470; GO:0004722	Uncharacterized protein
T3	Down	Solyc07g008380.1	K4CBV7_SOLLC	GO:0016747	Uncharacterized protein
T3	Down	Solyc01g090340.2	K4AYX5_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	Uncharacterized protein
T3	Down	Solyc07g007240.2	K4CBJ5_SOLLC		Uncharacterized protein
T3	Down	Solyc01g091320.2	K4AZ72_SOLLC	GO:0006633; GO:0016021; GO:0005506; GO:0016491	Uncharacterized protein
T3	Down	Solyc10g009150.2	K4CY91_SOLLC		Uncharacterized protein
T3	Down	Solyc04g082710.2	K4BVZ8_SOLLC	GO:0008234	Uncharacterized protein
T3	Down	Solyc04g078200.2	K4BUQ7_SOLLC		Uncharacterized protein
T3	Down	Solyc01g067460.1	K4AWZ5_SOLLC	GO:0045454; GO:0009055; GO:0015035	Uncharacterized protein
T3	Down	Solyc06g066420.2	K4C7R8_SOLLC		Uncharacterized protein
T3	Down	Solyc12g088840.1	K4DGV5_SOLLC	GO:0005509	Uncharacterized protein
T3	Down	Solyc10g008350.2	K4CY12_SOLLC		Uncharacterized protein
T3	Down	Solyc07g061800.2	K4CGL3_SOLLC		Uncharacterized protein

T1, T2, and T3 represent one, two, and four weeks after infestation, respectively.

Table A.9 List of DEGs with their associated GO terms resulted from the C vs L comparison

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T1	Up	Solyc05g043330.2	K4C0L5_SOLLC	GO:0016788; GO:0006629	Uncharacterized protein
T1	Up	Solyc09g055950.1	K4CT90_SOLLC	GO:0045156; GO:0009772	Uncharacterized protein
T1	Up	Solyc07g054310.1	K4CFX6_SOLLC		Uncharacterized protein
T1	Up	Solyc09g091110.2	K4CWD7_SOLLC		Uncharacterized protein
T1	Up	Solyc10g079350.1	K4D2H6_SOLLC	GO:0016758	Uncharacterized protein
T1	Up	Solyc12g039030.1	K4DEP9_SOLLC	GO:0045156; GO:0009772	Uncharacterized protein
T1	Down	Solyc07g007250.2	MCPI_SOLLC	GO:0004866	Metallocarboxypeptidase inhibitor (Carboxypeptidase inhibitor) (MCPI)
T1	Down	TD	THD1_SOLLC	GO:0004794; GO:0009507; GO:0009097; GO:0030170	Threonine dehydratase biosynthetic, chloroplastic (EC 4.3.1.19) (Threonine deaminase) (TD)
T1	Down	ARG2	Q5UNS1_SOLLC	GO:0016813; GO:0046872	Arginase 2 (Uncharacterized protein)
T1	Down	CBF1	Q8S9N5_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	CBF1 (Putative transcriptional activator CBF1) (Uncharacterized protein)
T1	Down	LOC544157	Q40159_SOLLC	GO:0009269	Late embryogenesis (Lea)-like protein (Uncharacterized protein)
T1	Down	Solyc03g006360.2	K4BE59_SOLLC		Uncharacterized protein
T1	Down	Solyc07g006570.2	K4CBC8_SOLLC	GO:0003723; GO:0033897	Uncharacterized protein
T1	Down	Solyc09g089510.2	K4CVX8_SOLLC	GO:0009611; GO:0004867	Uncharacterized protein
T1	Down	Solyc08g076730.2	K4CN34_SOLLC		Uncharacterized protein
T1	Down	Solyc06g007180.2	K4C3A1_SOLLC	GO:0005524; GO:0070981; GO:0004066; GO:0009063; GO:0006541; GO:0009646	Asparagine synthetase (EC 6.3.5.4)
T1	Down	Solyc02g067050.2	K4B737_SOLLC	GO:0009507	Uncharacterized protein
T1	Down	Solyc09g055950.1	K4CT90_SOLLC	GO:0045156; GO:0009772	Uncharacterized protein
T1	Down	Solyc12g039030.1	K4DEP9_SOLLC	GO:0045156; GO:0009772	Uncharacterized protein
T2	Up	Solyc09g065780.2	K4CUK4_SOLLC	GO:0006633; GO:0016020; GO:0016747	3-ketoacyl-CoA synthase (EC 2.3.1.-)
T2	Up	Solyc06g011350.2	E7EC27_SOLLC	GO:0016021; GO:0005215	Aquaporin (Plasmamembrane intrinsic protein 24) (Uncharacterized protein)
T2	Up	AS1	Q84N31_SOLLC	GO:0005524; GO:0070981; GO:0004066; GO:0009063; GO:0006541; GO:0009646	Asparagine synthetase (EC 6.3.5.4) (Fragment)

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T2	Up	Solyc08g021820.2	G9HPX2_SOLLC	GO:0009734; GO:0005634; GO:0006355; GO:0006351	Auxin-responsive protein
T2	Up	Solyc05g041540.2	K4C0D5_SOLLC	GO:0004185	Carboxypeptidase (EC 3.4.16.-)
T2	Up	Solyc04g080820.2	I0IUQ7_SOLLC	GO:0008762; GO:0009823; GO:0019139; GO:0005615; GO:0050660; GO:0009694; GO:0009753	Cytokinin oxidase/dehydrogenase-like (Uncharacterized protein)
T2	Up	Solyc03g020010.1	O48625_SOLLC	GO:0004866	Lemir (Uncharacterized protein)
T2	Up	Solyc08g029000.2	K4CJW3_SOLLC	GO:0046872; GO:0016702; GO:0031408	Lipoxygenase (EC 1.13.11.-)
T2	Up	Solyc03g044790.2	Q6ED34_SOLLC		Methylesterase (Uncharacterized protein)
T2	Up	THT1-3	Q8RXB8_SOLLC	GO:0008080	N-hydroxycinnamoyl-CoA:tyramine N-hydroxycinnamoyl transferase THT1-3 (Uncharacterized protein)
T2	Up	Solyc04g071890.2	K4BTH6_SOLLC	GO:0020037; GO:0046872; GO:0004601; GO:0006979	Peroxidase (EC 1.11.1.7)
T2	Up	Solyc02g092580.2	K4BD54_SOLLC	GO:0005576; GO:0020037; GO:0046872; GO:0004601; GO:0006979	Peroxidase (EC 1.11.1.7)
T2	Up	Solyc03g025380.2	K4BF11_SOLLC	GO:0005576; GO:0020037; GO:0046872; GO:0004601; GO:0006979	Peroxidase (EC 1.11.1.7)
T2	Up	ppo	Q6ZXV2_SOLLC	GO:0004097	Polyphenol oxidase (EC 1.10.3.1) (Fragment)
T2	Up	PR-5	Q8LPU1_SOLLC		PR-5x (Uncharacterized protein)
T2	Up	Solyc04g007000.1	E1U2K4_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	RAV1 (Uncharacterized protein)
T2	Up	RNALE	Q6A3R1_SOLLC	GO:0003723; GO:0009718; GO:0005618; GO:0005576; GO:0005886; GO:0015824; GO:0006950; GO:0033897	Ribonuclease T2 (EC 3.1.27.1)
T2	Up	Solyc09g090970.2	Q53U35_SOLLC	GO:0006952; GO:0009607	Similar to pathogenesis-related protein STH-2 (Uncharacterized protein)
T2	Up	Solyc07g054720.1	K4CG14_SOLLC	GO:0004867	Uncharacterized protein

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T2	Up	Solyc08g079900.1	K4CNZ0_SOLLC	GO:0004252	Uncharacterized protein
T2	Up	Solyc03g119520.2	K4BMA1_SOLLC		Uncharacterized protein
T2	Up	Solyc04g074410.1	K4BTX9_SOLLC		Uncharacterized protein
T2	Up	Solyc06g060830.2	K4C6R3_SOLLC	GO:0005634; GO:0043565; GO:0003700; GO:0006351	Uncharacterized protein
T2	Up	Solyc02g071470.2	K4B8C3_SOLLC	GO:0046872; GO:0016706	Uncharacterized protein
T2	Up	Solyc08g077330.2	K4CN93_SOLLC	GO:0005576	Uncharacterized protein
T2	Up	Solyc02g077590.1	K4B8Y4_SOLLC	GO:0005634; GO:0006355; GO:0043565	Uncharacterized protein
T2	Up	PR-5	K4CP64_SOLLC		Uncharacterized protein
T2	Up	Solyc03g006360.2	K4BE59_SOLLC		Uncharacterized protein
T2	Up	Solyc08g077900.2	K4CNE9_SOLLC	GO:0005576	Uncharacterized protein
T2	Up	Solyc12g045030.1	K4DFI3_SOLLC	GO:0016491	Uncharacterized protein
T2	Up	Solyc09g065540.2	K4CUI0_SOLLC	GO:0005524; GO:0004075; GO:0050897; GO:0022626; GO:0006552; GO:0004485; GO:0005759; GO:0009750; GO:0009744	Uncharacterized protein
T2	Up	Solyc02g070110.1	K4B7Z3_SOLLC	GO:0008762; GO:0050660	Uncharacterized protein
T2	Up	Solyc10g083690.2	K4D3F5_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T2	Up	Solyc06g062460.2	K4C6X7_SOLLC		Uncharacterized protein
T2	Up	Solyc02g078650.2	K4B989_SOLLC	GO:0004097; GO:0046872; GO:0046148	Uncharacterized protein
T2	Up	Solyc07g063410.2	K4CH24_SOLLC	GO:0003677; GO:0005634; GO:0006355; GO:0006351	Uncharacterized protein
T2	Up	Solyc05g007770.2	K4BWV2_SOLLC	GO:0003677; GO:0005634; GO:0006355; GO:0006351	Uncharacterized protein
T2	Up	Solyc04g005610.2	K4BNG7_SOLLC	GO:0003677; GO:0005634; GO:0006355; GO:0006351	Uncharacterized protein
T2	Up	Solyc08g062180.1	K4CL07_SOLLC		Uncharacterized protein
T2	Up	Solyc01g079940.2	K4AXN9_SOLLC	GO:0004190	Uncharacterized protein
T2	Up	Solyc05g009790.1	K4BXF3_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	Uncharacterized protein

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T2	Up	Solyc03g098730.1	K4BJT6_SOLLC	GO:0004866	Uncharacterized protein
T2	Up	Solyc01g005470.2	K4ASB4_SOLLC		Uncharacterized protein
T2	Up	Solyc10g017960.1	K4CYS0_SOLLC		Uncharacterized protein
T2	Up	Solyc08g079230.1	K4CNT1_SOLLC		Uncharacterized protein
T2	Up	Solyc03g078490.2	K4BHS7_SOLLC	GO:0016758	Uncharacterized protein
T2	Up	Solyc03g098740.1	K4BJT7_SOLLC	GO:0004866	Uncharacterized protein
T2	Up	Solyc05g052680.1	K4C1U9_SOLLC	GO:0016747	Uncharacterized protein
T2	Up	Solyc04g040180.2	K4BRF6_SOLLC	GO:0008168	Uncharacterized protein
T2	Up	Solyc10g008400.1	K4CY17_SOLLC	GO:0008270	Uncharacterized protein
T2	Up	Solyc04g076220.2	K4BU60_SOLLC		Uncharacterized protein
T2	Up	Solyc08g080670.1	K4CP65_SOLLC		Uncharacterized protein
T2	Up	Solyc02g062390.2	K4B6C8_SOLLC	GO:0006950; GO:0009415	Uncharacterized protein
T2	Up	Solyc07g006560.2	K4CBC7_SOLLC	GO:0003723; GO:0033897	Uncharacterized protein
T2	Up	Solyc06g068500.2	K4C825_SOLLC		Uncharacterized protein
T2	Up	Solyc06g009140.2	K4C3U4_SOLLC	GO:0006950	Uncharacterized protein
T2	Up	Solyc07g005100.2	K4CAY2_SOLLC	GO:0005975; GO:0006032; GO:0004568	Uncharacterized protein
T2	Up	Solyc07g054730.1	K4CG15_SOLLC		Uncharacterized protein
T2	Up	Solyc05g052670.1	K4C1U8_SOLLC	GO:0016747	Uncharacterized protein
T2	Up	Solyc02g064690.2	K4B6Q5_SOLLC	GO:0008080	Uncharacterized protein
T2	Up	Solyc03g031890.2	K4BFG0_SOLLC		Uncharacterized protein
T2	Up	Solyc09g097760.2	K4CWU8_SOLLC		Uncharacterized protein
T2	Up	Solyc05g008110.2	K4BWY5_SOLLC		Uncharacterized protein
T2	Up	Solyc04g011770.2	K4BPN0_SOLLC		Uncharacterized protein
T2	Up	Solyc04g064880.2	K4BT79_SOLLC		Uncharacterized protein
T2	Up	Solyc04g078340.2	K4BUS0_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T2	Up	Solyc02g082900.2	K4BAG0_SOLLC	GO:0009058; GO:0016844	Uncharacterized protein
T2	Up	Solyc06g067910.2	K4C7W6_SOLLC		Uncharacterized protein
T2	Up	Solyc07g062490.1	K4CGT2_SOLLC		Uncharacterized protein
T2	Up	Solyc09g098510.2	K4CX21_SOLLC	GO:0009664; GO:0005199	Uncharacterized protein
T2	Up	Solyc08g078870.1	K4CNP6_SOLLC		Uncharacterized protein
T2	Up	Solyc02g078150.2	K4B940_SOLLC		Uncharacterized protein
T2	Up	Solyc04g079860.1	K4BV65_SOLLC	GO:0016757	Uncharacterized protein

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T2	Up	BR1	K4CWS8_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T2	Up	ACI25	Q3SC86_SOLLC	GO:0004190	Xyloglucan-specific fungal endoglucanase inhibitor protein
T2	Down	Solyc06g069730.2	Q7M1K8_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0046872; GO:0009765; GO:0009522; GO:0009523; GO:0018298	Chlorophyll a/b-binding protein (cab-12) (Uncharacterized protein)
T2	Down	Solyc02g080210.2	K4B9P2_SOLLC	GO:0045330; GO:0005618; GO:0042545; GO:0004857; GO:0045490; GO:0030599	Pectinesterase (EC 3.1.1.11)
T2	Down	PSBS	PSBS_SOLLC	GO:0009517; GO:0016168; GO:0019344; GO:0016021; GO:0000023; GO:0010196; GO:0009523; GO:0010207; GO:0043085; GO:0006364; GO:0019252; GO:0010103; GO:0010027; GO:0051738	Photosystem II 22 kDa protein, chloroplastic (CP22)
T2	Down	Solyc01g102610.2	K4B1I9_SOLLC	GO:0016021; GO:0016491	Uncharacterized protein
T2	Down	Solyc06g072710.2	K4C8Z1_SOLLC	GO:0003677; GO:0006352; GO:0003700; GO:0016987	Uncharacterized protein
T2	Down	Solyc01g006330.2	K4ASJ9_SOLLC	GO:0009941; GO:0009535; GO:0006098; GO:0005198; GO:0010027	Uncharacterized protein
T2	Down	Solyc02g070980.1	K4B876_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0046872; GO:0009765; GO:0009522; GO:0009523; GO:0018298	Uncharacterized protein
T2	Down	Solyc09g011080.2	K4CRD4_SOLLC	GO:0005524	Uncharacterized protein
T2	Down	Solyc01g087710.2	K4AYG1_SOLLC		Uncharacterized protein
T2	Down	Solyc05g043330.2	K4C0L5_SOLLC	GO:0016788; GO:0006629	Uncharacterized protein
T2	Down	Solyc05g050770.2	K4C1A9_SOLLC	GO:0004185	Uncharacterized protein

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T2	Down	Solyc07g055260.2	K4CG65_SOLLC	GO:0009507; GO:0009055; GO:0005506; GO:0051536; GO:0006950	Uncharacterized protein
T2	Down	Solyc03g114130.1	K4BKR5_SOLLC		Uncharacterized protein
T2	Down	Solyc05g047680.2	K4C100_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T2	Down	Solyc04g007780.2	K4BNT5_SOLLC	GO:0006952; GO:0009607	Uncharacterized protein
T2	Down	Solyc12g098900.1	K4DHR3_SOLLC		Uncharacterized protein
T2	Down	Solyc01g095320.2	K4AZS1_SOLLC	GO:0050832; GO:0010286; GO:0012502; GO:0009506; GO:0006457; GO:0034976; GO:0010228	Uncharacterized protein
T2	Down	Solyc06g060310.2	K4C6L2_SOLLC	GO:0051537; GO:0010277; GO:0005506; GO:0016705	Uncharacterized protein
T2	Down	Solyc07g042520.2	K4CEB3_SOLLC	GO:0009058; GO:0005985; GO:0016157	Uncharacterized protein
T2	Down	Solyc06g068950.2	K4C868_SOLLC	GO:0006656; GO:0000234	Uncharacterized protein
T2	Down	Solyc03g005790.2	K4BE02_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0009765; GO:0009523; GO:0018298	Uncharacterized protein
T2	Down	Solyc01g005520.2	K4ASB8_SOLLC	GO:0016117; GO:0009941; GO:0009570; GO:0009535; GO:0010264; GO:0015979	Uncharacterized protein
T2	Down	Solyc07g056640.1	K4CGJ6_SOLLC		Uncharacterized protein
T2	Down	Solyc02g070990.1	K4B877_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0046872; GO:0009765; GO:0009522; GO:0009523; GO:0018298	Uncharacterized protein
T2	Down	Solyc09g008320.2	K4CQM0_SOLLC	GO:0048046; GO:0005618; GO:0042546; GO:0016998; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Up	ACO4	ACCO4_SOLLC	GO:0009815; GO:0031418; GO:0009693; GO:0009835; GO:0046872; GO:0016706	1-aminocyclopropane-1-carboxylate oxidase 4 (ACC oxidase 4) (EC 1.14.17.4) (Ethylene-forming enzyme) (EFE) (Protein pHTOM5)
T3	Up	TFT10	14310_SOLLC		14-3-3 protein 10
T3	Up	Solyc06g065560.1	K4C7I5_SOLLC	GO:0006633; GO:0016020; GO:0016747	3-ketoacyl-CoA synthase (EC 2.3.1.-)
T3	Up	CHI3	CHIA_SOLLC	GO:0016998; GO:0006032; GO:0004568; GO:0006952; GO:0005615; GO:0000272; GO:0009607	Acidic 26 kDa endochitinase (EC 3.2.1.14)
T3	Up	Solyc10g076480.1	K4D1Z0_SOLLC	GO:0006888; GO:0000165; GO:0009738; GO:0043090; GO:0015802; GO:0006995; GO:0042742; GO:0050832; GO:0009595; GO:0009581; GO:0030968; GO:0015398; GO:0016021; GO:0009867; GO:0031348; GO:0043069; GO:0006862; GO:0005886; GO:0009506; GO:0006612; GO:0010310; GO:0043269; GO:0043900; GO:0010363; GO:0010200; GO:0009409; GO:0009750; GO:0009749; GO:0002237; GO:0009744; GO:0009697; GO:0009862	Ammonium transporter
T3	Up	AGP-1c	Q43719_SOLLC		Arabinogalactan (Putative arabinogalactan-protein) (Uncharacterized protein)
T3	Up	AADC1A	Q1KSC6_SOLLC	GO:0016831; GO:0019752; GO:0030170	Aromatic amino acid decarboxylase 1A (Uncharacterized protein)
T3	Up	Solyc06g062920.2	Q94FU1_SOLLC	GO:0005524; GO:0004674	Auxin-regulated dual specificity cytosolic kinase (Uncharacterized protein)
T3	Up	ZIP	C0KYN1_SOLLC	GO:0043565; GO:0003700	BZIP transcription factor (Uncharacterized protein)

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Up	Solyc02g064680.2	K4B6Q4_SOLLC	GO:0005524; GO:0005388; GO:0016021; GO:0046872	Calcium-transporting ATPase (EC 3.6.3.8)
T3	Up	CHS2	K4C235_SOLLC	GO:0009058; GO:0016747	Chalcone synthase 2
T3	Up	Solyc04g080820.2	I0IUQ7_SOLLC	GO:0008762; GO:0009823; GO:0019139; GO:0005615; GO:0050660; GO:0009694; GO:0009753	Cytokinin oxidase/dehydrogenase-like (Uncharacterized protein)
T3	Up	ERF1	Q8S9H4_SOLLC	GO:0003677; GO:0009873; GO:0009740; GO:0005634; GO:0010162; GO:0003700; GO:0006351	Ethylene response factor 1 (Ethylene-responsive transcription factor 1)
T3	Up	hsc70.3	H1ZXA9_SOLLC	GO:0005524	Heat shock protein 70 isoform 3 (Uncharacterized protein)
T3	Up	ht2	Q9STA8_SOLLC	GO:0043090; GO:0005358; GO:0016021; GO:0005886; GO:0009506	Hexose transporter (Uncharacterized protein)
T3	Up	Solyc03g026230.1	K4BF96_SOLLC	GO:0015297; GO:0015238; GO:0016021	MATE efflux family protein
T3	Up	Solyc02g092800.2	Q84LR0_SOLLC	GO:0016020; GO:0005215	Metal transporter (Uncharacterized protein)
T3	Up	THT1-3	Q8RXB8_SOLLC	GO:0008080	N-hydroxycinnamoyl-CoA:tyramine N-hydroxycinnamoyl transferase THT1-3 (Uncharacterized protein)
T3	Up	Solyc08g067310.1	K4CLV7_SOLLC	GO:0005524; GO:0004674; GO:0007165	Non-specific serine/threonine protein kinase (EC 2.7.11.1)
T3	Up	Solyc02g090490.2	K4BCJ8_SOLLC	GO:0016787; GO:0016042	Patatin (EC 3.1.1.-)
T3	Up	PTI5	PTI5_SOLLC	GO:0003677; GO:0006952; GO:0005634; GO:0003700; GO:0006351	Pathogenesis-related genes transcriptional activator PTI5 (PTO-interacting protein 5)
T3	Up	Solyc09g007010.1	PR04_SOLLC	GO:0006952; GO:0005576; GO:0009607	Pathogenesis-related leaf protein 4 (P4)
T3	Up	Solyc09g082870.1	K4CVR3_SOLLC	GO:0005524; GO:0005388; GO:0016021; GO:0046872	Calcium-transporting ATPase (EC 3.6.3.8)
T3	Up	Solyc01g097240.2	PRP2_SOLLC	GO:0005618; GO:0042742; GO:0050832; GO:0005576	Pathogenesis-related protein P2

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Up	Solyc02g093580.2	K4BDF4_SOLLC	GO:0046872; GO:0030570; GO:0045490	Pectate lyase (EC 4.2.2.2)
T3	Up	Solyc03g006700.2	K4BE93_SOLLC	GO:0005576; GO:0020037; GO:0046872; GO:0004601; GO:0006979	Peroxidase (EC 1.11.1.7)
T3	Up	Solyc02g092580.2	K4BD54_SOLLC	GO:0005576; GO:0020037; GO:0046872; GO:0004601; GO:0006979	Peroxidase (EC 1.11.1.7)
T3	Up	Solyc06g050440.2	K4C5I8_SOLLC	GO:0005576; GO:0020037; GO:0046872; GO:0004601; GO:0006979	Peroxidase (EC 1.11.1.7)
T3	Up	CEVI-1	K4ASJ6_SOLLC	GO:0005576; GO:0020037; GO:0046872; GO:0004601; GO:0006979	Peroxidase (EC 1.11.1.7)
T3	Up	Solyc09g090980.2	K4CWC4_SOLLC	GO:0006952; GO:0009607	PR10 protein (Uncharacterized protein)
T3	Up	Solyc09g090990.2	K4CWC5_SOLLC	GO:0006952; GO:0009607	PR10 protein (Uncharacterized protein)
T3	Up	Asc-1	K4BKW2_SOLLC	GO:0016021	Protein ASC1
T3	Up	Solyc06g069040.2	Q9FT20_SOLLC	GO:0016740	Putative glutathione S-transferase T4 (Uncharacterized protein)
T3	Up	Solyc04g077270.2	K4BUG4_SOLLC	GO:0005524; GO:0004674; GO:0048544	Serine/threonine-protein kinase (EC 2.7.11.1)
T3	Up	Solyc03g097610.2	K4BJH8_SOLLC	GO:0008643; GO:0016021	Sugar transporter SWEET
T3	Up	Solyc07g009500.1	K4CC70_SOLLC	GO:0008061	Uncharacterized protein
T3	Up	Solyc08g079900.1	K4CNZ0_SOLLC	GO:0004252	Uncharacterized protein
T3	Up	Solyc05g051530.2	K4C1I4_SOLLC	GO:0005524; GO:0016887; GO:0016020	Uncharacterized protein
T3	Up	Solyc03g122120.2	K4BN10_SOLLC	GO:0006633; GO:0016747	Uncharacterized protein
T3	Up	Solyc06g030470.2	K4C4H1_SOLLC	GO:0005886	Uncharacterized protein
T3	Up	Solyc05g005200.2	K4BW51_SOLLC	GO:0005829; GO:0006635; GO:0046482; GO:0016920	Uncharacterized protein
T3	Up	Solyc03g116700.2	K4BLH2_SOLLC	GO:0009055	Uncharacterized protein
T3	Up	Solyc03g097170.2	K4BJD4_SOLLC	GO:0003854; GO:0006694	Uncharacterized protein
T3	Up	Solyc05g041910.2	K4C0H2_SOLLC	GO:0016021; GO:0055114	Uncharacterized protein
T3	Up	Solyc08g067340.2	K4CLW0_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Up	Solyc02g093860.2	K4BDI2_SOLLC	GO:0016021	Uncharacterized protein
T3	Up	Solyc08g077110.2	K4CN71_SOLLC	GO:0003677; GO:0005634; GO:0006355; GO:0006351	Uncharacterized protein
T3	Up	Solyc12g057160.1	K4DG46_SOLLC		Uncharacterized protein
T3	Up	Solyc04g078290.2	K4BUR6_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T3	Up	Solyc05g051460.2	K4C1H7_SOLLC	GO:0005634; GO:0043565; GO:0003700; GO:0006351	Uncharacterized protein
T3	Up	Solyc02g093230.2	K4BDB9_SOLLC	GO:0008171	Uncharacterized protein
T3	Up	Solyc04g074680.1	K4BU06_SOLLC		Uncharacterized protein
T3	Up	Solyc08g067360.2	K4CLW2_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T3	Up	Solyc07g008140.2	K4CBT3_SOLLC	GO:0009055	Uncharacterized protein
T3	Up	Solyc06g008870.2	K4C3R7_SOLLC	GO:0016787	Uncharacterized protein
T3	Up	Solyc05g009420.1	K4BXB6_SOLLC		Uncharacterized protein
T3	Up	Solyc11g010390.1	K4D5K0_SOLLC		Uncharacterized protein
T3	Up	Solyc07g008590.1	K4CBX8_SOLLC		Uncharacterized protein
T3	Up	Solyc02g090820.2	K4BCN1_SOLLC	GO:0030968; GO:0042538; GO:0045892; GO:0005634; GO:0009737; GO:0010583; GO:0009408; GO:0009414; GO:0043565; GO:0003700; GO:0009407; GO:0006351	Uncharacterized protein
T3	Up	AO	K4BSL7_SOLLC	GO:0005507; GO:0005576; GO:0016491	Uncharacterized protein
T3	Up	Solyc10g055740.1	K4D1G4_SOLLC	GO:0016021	Uncharacterized protein
T3	Up	Solyc02g063440.2	K4B6M9_SOLLC		Uncharacterized protein
T3	Up	Solyc09g011590.2	K4CRI5_SOLLC		Uncharacterized protein
T3	Up	Solyc03g113520.2	K4BKK4_SOLLC	GO:0005794; GO:0030246; GO:0008378; GO:0016021; GO:0006486	Uncharacterized protein
T3	Up	Solyc03g117860.2	K4BLT7_SOLLC	GO:0003676; GO:0008270	Uncharacterized protein
T3	Up	Solyc05g009040.2	K4BX78_SOLLC	GO:0005524; GO:0004674	Uncharacterized protein
T3	Up	Solyc03g097050.2	K4BJC2_SOLLC	GO:0030244; GO:0016760; GO:0016021	Uncharacterized protein

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Up	Solyc04g079940.2	K4BV73_SOLLC	GO:0003677; GO:0005634; GO:0006355; GO:0006351	Uncharacterized protein
T3	Up	Solyc02g078400.2	K4B964_SOLLC	GO:0000256; GO:0004038; GO:0050897; GO:0005783; GO:0010136; GO:0008270	Uncharacterized protein
T3	Up	Solyc07g056190.2	K4CGF2_SOLLC		Uncharacterized protein
T3	Up	Solyc03g013160.2	K4BEN7_SOLLC	GO:0016021	Uncharacterized protein
T3	Up	Solyc09g005730.2	K4CQ63_SOLLC		Uncharacterized protein
T3	Up	Solyc03g094160.2	K4BIU1_SOLLC	GO:0004197	Uncharacterized protein
T3	Up	Solyc09g097960.2	K4CWW8_SOLLC		Uncharacterized protein
T3	Up	Solyc02g036480.1	K4B5U1_SOLLC		Uncharacterized protein
T3	Up	Solyc03g033790.2	K4BFQ1_SOLLC	GO:0005524	Uncharacterized protein
T3	Up	Solyc10g075150.1	K4D1V6_SOLLC	GO:0008289; GO:0006869	Uncharacterized protein
T3	Up	Solyc10g005320.2	K4CX65_SOLLC	GO:0004834	Uncharacterized protein
T3	Up	Solyc03g082370.1	K4BI14_SOLLC		Uncharacterized protein
T3	Up	Solyc10g055200.1	K4D1B3_SOLLC		Uncharacterized protein
T3	Up	Solyc12g056360.1	K4DFW7_SOLLC		Uncharacterized protein
T3	Up	Solyc03g025670.2	K4BF40_SOLLC		Uncharacterized protein
T3	Up	Solyc03g083400.2	K4BIB6_SOLLC		Uncharacterized protein
T3	Up	Solyc07g041620.1	K4CE30_SOLLC		Uncharacterized protein
T3	Up	Solyc07g045530.1	K4CEV9_SOLLC		Uncharacterized protein
T3	Up	Solyc01g108050.2	K4B321_SOLLC		Uncharacterized protein
T3	Up	Solyc03g083560.1	K4BID2_SOLLC		Uncharacterized protein
T3	Up	TOMQ`B	K4D2M7_SOLLC	GO:0005975; GO:0004553	Uncharacterized protein
T3	Up	Solyc01g010060.2	K4ATK1_SOLLC		Uncharacterized protein
T3	Up	Wiv-1	Q8LRN8_SOLLC	GO:0005975; GO:0004553	Cell-wall invertase (Uncharacterized protein)
T3	Up	Solyc11g069940.1	K4DAF0_SOLLC	GO:0045454; GO:0009055; GO:0015035	Uncharacterized protein
T3	Up	Solyc05g007890.2	K4BWW4_SOLLC	GO:0003677; GO:0003682; GO:0009736; GO:0003700	Uncharacterized protein
T3	Up	Solyc02g032950.2	K4B5N8_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T3	Up	Solyc07g056200.2	K4CGF3_SOLLC		Uncharacterized protein
T3	Up	Solyc04g072070.2	K4BTJ4_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T3	Up	Solyc03g119600.1	K4BMA9_SOLLC		Uncharacterized protein

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Up	Solyc01g102310.2	K4B1F9_SOLLC		Uncharacterized protein
T3	Up	Solyc12g049030.1	K4DFI4_SOLLC	GO:0006629; GO:0016717	Uncharacterized protein
T3	Up	Solyc02g090360.2	K4BCI5_SOLLC	GO:0005507; GO:0016491	Uncharacterized protein
T3	Up	Solyc03g031420.1	K4BFB4_SOLLC	GO:0003824; GO:0030170	Uncharacterized protein
T3	Up	Solyc09g005260.2	K4CQ16_SOLLC	GO:0015369; GO:0016021	Uncharacterized protein
T3	Up	Solyc03g078490.2	K4BHS7_SOLLC	GO:0016758	Uncharacterized protein
T3	Up	Solyc01g010230.2	K4ATL8_SOLLC		Uncharacterized protein
T3	Up	Solyc10g076500.1	K4D1Z2_SOLLC		Uncharacterized protein
T3	Up	Solyc09g011490.2	K4CRH5_SOLLC		Uncharacterized protein
T3	Up	Solyc02g082740.1	K4BAE4_SOLLC		Uncharacterized protein
T3	Up	Solyc04g054500.2	K4BSK5_SOLLC	GO:0046872; GO:0030001	Uncharacterized protein
T3	Up	Solyc12g096960.1	K4DHG9_SOLLC	GO:0006952; GO:0009607	Uncharacterized protein
T3	Up	Solyc10g085010.1	K4D3T5_SOLLC		Uncharacterized protein
T3	Up	Solyc01g079580.2	K4AXK3_SOLLC		Uncharacterized protein
T3	Up	Solyc09g011860.2	K4CRL2_SOLLC		Uncharacterized protein
T3	Up	Solyc04g007380.1	K4BNP5_SOLLC	GO:0005524; GO:0004674	Uncharacterized protein
T3	Up	Solyc08g077480.2	K4CNA7_SOLLC		Uncharacterized protein
T3	Up	Solyc12g100270.1	K4DI48_SOLLC	GO:0006633; GO:0016021; GO:0005506; GO:0016491	Uncharacterized protein
T3	Up	Solyc01g088660.2	K4AYQ6_SOLLC		Uncharacterized protein
T3	Up	Solyc03g034370.1	K4BFV7_SOLLC		Uncharacterized protein
T3	Up	Solyc09g097810.2	K4CWV3_SOLLC		Uncharacterized protein
T3	Up	Solyc10g007280.2	K4CXQ7_SOLLC	GO:0005524	Uncharacterized protein
T3	Up	Solyc01g008620.2	K4AT60_SOLLC	GO:0005975; GO:0004553	Uncharacterized protein
T3	Up	Solyc03g121660.2	K4BMW5_SOLLC	GO:0046872; GO:0003676	Uncharacterized protein
T3	Up	Solyc04g077230.1	K4BUG0_SOLLC		Uncharacterized protein
T3	Up	Solyc06g062420.2	K4C6X3_SOLLC		Uncharacterized protein
T3	Up	Solyc07g054850.2	K4CG27_SOLLC	GO:0046658	Uncharacterized protein
T3	Up	Solyc04g051690.2	K4BSC8_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T3	Up	Solyc07g005100.2	K4CAY2_SOLLC	GO:0005975; GO:0006032; GO:0004568	Uncharacterized protein
T3	Up	pip1	K4B8T1_SOLLC	GO:0008234	Uncharacterized protein
T3	Up	Solyc01g087020.2	K4AY95_SOLLC		Uncharacterized protein

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Up	Solyc01g089880.2	K4AYS9_SOLLC		Uncharacterized protein
T3	Up	Solyc03g083460.2	K4BIC2_SOLLC	GO:0030247; GO:0008270	Uncharacterized protein
T3	Up	Solyc05g050130.2	K4C145_SOLLC	GO:0006032; GO:0004568; GO:0005615; GO:0050665; GO:0000272; GO:0016926; GO:0010228	Uncharacterized protein
T3	Up	Solyc02g062550.2	K4B6E3_SOLLC	GO:0005524	Uncharacterized protein
T3	Up	Solyc03g095770.2	K4BIZ9_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T3	Up	Solyc04g007140.1	K4BNM1_SOLLC		Uncharacterized protein
T3	Up	Solyc09g097760.2	K4CWU8_SOLLC		Uncharacterized protein
T3	Up	Solyc00g206460.1	K4ARX5_SOLLC		Uncharacterized protein
T3	Up	Solyc04g009640.2	K4BPB9_SOLLC	GO:0005524; GO:0016021; GO:0004674	Uncharacterized protein
T3	Up	Solyc10g009410.1	K4CYB7_SOLLC	GO:0004190	Uncharacterized protein
T3	Up	Solyc07g009230.2	K4CC42_SOLLC	GO:0006952	Uncharacterized protein
T3	Up	Solyc03g005980.2	K4BE21_SOLLC	GO:0016021; GO:0005215	Uncharacterized protein
T3	Up	Solyc08g068710.1	K4CM93_SOLLC	GO:0008080	Uncharacterized protein
T3	Up	Solyc03g122350.2	K4BN33_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T3	Up	Solyc03g115930.1	K4BL95_SOLLC	GO:0005509	Uncharacterized protein
T3	Up	ail	K4CKN7_SOLLC		Uncharacterized protein
T3	Up	Solyc09g065890.2	K4CUL5_SOLLC	GO:0016787; GO:0006629	Uncharacterized protein
T3	Up	Solyc03g119590.1	K4BMA8_SOLLC		Uncharacterized protein
T3	Up	Solyc09g091000.2	K4CWC6_SOLLC	GO:0006952; GO:0009607	Uncharacterized protein
T3	Up	Solyc04g071780.2	K4BTG8_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T3	Up	Solyc09g011560.2	K4CRI2_SOLLC		Uncharacterized protein
T3	Up	Solyc12g057150.1	K4DG45_SOLLC		Uncharacterized protein
T3	Up	Solyc04g054760.2	K4BSM4_SOLLC		Uncharacterized protein
T3	Up	Solyc04g078340.2	K4BUS0_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T3	Up	Solyc11g005150.1	K4D4C8_SOLLC		Uncharacterized protein
T3	Up	Solyc12g036390.1	K4DE96_SOLLC		Uncharacterized protein

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Up	Solyc11g018800.1	K4D6T3_SOLLC	GO:0020037; GO:0004601; GO:0006979	Uncharacterized protein
T3	Up	Solyc07g062490.1	K4CGT2_SOLLC		Uncharacterized protein
T3	Up	Solyc11g030730.1	K4D7K8_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T3	Up	Solyc04g005100.2	K4BNB6_SOLLC	GO:0003677; GO:0003682	Uncharacterized protein
T3	Up	Solyc08g068770.1	K4CM99_SOLLC	GO:0008080	Uncharacterized protein
T3	Up	Solyc04g077140.2	K4BUF1_SOLLC		Uncharacterized protein
T3	Up	Solyc03g114100.1	K4BKR2_SOLLC		Uncharacterized protein
T3	Up	GGPS1	K4D5T0_SOLLC	GO:0008299; GO:0016740	Uncharacterized protein
T3	Up	Solyc02g069800.1	K4B7W2_SOLLC	GO:0016787	Uncharacterized protein
T3	Up	Solyc02g091380.1	K4BCT6_SOLLC		Uncharacterized protein
T3	Up	Solyc06g074530.1	K4C9H1_SOLLC	GO:0009094; GO:0016597; GO:0004664	Uncharacterized protein
T3	Up	Solyc09g014990.2	K4CRX3_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T3	Up	Solyc06g007620.2	K4C3E3_SOLLC		Uncharacterized protein
T3	Up	Solyc08g007460.2	K4CIN3_SOLLC		Uncharacterized protein
T3	Up	Solyc01g100010.2	K4B135_SOLLC		Uncharacterized protein
T3	Up	Solyc05g006510.1	K4BWH7_SOLLC	GO:0016757	Uncharacterized protein
T3	Up	Solyc01g086640.2	K4AY57_SOLLC		Uncharacterized protein
T3	Up	Solyc06g048820.1	K4C5C8_SOLLC		Uncharacterized protein
T3	Up	Solyc07g042490.1	K4CEB0_SOLLC		Uncharacterized protein
T3	Up	Solyc07g054470.1	K4CFZ2_SOLLC		Uncharacterized protein
T3	Up	Solyc09g075910.1	K4CVG8_SOLLC	GO:0005524; GO:0004674; GO:0048544	Uncharacterized protein
T3	Up	Solyc12g042480.1	K4DF40_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T3	Up	Solyc07g014670.2	K4CC86_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T3	Up	Solyc03g121620.1	K4BMW1_SOLLC	GO:0005886; GO:0009506	Uncharacterized protein
T3	Up	Solyc06g061230.2	K4C6V3_SOLLC		Uncharacterized protein

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Up	Solyc04g079110.1	K4BUZ5_SOLLC	GO:0009742; GO:0005829; GO:0006629; GO:0010423; GO:0005886	Uncharacterized protein
T3	Up	Solyc09g015770.2	I3NN77_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein (WRKY3)
T3	Up	tXET-B2	Q43528_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T3	Up	LeXET2	Q9FZ05_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T3	Up	Solyc03g093120.2	K4BII9_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T3	Up	BR1	K4CWS8_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T3	Up	Solyc03g093110.2	K4BII8_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T3	Up	Solyc12g011030.1	K4DCI9_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T3	Down	Solyc05g009270.2	K4BXA1_SOLLC	GO:0006633; GO:0016020; GO:0016747	3-ketoacyl-CoA synthase (EC 2.3.1.-)
T3	Down	CYP707A1	A9QNE7_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	ABA 8'-hydroxylase (Uncharacterized protein)
T3	Down	LEAGAL	K4BEV1_SOLLC	GO:0009965; GO:0000023; GO:0007020; GO:0009505; GO:0043085; GO:0009911; GO:0052692; GO:0019252	Alpha-galactosidase (EC 3.2.1.22) (Melibiase)
T3	Down	Solyc06g053840.2	G9HPV5_SOLLC	GO:0009734; GO:0005634; GO:0006355; GO:0006351	Auxin-responsive protein
T3	Down	Solyc06g053830.2	G9HPV6_SOLLC	GO:0009734; GO:0005634; GO:0006355; GO:0006351	Auxin-responsive protein

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Down	Solyc06g072350.2	K4C8V5_SOLLC	GO:0016021; GO:0005886	CASP-like protein
T3	Down	cathDInh	Q9LEG1_SOLLC	GO:0004866	Cathepsin D Inhibitor (Uncharacterized protein)
T3	Down	CAB1B	CB2B_SOLLC	GO:0016168; GO:0009535; GO:0016021; GO:0046872; GO:0009765; GO:0009522; GO:0009523; GO:0018298	Chlorophyll a-b binding protein 1B, chloroplastic (LHCII type I CAB-1B) (LHCP)
T3	Down	Solyc06g069730.2	Q7M1K8_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0046872; GO:0009765; GO:0009522; GO:0009523; GO:0018298	Chlorophyll a/b-binding protein (cab-12) (Uncharacterized protein)
T3	Down	Solyc07g006630.2	B2MW87_SOLLC	GO:0005622; GO:0008270	CONSTANS-like protein (Hop-interacting protein THI010) (Uncharacterized protein)
T3	Down	Solyc11g006250.1	G1DEX3_SOLLC	GO:0005576; GO:0016788; GO:0016042	Cutin-deficient 1 protein (Uncharacterized protein)
T3	Down	Cel1	Q42871_SOLLC	GO:0008810; GO:0030245	Endoglucanase (EC 3.2.1.4)
T3	Down	Solyc09g075360.2	Q42875_SOLLC	GO:0008810; GO:0030245	Endoglucanase (EC 3.2.1.4)
T3	Down	Solyc04g081300.2	K4BVK9_SOLLC	GO:0008810; GO:0030245	Endoglucanase (EC 3.2.1.4)
T3	Down	Solyc01g110340.2	K4B3P7_SOLLC	GO:0008810; GO:0030245	Endoglucanase (EC 3.2.1.4)
T3	Down	ERF4	Q84XB0_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	Ethylene response factor 4 (Uncharacterized protein)
T3	Down	LeEXP2 EXP2 exp2	O82625_SOLLC	GO:0005618; GO:0005576; GO:0016020; GO:0009664	Expansin (Expansin2) (Uncharacterized protein)
T3	Down	EXPA4	Q9ZP32_SOLLC	GO:0005618; GO:0005576; GO:0016020; GO:0009664	Expansin (Uncharacterized protein)
T3	Down	GA20OX1	Q9ZPP4_SOLLC	GO:0005506; GO:0016706	Gibberellin 20-oxidase-1 (Uncharacterized protein)
T3	Down	Solyc04g014510.2	K4BPV5_SOLLC	GO:0005524; GO:0004356; GO:0006542	Glutamine synthetase (EC 6.3.1.2)
T3	Down	Solyc08g076820.2	G8Z255_SOLLC	GO:0003677; GO:0007275; GO:0005634; GO:0003700; GO:0006351	Hop-interacting protein THI018 (Uncharacterized protein)
T3	Down	Solyc08g067530.1	K4CLX9_SOLLC	GO:0008289; GO:0006869	Non-specific lipid-transfer protein

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Down	Solyc06g007440.2	K4C3C6_SOLLC	GO:0005524; GO:0004674; GO:0007165	Non-specific serine/threonine protein kinase (EC 2.7.11.1)
T3	Down	Solyc02g072540.2	K4B8M8_SOLLC	GO:0005524; GO:0004674; GO:0007165	Non-specific serine/threonine protein kinase (EC 2.7.11.1)
T3	Down	Solyc05g014000.2	K4BYC1_SOLLC	GO:0046872; GO:0030570; GO:0045490	Pectate lyase (EC 4.2.2.2)
T3	Down	Solyc02g080210.2	K4B9P2_SOLLC	GO:0045330; GO:0005618; GO:0042545; GO:0004857; GO:0045490; GO:0030599	Pectinesterase (EC 3.1.1.11)
T3	Down	GP3	GP3_SOLLC	GO:0048046; GO:0005618; GO:0071555	Polygalacturonase non-catalytic subunit AroGP3
T3	Down	ARPI	IP22_SOLLC	GO:0004867	Proteinase inhibitor type-2 TR8 (Proteinase inhibitor type II TR8)
T3	Down	spe4	Q70AG5_SOLLC	GO:0003824	Putative spermine synthase (Uncharacterized protein)
T3	Down	Solyc06g053260.1	I3RSI1_SOLLC		Small auxin-up protein 58 (Uncharacterized protein)
T3	Down	Solyc05g024260.2	K4BZR4_SOLLC	GO:0071470; GO:0005887; GO:0008515	Sugar transporter SWEET
T3	Down	Solyc06g071320.2	Q53J17_SOLLC		T10O24.15, related (Uncharacterized protein)
T3	Down	TD	THD1_SOLLC	GO:0004794; GO:0009507; GO:0009097; GO:0030170	Threonine dehydratase biosynthetic, chloroplastic (EC 4.3.1.19) (Threonine deaminase) (TD)
T3	Down	Solyc07g007150.1	K4CBI6_SOLLC		Uncharacterized protein
T3	Down	Solyc01g102610.2	K4B1I9_SOLLC	GO:0016021; GO:0016491	Uncharacterized protein
T3	Down	Solyc12g096490.1	K4DHC2_SOLLC		Uncharacterized protein
T3	Down	Solyc04g008260.2	K4BNY2_SOLLC	GO:0003993	Uncharacterized protein
T3	Down	Solyc06g083470.2	K4CAK2_SOLLC	GO:0016491	Uncharacterized protein
T3	Down	Solyc01g007810.1	K4ASX9_SOLLC		Uncharacterized protein
T3	Down	Solyc05g012110.2	K4BXT4_SOLLC	GO:0017057; GO:0005975; GO:0006098	Uncharacterized protein
T3	Down	Solyc11g072110.1	K4DAR8_SOLLC	GO:0046872; GO:0016706	Uncharacterized protein

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Down	Solyc06g072710.2	K4C8Z1_SOLLC	GO:0003677; GO:0006352; GO:0003700; GO:0016987	Uncharacterized protein
T3	Down	Solyc03g121900.1	K4BMY8_SOLLC		Uncharacterized protein
T3	Down	Solyc01g095530.2	K4AZU2_SOLLC		Uncharacterized protein
T3	Down	Solyc06g051940.2	K4C5Y0_SOLLC	GO:0046872; GO:0006470; GO:0004722	Uncharacterized protein
T3	Down	Solyc01g111570.2	K4B419_SOLLC	GO:0005524; GO:0004674; GO:0006950	Uncharacterized protein
T3	Down	Solyc04g015620.2	K4BQ64_SOLLC		Uncharacterized protein
T3	Down	Solyc12g044330.1	K4DFC1_SOLLC	GO:0016021; GO:0005215	Uncharacterized protein
T3	Down	Solyc02g071380.2	K4B8B4_SOLLC	GO:0046872; GO:0016706	Uncharacterized protein
T3	Down	Solyc02g070980.1	K4B876_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0046872; GO:0009765; GO:0009522; GO:0009523; GO:0018298	Uncharacterized protein
T3	Down	Solyc08g006160.2	K4CIA5_SOLLC	GO:0030003; GO:0009941; GO:0009534; GO:0019344; GO:0070838; GO:0019761; GO:0019684; GO:0035304; GO:0005198	Uncharacterized protein
T3	Down	Solyc11g010410.1	K4D5K2_SOLLC	GO:0046872; GO:0016706	Uncharacterized protein
T3	Down	Solyc07g049440.2	K4CF47_SOLLC	GO:0005576; GO:0016788; GO:0016042	Uncharacterized protein
T3	Down	Solyc07g007260.2	K4CBJ6_SOLLC		Uncharacterized protein
T3	Down	Solyc09g010220.2	K4CR50_SOLLC	GO:0008236	Uncharacterized protein
T3	Down	Solyc05g054320.2	K4C2B1_SOLLC	GO:0003824	Uncharacterized protein
T3	Down	Solyc07g005390.2	K4CB11_SOLLC	GO:0005737; GO:0008886	Uncharacterized protein
T3	Down	Solyc07g043130.2	K4CEH3_SOLLC	GO:0007030; GO:0006816; GO:0019344; GO:0005737; GO:0010227; GO:0048439; GO:0005634; GO:0009638; GO:0016567; GO:0009954; GO:0009651; GO:0004871	Uncharacterized protein
T3	Down	Solyc07g054210.2	K4CFW6_SOLLC	GO:0016630	Uncharacterized protein

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Down	Solyc03g119860.2	K4BMD5_SOLLC	GO:0009507; GO:0019288; GO:0016556; GO:0003755; GO:0006457	Uncharacterized protein
T3	Down	Solyc09g009420.1	K4CQX1_SOLLC	GO:0009813; GO:0010224; GO:0009744	Uncharacterized protein
T3	Down	Solyc07g007240.2	K4CBJ5_SOLLC		Uncharacterized protein
T3	Down	Solyc06g005750.2	K4C357_SOLLC	GO:0006633; GO:0016021; GO:0005506; GO:0016491	Uncharacterized protein
T3	Down	Solyc04g008040.2	K4BNW0_SOLLC	GO:0007010	Uncharacterized protein
T3	Down	Solyc04g007500.1	K4BNQ7_SOLLC	GO:0008270	Uncharacterized protein
T3	Down	Solyc01g009080.2	K4ATA4_SOLLC	GO:0009570; GO:0009535; GO:0000023; GO:0006098; GO:0010207; GO:0009657; GO:0043085; GO:0006364; GO:0019252; GO:0010103	Uncharacterized protein
T3	Down	Solyc02g071000.1	K4B878_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0046872; GO:0009765; GO:0009522; GO:0009523; GO:0018298	Uncharacterized protein
T3	Down	Solyc03g116730.2	K4BLH5_SOLLC	GO:0006633; GO:0016021; GO:0016717	Uncharacterized protein
T3	Down	Solyc01g087710.2	K4AYG1_SOLLC		Uncharacterized protein
T3	Down	Solyc05g043330.2	K4C0L5_SOLLC	GO:0016788; GO:0006629	Uncharacterized protein
T3	Down	Solyc07g021530.2	K4CD09_SOLLC		Uncharacterized protein
T3	Down	Solyc08g067320.1	K4CLV8_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0009765; GO:0009523; GO:0018298	Uncharacterized protein
T3	Down	Solyc03g097380.2	K4BJF5_SOLLC	GO:0046872; GO:0030001	Uncharacterized protein
T3	Down	Solyc09g007150.2	K4CQA5_SOLLC		Uncharacterized protein
T3	Down	Solyc06g084140.2	K4CAR9_SOLLC	GO:0009507; GO:0016021; GO:0008271	Uncharacterized protein
T3	Down	Solyc06g060640.1	K4C6P4_SOLLC		Uncharacterized protein
T3	Down	Solyc11g010960.1	K4D5Q4_SOLLC	GO:0016491; GO:0008270	Uncharacterized protein

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Down	Solyc09g014350.2	K4CRR2_SOLLC	GO:0010143; GO:0009908; GO:0090447; GO:0016021; GO:0016791; GO:0006655	Uncharacterized protein
T3	Down	Solyc12g009200.1	K4DC08_SOLLC	GO:0030003; GO:0016168; GO:0009507; GO:0070838; GO:0019761; GO:0016021; GO:0019288; GO:0046872; GO:0006098; GO:0009765; GO:0009522; GO:0009523; GO:0018298; GO:0006364; GO:0010155; GO:0009644; GO:0009744	Uncharacterized protein
T3	Down	Solyc10g005400.2	K4CX72_SOLLC	GO:0005737; GO:0019310; GO:0050113; GO:0005506	Uncharacterized protein
T3	Down	Solyc01g091320.2	K4AZ72_SOLLC	GO:0006633; GO:0016021; GO:0005506; GO:0016491	Uncharacterized protein
T3	Down	Solyc04g054370.1	K4BSJ2_SOLLC	GO:0008270	Uncharacterized protein
T3	Down	Solyc07g055260.2	K4CG65_SOLLC	GO:0009507; GO:0009055; GO:0005506; GO:0051536; GO:0006950	Uncharacterized protein
T3	Down	Solyc10g009150.2	K4CY91_SOLLC		Uncharacterized protein
T3	Down	Solyc12g011010.1	K4DCI7_SOLLC		Uncharacterized protein
T3	Down	Solyc04g015750.2	K4BQ77_SOLLC	GO:0005524; GO:0015995; GO:0009706; GO:0009570; GO:0016851; GO:0010007; GO:0005739; GO:0019684	Uncharacterized protein
T3	Down	Solyc01g073680.2	K4AXB4_SOLLC		Uncharacterized protein
T3	Down	Solyc06g069760.2	K4C8E8_SOLLC	GO:0003677; GO:0006355	Uncharacterized protein
T3	Down	Solyc03g110860.2	K4BJU9_SOLLC	GO:0016602; GO:0009738; GO:0043565; GO:0003700; GO:0006351	Uncharacterized protein
T3	Down	Solyc10g008440.2	K4CY21_SOLLC	GO:0005576; GO:0019953	Uncharacterized protein

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Down	Solyc01g086920.2	K4AY85_SOLLC	GO:0006281; GO:0009507; GO:0016301; GO:0000166; GO:0009411; GO:0042493	Uncharacterized protein
T3	Down	Solyc06g062370.2	K4C6W8_SOLLC	GO:0003993	Uncharacterized protein
T3	Down	Solyc06g069150.1	K4C888_SOLLC		Uncharacterized protein
T3	Down	Solyc07g052950.2	K4CFJ3_SOLLC		Uncharacterized protein
T3	Down	Solyc10g005030.2	K4CX37_SOLLC	GO:0000160	Uncharacterized protein
T3	Down	Solyc07g045080.2	K4CER6_SOLLC	GO:0016491; GO:0008270	Uncharacterized protein
T3	Down	Solyc06g064550.2	K4C785_SOLLC	GO:0050661; GO:0016597; GO:0004072; GO:0008652; GO:0016491	Uncharacterized protein
T3	Down	Solyc05g051580.2	K4C1I9_SOLLC	GO:0010588; GO:0010305; GO:0010087; GO:0080022; GO:0016567	Uncharacterized protein
T3	Down	Solyc03g111100.1	K4BJX3_SOLLC		Uncharacterized protein
T3	Down	Solyc01g017600.2	K4AUU1_SOLLC		Uncharacterized protein
T3	Down	Solyc02g063000.2	K4B6I8_SOLLC	GO:0016758	Uncharacterized protein
T3	Down	Solyc11g056680.1	K4D8X9_SOLLC		Uncharacterized protein
T3	Down	Solyc01g090970.2	K4AZ37_SOLLC	GO:0005576	Uncharacterized protein
T3	Down	Solyc07g042390.1	K4CEA0_SOLLC	GO:0004857; GO:0030599	Uncharacterized protein
T3	Down	Solyc01g106960.2	K4B2R3_SOLLC		Uncharacterized protein
T3	Down	Solyc05g056050.2	K4C2T0_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0046872; GO:0009765; GO:0009522; GO:0009523; GO:0018298	Uncharacterized protein
T3	Down	Solyc07g055950.2	K4CGC8_SOLLC		Uncharacterized protein
T3	Down	Solyc06g073290.1	K4C948_SOLLC	GO:0009073; GO:0016117; GO:0030154; GO:0015995; GO:0031969; GO:0010019; GO:0019344; GO:0009965; GO:0006098; GO:0010207; GO:0043085; GO:0045893; GO:0006364; GO:0046906	Uncharacterized protein
T3	Down	Solyc06g066420.2	K4C7R8_SOLLC		Uncharacterized protein

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Down	Solyc01g099020.2	K4B0T9_SOLLC	GO:0016788; GO:0006629	Uncharacterized protein
T3	Down	Solyc12g087940.1	K4DGL5_SOLLC	GO:0004190	Uncharacterized protein
T3	Down	Solyc10g008710.2	K4CY48_SOLLC	GO:0016298; GO:0006629	Uncharacterized protein
T3	Down	Solyc08g067330.1	K4CLV9_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0009765; GO:0009523; GO:0018298	Uncharacterized protein
T3	Down	Solyc03g005790.2	K4BE02_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0009765; GO:0009523; GO:0018298	Uncharacterized protein
T3	Down	Solyc04g015030.2	K4BQ06_SOLLC	GO:0046872; GO:0030001	Uncharacterized protein
T3	Down	Solyc02g081980.2	K4BA68_SOLLC	GO:0016787	Uncharacterized protein
T3	Down	Solyc07g006570.2	K4CBC8_SOLLC	GO:0003723; GO:0033897	Uncharacterized protein
T3	Down	Solyc07g063600.2	K4CH43_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0046872; GO:0009765; GO:0009522; GO:0009523; GO:0018298	Uncharacterized protein
T3	Down	Solyc03g043740.2	K4BFZ5_SOLLC		Uncharacterized protein
T3	Down	Solyc01g087040.2	K4AY97_SOLLC	GO:0005509; GO:0009543; GO:0019898; GO:0015979; GO:0009654	Uncharacterized protein
T3	Down	Solyc12g006140.1	K4DBF1_SOLLC	GO:0016020; GO:0009765	Uncharacterized protein
T3	Down	Solyc08g075490.2	K4CMR6_SOLLC		Uncharacterized protein
T3	Down	Solyc05g005230.2	K4BW54_SOLLC		Uncharacterized protein
T3	Down	Solyc03g118310.2	K4BLY2_SOLLC		Uncharacterized protein
T3	Down	Solyc02g070990.1	K4B877_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0046872; GO:0009765; GO:0009522; GO:0009523; GO:0018298	Uncharacterized protein
T3	Down	Solyc06g069790.2	K4C8F1_SOLLC		Uncharacterized protein
T3	Down	Solyc01g112060.2	K4B467_SOLLC	GO:0016117; GO:0009534; GO:0019288; GO:0010207; GO:0006364; GO:0009637; GO:0010218; GO:0010114; GO:0003743	Uncharacterized protein

Table A.9 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Down	Solyc05g055400.2	K4C2L6_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T3	Down	Solyc03g006490.2	K4BE72_SOLLC		Uncharacterized protein
T3	Down	Solyc03g111550.2	K4BK18_SOLLC	GO:0005576; GO:0016788; GO:0016042	Uncharacterized protein
T3	Down	Solyc06g075170.1	K4C9N3_SOLLC		Uncharacterized protein
T3	Down	Solyc04g071960.2	K4BTI3_SOLLC	GO:0016491	Uncharacterized protein
T3	Down	Solyc07g014730.2	K4CC92_SOLLC	GO:0005794; GO:0005509; GO:0005576; GO:0016042; GO:0004623; GO:0006644; GO:0005773	Uncharacterized protein
T3	Down	Solyc05g056300.2	K4C2V4_SOLLC	GO:0045454; GO:0006662; GO:0015035	Uncharacterized protein
T3	Down	Solyc02g077330.2	K4B8W0_SOLLC	GO:0042335; GO:0005576; GO:0016788; GO:0016042; GO:0000038	Uncharacterized protein
T3	Down	Solyc08g079280.2	K4CNT6_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T3	Down	Solyc08g078870.1	K4CNP6_SOLLC		Uncharacterized protein
T3	Down	Solyc12g056980.1	K4DG29_SOLLC	GO:0003700	Uncharacterized protein
T3	Down	Solyc05g053760.2	K4C256_SOLLC		Uncharacterized protein
T3	Down	Solyc03g025410.2	K4BF14_SOLLC	GO:0016491	Uncharacterized protein
T3	Down	Solyc12g019550.1	K4DDI0_SOLLC	GO:0009534	Uncharacterized protein
T3	Down	Solyc07g061800.2	K4CGL3_SOLLC		Uncharacterized protein
T3	Down	Solyc09g075750.1	K4CVF2_SOLLC	GO:0009742; GO:0019210; GO:0006629; GO:0005886	Uncharacterized protein
T3	Down	Solyc09g008320.2	K4CQM0_SOLLC	GO:0048046; GO:0005618; GO:0042546; GO:0016998; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)

T1, T2, and T3 represent one, two, and four weeks after infestation, respectively.

Table A.10 List of DEGs with their associated GO terms resulted from the P vs L comparison

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T1	Up	Solyc01g097240.2	PRP2_SOLLC	GO:0005618; GO:0042742; GO:0050832; GO:0005576	Pathogenesis-related protein P2
T1	Up	LeEXP2	O82625_SOLLC	GO:0005618; GO:0005576; GO:0016020; GO:0009664	Expansin (Expansin2) (Uncharacterized protein)
T1	Up	Solyc10g005400.2	K4CX72_SOLLC	GO:0005737; GO:0019310; GO:0050113; GO:0005506	Uncharacterized protein
T1	Up	Solyc03g078490.2	K4BHS7_SOLLC	GO:0016758	Uncharacterized protein
T1	Up	Solyc07g053640.1	K4CFQ9_SOLLC		Uncharacterized protein
T1	Up	Solyc07g056640.1	K4CGJ6_SOLLC		Uncharacterized protein
T1	Down	ARG2	Q5UNS1_SOLLC	GO:0016813; GO:0046872	Arginase 2 (Uncharacterized protein)
T1	Down	Solyc06g007180.2	K4C3A1_SOLLC	GO:0005524; GO:0070981; GO:0004066; GO:0009063; GO:0006541; GO:0009646	Asparagine synthetase (EC 6.3.5.4)
T1	Down	CZFP1	A6ZIC0_SOLLC	GO:0046872	C2H2-type zinc finger protein (Cold zinc finger protein 1) (Uncharacterized protein)
T1	Down	Solyc09g082870.1	K4CVR3_SOLLC	GO:0005524; GO:0005388; GO:0016021; GO:0046872	Calcium-transporting ATPase (EC 3.6.3.8)
T1	Down	Solyc02g064680.2	K4B6Q4_SOLLC	GO:0005524; GO:0005388; GO:0016021; GO:0046872	Calcium-transporting ATPase (EC 3.6.3.8)
T1	Down	CBF1	Q8S9N5_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	CBF1 (Putative transcriptional activator CBF1) (Uncharacterized protein)
T1	Down	ERF3	Q84XB1_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	Ethylene response factor 3
T1	Down	EXLA1	A7X331_SOLLC	GO:0005576; GO:0019953	Expansin-like protein (Uncharacterized protein)
T1	Down	GRAS4	Q00LP5_SOLLC	GO:0006355; GO:0006351	GRAS4 (Uncharacterized protein)
T1	Down	Solyc12g005340.1	G8Z267_SOLLC	GO:0006355; GO:0006351	Hop-interacting protein THI039 (Uncharacterized protein)
T1	Down	LEMMI9	Q40159_SOLLC	GO:0009269	Late embryogenesis (Lea)-like protein (Uncharacterized protein)
T1	Down	LeMKK4 MKK4	Q66MH6_SOLLC	GO:0005524; GO:0004674	MAPKK (Uncharacterized protein)
T1	Down	Solyc04g005040.1	I7KJ40_SOLLC	GO:0031012; GO:0004222; GO:0008270	Matrix metalloproteinase (Uncharacterized protein)

Table A.10 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T1	Down	Solyc07g007250.2	MCPI_SOLLC	GO:0004866	Metallocarboxypeptidase inhibitor (Carboxypeptidase inhibitor) (MCPI)
T1	Down	Solyc04g071890.2	K4BTH6_SOLLC	GO:0020037; GO:0046872; GO:0004601; GO:0006979	Peroxidase (EC 1.11.1.7)
T1	Down	Solyc04g007000.1	E1U2K4_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	RAV1 (Uncharacterized protein)
T1	Down	Solyc01g086960.2	B6JU38_SOLLC	GO:0003677; GO:0006007; GO:0005634; GO:0051865; GO:0009414; GO:0004842; GO:0008270	Stress-associated protein 1 (Uncharacterized protein)
T1	Down	TD	THD1_SOLLC	GO:0004794; GO:0009507; GO:0009097; GO:0030170	Threonine dehydratase biosynthetic, chloroplastic (EC 4.3.1.19) (Threonine deaminase) (TD)
T1	Down	Solyc03g006360.2	K4BE59_SOLLC		Uncharacterized protein
T1	Down	Solyc06g007190.2	K4C3A2_SOLLC	GO:0046872; GO:0006470; GO:0004722	Uncharacterized protein
T1	Down	Solyc10g074740.1	K4D1R6_SOLLC	GO:0005509	Uncharacterized protein
T1	Down	Solyc06g048820.1	K4C5C8_SOLLC		Uncharacterized protein
T1	Down	Solyc04g071030.1	K4BT95_SOLLC	GO:0016874; GO:0004842	Uncharacterized protein
T1	Down	Solyc07g042170.2	K4CE80_SOLLC		Uncharacterized protein
T1	Down	Solyc07g045100.1	K4CER8_SOLLC	GO:0004190	Uncharacterized protein
T1	Down	Solyc01g065530.2	K4AWF7_SOLLC	GO:0031225; GO:0016049; GO:0010215	Uncharacterized protein
T1	Down	Solyc02g094400.2	K4BDN5_SOLLC	GO:0006629; GO:0008081	Uncharacterized protein
T1	Down	Solyc05g006030.2	K4BWD0_SOLLC		Uncharacterized protein
T1	Down	Solyc06g075610.1	K4C9S6_SOLLC	GO:0000145; GO:0006887	Uncharacterized protein
T1	Down	Solyc08g083050.1	K4CPV1_SOLLC		Uncharacterized protein
T1	Down	Solyc09g015040.1	K4CRX8_SOLLC	GO:0048193; GO:0008168	Uncharacterized protein
T1	Down	Solyc08g006320.2	K4CIC1_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T1	Down	Solyc01g057770.2	K4AVY8_SOLLC	GO:0005452; GO:0016021; GO:0005886	Uncharacterized protein
T1	Down	Solyc04g025650.2	K4BR09_SOLLC	GO:0016491	Uncharacterized protein
T1	Down	Solyc01g079940.2	K4AXN9_SOLLC	GO:0004190	Uncharacterized protein
T1	Down	Solyc02g093230.2	K4BDB9_SOLLC	GO:0008171	Uncharacterized protein

Table A.10 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T1	Down	Solyc07g006570.2	K4CBC8_SOLLC	GO:0003723; GO:0033897	Uncharacterized protein
T1	Down	Solyc07g053740.1	K4CFR9_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	Uncharacterized protein
T1	Down	Solyc09g089510.2	K4CVX8_SOLLC	GO:0009611; GO:0004867	Uncharacterized protein
T1	Down	Solyc03g118810.1	K4BM30_SOLLC	GO:0005509	Uncharacterized protein
T1	Down	Solyc08g068600.2	K4CM83_SOLLC	GO:0016831; GO:0019752; GO:0030170	Uncharacterized protein
T1	Down	Solyc04g005480.1	K4BNF4_SOLLC		Uncharacterized protein
T1	Down	Solyc08g077020.1	K4CN62_SOLLC	GO:0009741	Uncharacterized protein
T1	Down	Solyc12g006260.1	K4DBG3_SOLLC		Uncharacterized protein
T1	Down	Solyc05g009790.1	K4BXF3_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	Uncharacterized protein
T1	Down	Solyc03g093550.1	K4BIN2_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	Uncharacterized protein
T1	Down	Solyc01g079600.2	K4AXK5_SOLLC	GO:0016787; GO:0006629	Uncharacterized protein
T1	Down	Solyc03g098730.1	K4BJT6_SOLLC	GO:0004866	Uncharacterized protein
T1	Down	Solyc03g005570.2	K4BDY1_SOLLC	GO:0003677; GO:0003682	Uncharacterized protein
T1	Down	Solyc06g066370.2	K4C7R3_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T1	Down	Solyc10g008400.1	K4CY17_SOLLC	GO:0008270	Uncharacterized protein
T1	Down	Solyc06g074030.1	K4C9C1_SOLLC	GO:0003676; GO:0005634	Uncharacterized protein
T1	Down	Solyc08g081230.1	K4CPC0_SOLLC	GO:0051260	Uncharacterized protein
T1	Down	Solyc10g009550.2	K4CYD1_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T1	Down	Solyc11g020230.1	K4D6X5_SOLLC	GO:0005524; GO:0009693; GO:0016021; GO:0004674; GO:0010200	Uncharacterized protein
T1	Down	Solyc10g006130.1	K4CXE5_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	Uncharacterized protein
T1	Down	Solyc08g068770.1	K4CM99_SOLLC	GO:0008080	Uncharacterized protein
T1	Down	Solyc03g114100.1	K4BKR2_SOLLC		Uncharacterized protein
T1	Down	Solyc08g008370.2	K4CIX1_SOLLC		Uncharacterized protein
T1	Down	Solyc06g060680.1	K4C6P8_SOLLC	GO:0005524; GO:0004672	Uncharacterized protein
T1	Down	Solyc03g093610.1	K4BIN7_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	Uncharacterized protein
T1	Down	Solyc02g091500.1	K4BCU8_SOLLC	GO:0005509	Uncharacterized protein

Table A.10 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T1	Down	Solyc01g079580.2	K4AXK3_SOLLC		Uncharacterized protein
T1	Down	Solyc10g077130.1	K4D255_SOLLC		Uncharacterized protein
T1	Down	Solyc09g014990.2	K4CRX3_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T1	Down	Solyc01g100010.2	K4B135_SOLLC		Uncharacterized protein
T1	Down	Solyc03g119250.2	K4BM74_SOLLC		Uncharacterized protein
T1	Down	Solyc03g083470.2	K4BIC3_SOLLC	GO:0005524; GO:0004674	Uncharacterized protein
T1	Down	Solyc08g077480.2	K4CNA7_SOLLC		Uncharacterized protein
T1	Down	Solyc05g005260.1	K4BW57_SOLLC		Uncharacterized protein
T1	Down	Solyc01g066430.2	K4AWP6_SOLLC	GO:0008270	Uncharacterized protein
T1	Down	Solyc01g102840.2	K4B1L0_SOLLC	GO:0043531; GO:0007165	Uncharacterized protein
T1	Down	Solyc06g009140.2	K4C3U4_SOLLC	GO:0006950	Uncharacterized protein
T1	Down	Solyc10g009340.1	K4CYB0_SOLLC	GO:0005509; GO:0042744; GO:0010091	Uncharacterized protein
T1	Down	Solyc02g067050.2	K4B737_SOLLC	GO:0009507	Uncharacterized protein
T1	Down	Solyc03g097170.2	K4BJD4_SOLLC	GO:0003854; GO:0006694	Uncharacterized protein
T1	Down	Solyc06g067910.2	K4C7W6_SOLLC		Uncharacterized protein
T1	Down	Solyc05g051400.2	K4C1H1_SOLLC	GO:0016021; GO:0031966; GO:0006839	Uncharacterized protein
T1	Down	Solyc12g009000.1	K4DBY8_SOLLC		Uncharacterized protein
T1	Down	Solyc01g099370.2	K4B0X4_SOLLC		Uncharacterized protein
T1	Down	Solyc04g078420.1	K4BUS7_SOLLC	GO:0003677; GO:0003682	Uncharacterized protein
T1	Down	Solyc11g010500.1	K4D5L1_SOLLC	GO:0016021; GO:0031966; GO:0006839	Uncharacterized protein
T1	Down	Solyc01g111980.2	K4B460_SOLLC	GO:0016021	Uncharacterized protein
T1	Down	Solyc03g083480.2	K4BIC4_SOLLC	GO:0030247	Uncharacterized protein
T1	Down	Solyc03g112340.1	K4BK88_SOLLC	GO:0008270	Uncharacterized protein
T1	Down	Solyc12g010540.1	K4DCE1_SOLLC	GO:0005975; GO:0050662; GO:0016857	Uncharacterized protein
T1	Down	Solyc03g007870.2	K4BEK9_SOLLC	GO:0046872; GO:0030001	Uncharacterized protein
T1	Down	Solyc11g010250.1	K4D5I6_SOLLC		Uncharacterized protein
T1	Down	Solyc08g078190.1	K4CNH8_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	Uncharacterized protein
T1	Down	Solyc08g079700.1	K4CNX0_SOLLC	GO:0003677; GO:0008270	Uncharacterized protein
T1	Down	Solyc01g087580.2	K4AYE8_SOLLC		Uncharacterized protein

Table A.10 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T1	Down	Solyc11g068710.1	K4DA28_SOLLC	GO:0009738; GO:0009693; GO:0009873; GO:0010286; GO:0042538; GO:0002679; GO:0010200; GO:0009414	Uncharacterized protein
T1	Down	Solyc06g061230.2	K4C6V3_SOLLC		Uncharacterized protein
T1	Down	Solyc03g097050.2	K4BJC2_SOLLC	GO:0030244; GO:0016760; GO:0016021	Uncharacterized protein
T1	Down	Solyc05g052040.1	K4C1N5_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	Uncharacterized protein
T1	Down	Solyc03g082370.1	K4BI14_SOLLC		Uncharacterized protein
T1	Down	Solyc00g206460.1	K4ARX5_SOLLC		Uncharacterized protein
T1	Down	Solyc01g091590.2	K4AZ99_SOLLC		Uncharacterized protein
T1	Down	Solyc02g091180.1	K4BCR7_SOLLC		Uncharacterized protein
T1	Down	Solyc04g018110.1	K4BQL0_SOLLC	GO:0005509	Uncharacterized protein
T1	Down	Solyc08g078670.2	K4CNM6_SOLLC	GO:0004190; GO:0009505	Uncharacterized protein
T1	Down	Solyc05g051750.2	K4C1K6_SOLLC		Uncharacterized protein
T1	Down	Solyc07g007130.1	K4CBI4_SOLLC		Uncharacterized protein
T1	Down	Solyc06g036310.2	K4C4Z8_SOLLC	GO:0046872; GO:0030001	Uncharacterized protein
T1	Down	Solyc01g080870.2	K4AXY0_SOLLC	GO:0016020; GO:0005215	Uncharacterized protein
T1	Down	Solyc08g008100.2	K4CIU4_SOLLC	GO:0009058; GO:0003824; GO:0030170	Uncharacterized protein
T1	Down	Solyc02g073580.1	K4B8N3_SOLLC	GO:0043565; GO:0006351	Uncharacterized protein
T1	Down	Solyc12g057150.1	K4DG45_SOLLC		Uncharacterized protein
T1	Down	Solyc11g051180.1	K4D8S8_SOLLC		Uncharacterized protein
T1	Down	Solyc06g068460.2	K4C821_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T1	Down	Solyc08g062680.1	K4CL55_SOLLC	GO:0009507; GO:0005886; GO:0015824; GO:0005774	Uncharacterized protein
T1	Down	Solyc04g077620.1	K4BUJ9_SOLLC		Uncharacterized protein
T1	Down	SLSRG2	K4CDX3_SOLLC		Uncharacterized protein
T1	Down	Solyc07g006560.2	K4CBC7_SOLLC	GO:0003723; GO:0033897	Uncharacterized protein
T1	Down	Solyc10g080370.1	K4D2S7_SOLLC		Uncharacterized protein
T1	Down	Solyc10g081040.1	K4D2Z1_SOLLC		Uncharacterized protein
T1	Down	Solyc10g006700.1	K4CXK1_SOLLC	GO:0005509	Uncharacterized protein
T1	Down	Solyc06g005650.2	K4C347_SOLLC		Uncharacterized protein

Table A.10 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T1	Down	Solyc06g059870.1	K4C6H3_SOLLC		Uncharacterized protein
T1	Down	Solyc10g079420.1	K4D2I3_SOLLC	GO:0005509	Uncharacterized protein
T1	Down	Solyc11g010390.1	K4D5K0_SOLLC		Uncharacterized protein
T1	Down	Solyc06g051680.1	K4C5V8_SOLLC		Uncharacterized protein
T1	Down	Solyc03g121660.2	K4BMW5_SOLLC	GO:0046872; GO:0003676	Uncharacterized protein
T1	Down	Solyc06g060690.2	K4C6P9_SOLLC	GO:0005524; GO:0004672	Uncharacterized protein
T1	Down	LOC100134881	K4D3S2_SOLLC		Uncharacterized protein
T1	Down	WRKY3	D3YEX5_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein (WRKY transcription factor)
T1	Down	Solyc09g015770.2	I3NN77_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein (WRKY3)
T1	Down	tXET-B2	Q43528_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T1	Down	tXET-B1	K4DD58_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T1	Down	Solyc03g093110.2	K4BII8_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T1	Down	Solyc12g011030.1	K4DCI9_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T1	Down	tXET-B1	Q43527_SOLLC	GO:0048046; GO:0005618; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T2	Up	Solyc06g011350.2	E7EC27_SOLLC	GO:0016021; GO:0005215	Aquaporin (Plasmamembrane intrinsic protein 24) (Uncharacterized protein)
T2	Up	Solyc08g021820.2	G9HPX2_SOLLC	GO:0009734; GO:0005634; GO:0006355; GO:0006351	Auxin-responsive protein
T2	Up	Solyc05g041540.2	K4C0D5_SOLLC	GO:0004185	Carboxypeptidase (EC 3.4.16.-)
T2	Up	Solyc01g059980.2	E13B_SOLLC	GO:0005975; GO:0006952; GO:0042973; GO:0005773	Glucan endo-1,3-beta-glucosidase B (EC 3.2.1.39)
T2	Up	Solyc03g020010.1	O48625_SOLLC	GO:0004866	Lemir (Uncharacterized protein)

Table A.10 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T2	Up	Solyc08g029000.2	K4CJW3_SOLLC	GO:0046872; GO:0016702; GO:0031408	Lipoxygenase (EC 1.13.11.-)
T2	Up	Solyc03g044790.2	Q6ED34_SOLLC		Methylesterase (Uncharacterized protein)
T2	Up	Solyc09g007010.1	PR04_SOLLC	GO:0006952; GO:0005576; GO:0009607	Pathogenesis-related leaf protein 4 (P4)
T2	Up	Solyc01g097240.2	PRP2_SOLLC	GO:0005618; GO:0042742; GO:0050832; GO:0005576	Pathogenesis-related protein P2
T2	Up	Solyc02g093580.2	K4BDF4_SOLLC	GO:0046872; GO:0030570; GO:0045490	Pectate lyase (EC 4.2.2.2)
T2	Up	Solyc02g092580.2	K4BD54_SOLLC	GO:0005576; GO:0020037; GO:0046872; GO:0004601; GO:0006979	Peroxidase (EC 1.11.1.7)
T2	Up	Solyc03g025380.2	K4BF11_SOLLC	GO:0005576; GO:0020037; GO:0046872; GO:0004601; GO:0006979	Peroxidase (EC 1.11.1.7)
T2	Up	Solyc03g006700.2	K4BE93_SOLLC	GO:0005576; GO:0020037; GO:0046872; GO:0004601; GO:0006979	Peroxidase (EC 1.11.1.7)
T2	Up	Solyc09g090980.2	K4CWC4_SOLLC	GO:0006952; GO:0009607	PR10 protein (Uncharacterized protein)
T2	Up	Solyc04g007000.1	E1U2K4_SOLLC	GO:0003677; GO:0005634; GO:0003700; GO:0006351	RAV1 (Uncharacterized protein)
T2	Up	Solyc09g090970.2	Q53U35_SOLLC	GO:0006952; GO:0009607	Similar to pathogenesis-related protein STH-2 (Uncharacterized protein)
T2	Up	Solyc02g078650.2	K4B989_SOLLC	GO:0004097; GO:0046872; GO:0046148	Uncharacterized protein
T2	Up	Solyc06g060830.2	K4C6R3_SOLLC	GO:0005634; GO:0043565; GO:0003700; GO:0006351	Uncharacterized protein
T2	Up	Solyc00g187050.2	K4ARV8_SOLLC	GO:0004177; GO:0005737; GO:0030145; GO:0008235	Uncharacterized protein
T2	Up	Solyc08g077330.2	K4CN93_SOLLC	GO:0005576	Uncharacterized protein
T2	Up	Solyc09g097960.2	K4CWW8_SOLLC		Uncharacterized protein
T2	Up	Solyc06g068500.2	K4C825_SOLLC		Uncharacterized protein
T2	Up	Solyc08g077900.2	K4CNE9_SOLLC	GO:0005576	Uncharacterized protein

Table A.10 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T2	Up	Solyc04g078340.2	K4BUS0_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T2	Up	Solyc06g062460.2	K4C6X7_SOLLC		Uncharacterized protein
T2	Up	Solyc10g083690.2	K4D3F5_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T2	Up	Solyc09g091000.2	K4CWC6_SOLLC	GO:0006952; GO:0009607	Uncharacterized protein
T2	Up	Solyc05g050130.2	K4C145_SOLLC	GO:0006032; GO:0004568; GO:0005615; GO:0050665; GO:0000272; GO:0016926; GO:0010228	Uncharacterized protein
T2	Up	Solyc04g040180.2	K4BRF6_SOLLC	GO:0008168	Uncharacterized protein
T2	Up	Solyc02g082900.2	K4BAG0_SOLLC	GO:0009058; GO:0016844	Uncharacterized protein
T2	Up	Solyc12g049030.1	K4DFI4_SOLLC	GO:0006629; GO:0016717	Uncharacterized protein
T2	Up	Solyc10g055820.1	K4D1H1_SOLLC	GO:0005975; GO:0016998; GO:0008061; GO:0006032; GO:0004568	Uncharacterized protein
T2	Up	Solyc12g045020.1	K4DFI2_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T2	Up	Solyc08g079900.1	K4CNZ0_SOLLC	GO:0004252	Uncharacterized protein
T2	Up	Solyc12g042480.1	K4DF40_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T2	Up	Solyc02g077590.1	K4B8Y4_SOLLC	GO:0005634; GO:0006355; GO:0043565	Uncharacterized protein
T2	Up	Solyc02g070110.1	K4B7Z3_SOLLC	GO:0008762; GO:0050660	Uncharacterized protein
T2	Up	Solyc03g098740.1	K4BJT7_SOLLC	GO:0004866	Uncharacterized protein
T2	Up	Solyc10g017960.1	K4CYS0_SOLLC		Uncharacterized protein
T2	Up	Solyc05g007770.2	K4BWV2_SOLLC	GO:0003677; GO:0005634; GO:0006355; GO:0006351	Uncharacterized protein
T2	Up	Solyc07g005100.2	K4CAY2_SOLLC	GO:0005975; GO:0006032; GO:0004568	Uncharacterized protein
T2	Up	Solyc04g005610.2	K4BNG7_SOLLC	GO:0003677; GO:0005634; GO:0006355; GO:0006351	Uncharacterized protein
T2	Up	Solyc03g006210.1	K4BE44_SOLLC	GO:0008234	Uncharacterized protein
T2	Up	Solyc09g097760.2	K4CWU8_SOLLC		Uncharacterized protein

Table A.10 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T2	Up	Solyc09g089540.2	K4CVY1_SOLLC	GO:0009611; GO:0004867	Uncharacterized protein
T2	Up	Solyc08g078670.2	K4CNM6_SOLLC	GO:0004190; GO:0009505	Uncharacterized protein
T2	Up	Solyc04g076220.2	K4BU60_SOLLC		Uncharacterized protein
T2	Up	Solyc04g077860.2	K4BUM3_SOLLC	GO:0009805; GO:0016787; GO:0015824; GO:0009611; GO:0010223; GO:1901601	Uncharacterized protein
T2	Up	Solyc07g056200.2	K4CGF3_SOLLC		Uncharacterized protein
T2	Up	Solyc02g078150.2	K4B940_SOLLC		Uncharacterized protein
T2	Up	Solyc02g062390.2	K4B6C8_SOLLC	GO:0006950; GO:0009415	Uncharacterized protein
T2	Up	Solyc03g078490.2	K4BHS7_SOLLC	GO:0016758	Uncharacterized protein
T2	Up	Solyc07g054720.1	K4CG14_SOLLC	GO:0004867	Uncharacterized protein
T2	Up	Solyc03g114890.2	K4BKZ1_SOLLC	GO:0031225; GO:0016049; GO:0010215	Uncharacterized protein
T2	Up	Solyc05g052670.1	K4C1U8_SOLLC	GO:0016747	Uncharacterized protein
T2	Up	Solyc05g052680.1	K4C1U9_SOLLC	GO:0016747	Uncharacterized protein
T2	Up	Solyc01g110180.2	K4B3N1_SOLLC	GO:0005622; GO:0008270	Uncharacterized protein
T2	Up	Solyc08g007460.2	K4CIN3_SOLLC		Uncharacterized protein
T2	Up	Solyc03g025670.2	K4BF40_SOLLC		Uncharacterized protein
T2	Up	Solyc03g006360.2	K4BE59_SOLLC		Uncharacterized protein
T2	Up	Solyc07g006370.1	K4CBA8_SOLLC	GO:0016021; GO:0055085	Uncharacterized protein
T2	Up	Solyc09g098510.2	K4CX21_SOLLC	GO:0009664; GO:0005199	Uncharacterized protein
T2	Up	Solyc08g062180.1	K4CL07_SOLLC		Uncharacterized protein
T2	Up	Solyc04g071110.1	K4BTA3_SOLLC		Uncharacterized protein
T2	Up	Solyc08g080670.1	K4CP65_SOLLC		Uncharacterized protein
T2	Up	Solyc01g008620.2	K4AT60_SOLLC	GO:0005975; GO:0004553	Uncharacterized protein
T2	Down	Solyc06g069730.2	Q7M1K8_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0046872; GO:0009765; GO:0009522; GO:0009523; GO:0018298	Chlorophyll a/b-binding protein (cab-12) (Uncharacterized protein)
T2	Down	ER5	P93220_SOLLC	GO:0009269	Ethylene-responsive late embryogenesis-like protein (Uncharacterized protein)
T2	Down	Solyc03g120990.2	K4BMP8_SOLLC	GO:0051287; GO:0004471; GO:0006108; GO:0046872	Malic enzyme

Table A.10 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T2	Down	Solyc02g080210.2	K4B9P2_SOLLC	GO:0045330; GO:0005618; GO:0042545; GO:0004857; GO:0045490; GO:0030599	Pectinesterase (EC 3.1.1.11)
T2	Down	PSBS	PSBS_SOLLC	GO:0009517; GO:0016168; GO:0019344; GO:0016021; GO:0000023; GO:0010196; GO:0009523; GO:0010207; GO:0043085; GO:0006364; GO:0019252; GO:0010103; GO:0010027; GO:0051738	Photosystem II 22 kDa protein, chloroplastic (CP22)
T2	Down	yfe37	Q9LEG3_SOLLC	GO:0016491	Putative alcohol dehydrogenase (Uncharacterized protein)
T2	Down	Solyc06g072710.2	K4C8Z1_SOLLC	GO:0003677; GO:0006352; GO:0003700; GO:0016987	Uncharacterized protein
T2	Down	Solyc01g087590.2	K4AYE9_SOLLC	GO:0052895; GO:0050660; GO:0052894; GO:0046592; GO:0046208; GO:0052901	Uncharacterized protein
T2	Down	Solyc02g070980.1	K4B876_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0046872; GO:0009765; GO:0009522; GO:0009523; GO:0018298	Uncharacterized protein
T2	Down	Solyc11g010410.1	K4D5K2_SOLLC	GO:0046872; GO:0016706	Uncharacterized protein
T2	Down	Solyc07g007260.2	K4CBJ6_SOLLC		Uncharacterized protein
T2	Down	Solyc06g007190.2	K4C3A2_SOLLC	GO:0046872; GO:0006470; GO:0004722	Uncharacterized protein
T2	Down	Solyc01g009080.2	K4ATA4_SOLLC	GO:0009570; GO:0009535; GO:0000023; GO:0006098; GO:0010207; GO:0009657; GO:0043085; GO:0006364; GO:0019252; GO:0010103	Uncharacterized protein
T2	Down	Solyc03g116730.2	K4BLH5_SOLLC	GO:0006633; GO:0016021; GO:0016717	Uncharacterized protein
T2	Down	Solyc07g055740.1	K4CGA7_SOLLC	GO:0009058; GO:0016844	Uncharacterized protein

Table A.10 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T2	Down	Solyc01g087710.2	K4AYG1_SOLLC		Uncharacterized protein
T2	Down	Solyc05g043330.2	K4C0L5_SOLLC	GO:0016788; GO:0006629	Uncharacterized protein
T2	Down	Solyc05g050770.2	K4C1A9_SOLLC	GO:0004185	Uncharacterized protein
T2	Down	Solyc12g009200.1	K4DC08_SOLLC	GO:0030003; GO:0016168; GO:0009507; GO:0070838; GO:0019761; GO:0016021; GO:0019288; GO:0046872; GO:0006098; GO:0009765; GO:0009522; GO:0009523; GO:0018298; GO:0006364; GO:0010155; GO:0009644; GO:0009744	Uncharacterized protein
T2	Down	Solyc07g042440.2	K4CEA5_SOLLC	GO:0016209; GO:0016491	Uncharacterized protein
T2	Down	Solyc01g103100.2	K4B1N6_SOLLC	GO:0042335; GO:0005829; GO:0006760; GO:0016616; GO:0009409; GO:0000038	Uncharacterized protein
T2	Down	Solyc01g005590.2	K4ASC5_SOLLC		Uncharacterized protein
T2	Down	Solyc07g055260.2	K4CG65_SOLLC	GO:0009507; GO:0009055; GO:0005506; GO:0051536; GO:0006950	Uncharacterized protein
T2	Down	Solyc10g009150.2	K4CY91_SOLLC		Uncharacterized protein
T2	Down	Solyc03g007030.2	K4BEC6_SOLLC	GO:0051537; GO:0009570; GO:0055072; GO:0010150; GO:0016556; GO:0005739; GO:0006098; GO:0072593	Uncharacterized protein
T2	Down	Solyc10g078580.1	K4D2A0_SOLLC		Uncharacterized protein
T2	Down	Solyc06g066800.1	K4C7V4_SOLLC		Uncharacterized protein
T2	Down	Solyc07g045080.2	K4CER6_SOLLC	GO:0016491; GO:0008270	Uncharacterized protein
T2	Down	Solyc11g071740.1	K4DAN1_SOLLC	GO:0005509	Uncharacterized protein
T2	Down	Solyc02g063000.2	K4B6I8_SOLLC	GO:0016758	Uncharacterized protein

Table A.10 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T2	Down	Solyc08g079090.2	K4CNR8_SOLLC	GO:0046658; GO:0043481; GO:0048046; GO:0009932; GO:0071555; GO:0030243; GO:0005507; GO:0009825; GO:0016491; GO:0009505; GO:0009506; GO:0000271; GO:0010817; GO:0048767; GO:0005774	Uncharacterized protein
T2	Down	Solyc07g042520.2	K4CEB3_SOLLC	GO:0009058; GO:0005985; GO:0016157	Uncharacterized protein
T2	Down	Solyc03g034070.1	K4BFS9_SOLLC	GO:0016117; GO:0019761; GO:0046777	Uncharacterized protein
T2	Down	Solyc06g068950.2	K4C868_SOLLC	GO:0006656; GO:0000234	Uncharacterized protein
T2	Down	Solyc01g099020.2	K4B0T9_SOLLC	GO:0016788; GO:0006629	Uncharacterized protein
T2	Down	Solyc03g005790.2	K4BE02_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0009765; GO:0009523; GO:0018298	Uncharacterized protein
T2	Down	Solyc02g081980.2	K4BA68_SOLLC	GO:0016787	Uncharacterized protein
T2	Down	Solyc03g025710.2	K4BF44_SOLLC	GO:0008080	Uncharacterized protein
T2	Down	Solyc02g070990.1	K4B877_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0046872; GO:0009765; GO:0009522; GO:0009523; GO:0018298	Uncharacterized protein
T2	Down	Solyc07g052610.2	K4CFG0_SOLLC	GO:0007049; GO:0051301; GO:0000079; GO:0010440	Uncharacterized protein
T2	Down	Solyc11g018800.1	K4D6T3_SOLLC	GO:0020037; GO:0004601; GO:0006979	Uncharacterized protein
T2	Down	Solyc12g096770.1	K4DHF0_SOLLC	GO:0016747	Uncharacterized protein
T2	Down	Solyc04g071960.2	K4BTI3_SOLLC	GO:0016491	Uncharacterized protein
T2	Down	hsc70	K4C9W3_SOLLC	GO:0005524	Uncharacterized protein
T2	Down	Solyc09g008320.2	K4CQM0_SOLLC	GO:0048046; GO:0005618; GO:0042546; GO:0016998; GO:0071555; GO:0006073; GO:0004553; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)

Table A.10 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Up	ACO4 ACO3	ACCO4_SOLLC	GO:0009815; GO:0031418; GO:0009693; GO:0009835; GO:0046872; GO:0016706	1-aminocyclopropane-1-carboxylate oxidase 4 (ACC oxidase 4) (EC 1.14.17.4) (Ethylene-forming enzyme) (EFE) (Protein pHTOM5)
T3	Up	CHI3	CHIA_SOLLC	GO:0016998; GO:0006032; GO:0004568; GO:0006952; GO:0005615; GO:0000272; GO:0009607	Acidic 26 kDa endochitinase (EC 3.2.1.14)
T3	Up	ZIP	C0KYN1_SOLLC	GO:0043565; GO:0003700	BZIP transcription factor (Uncharacterized protein)
T3	Up	Lin6 Wiv-1	Q8LRN8_SOLLC	GO:0005975; GO:0004553	Cell-wall invertase (Uncharacterized protein)
T3	Up	CHS2	K4C235_SOLLC	GO:0009058; GO:0016747	Chalcone synthase 2
T3	Up	Rcr3	Q8S333_SOLLC	GO:0008234	Cysteine protease (Uncharacterized protein)
T3	Up	Solyc09g011600.2	A8DUB0_SOLLC	GO:0016740	Glutathione S-transferase-like protein (Uncharacterized protein)
T3	Up	Solyc02g093580.2	K4BDF4_SOLLC	GO:0046872; GO:0030570; GO:0045490	Pectate lyase (EC 4.2.2.2)
T3	Up	Solyc06g050440.2	K4C5I8_SOLLC	GO:0005576; GO:0020037; GO:0046872; GO:0004601; GO:0006979	Peroxidase (EC 1.11.1.7)
T3	Up	CEVI-1	K4ASJ6_SOLLC	GO:0005576; GO:0020037; GO:0046872; GO:0004601; GO:0006979	Peroxidase (EC 1.11.1.7)
T3	Up	Solyc09g090990.2	K4CWC5_SOLLC	GO:0006952; GO:0009607	PR10 protein (Uncharacterized protein)
T3	Up	Solyc06g069040.2	Q9FT20_SOLLC	GO:0016740	Putative glutathione S-transferase T4 (Uncharacterized protein)
T3	Up	PSK1	Q7PCA9_SOLLC	GO:0008283; GO:0005576	Putative phytosulfokine peptide (Uncharacterized protein)
T3	Up	Solyc03g097610.2	K4BJH8_SOLLC	GO:0008643; GO:0016021	Sugar transporter SWEET
T3	Up	Solyc05g006870.2	K4BWL3_SOLLC	GO:0045454; GO:0006662; GO:0015035	Thioredoxin
T3	Up	Solyc07g009500.1	K4CC70_SOLLC	GO:0008061	Uncharacterized protein
T3	Up	Solyc08g079900.1	K4CNZ0_SOLLC	GO:0004252	Uncharacterized protein
T3	Up	Solyc02g061780.2	K4B668_SOLLC	GO:0003677; GO:0005634; GO:0006355; GO:0006351	Uncharacterized protein

Table A.10 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Up	Solyc05g051530.2	K4C1I4_SOLLC	GO:0005524; GO:0016887; GO:0016020	Uncharacterized protein
T3	Up	Solyc12g087870.1	K4DGK8_SOLLC	GO:0016021; GO:0005215	Uncharacterized protein
T3	Up	Solyc08g067340.2	K4CLW0_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T3	Up	Solyc04g078290.2	K4BUR6_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T3	Up	Solyc05g051460.2	K4C1H7_SOLLC	GO:0005634; GO:0043565; GO:0003700; GO:0006351	Uncharacterized protein
T3	Up	Solyc08g067360.2	K4CLW2_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T3	Up	Solyc07g008140.2	K4CBT3_SOLLC	GO:0009055	Uncharacterized protein
T3	Up	Solyc10g055740.1	K4D1G4_SOLLC	GO:0016021	Uncharacterized protein
T3	Up	Solyc02g063440.2	K4B6M9_SOLLC		Uncharacterized protein
T3	Up	Solyc09g011590.2	K4CRI5_SOLLC		Uncharacterized protein
T3	Up	Solyc05g009040.2	K4BX78_SOLLC	GO:0005524; GO:0004674	Uncharacterized protein
T3	Up	Solyc03g013160.2	K4BEN7_SOLLC	GO:0016021	Uncharacterized protein
T3	Up	Solyc09g090080.1	K4CW34_SOLLC	GO:0005315; GO:0016021; GO:0006817	Uncharacterized protein
T3	Up	Solyc03g033790.2	K4BFQ1_SOLLC	GO:0005524	Uncharacterized protein
T3	Up	Solyc10g075150.1	K4D1V6_SOLLC	GO:0008289; GO:0006869	Uncharacterized protein
T3	Up	Solyc01g098590.2	K4B0P6_SOLLC	GO:0003824	Uncharacterized protein
T3	Up	Solyc10g055200.1	K4D1B3_SOLLC		Uncharacterized protein
T3	Up	Solyc03g025670.2	K4BF40_SOLLC		Uncharacterized protein
T3	Up	Solyc07g045530.1	K4CEV9_SOLLC		Uncharacterized protein
T3	Up	TOMQ`B	K4D2M7_SOLLC	GO:0005975; GO:0004553	Uncharacterized protein
T3	Up	Solyc11g069940.1	K4DAF0_SOLLC	GO:0045454; GO:0009055; GO:0015035	Uncharacterized protein
T3	Up	Solyc07g056200.2	K4CGF3_SOLLC		Uncharacterized protein
T3	Up	Solyc04g072070.2	K4BTJ4_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T3	Up	Solyc03g119600.1	K4BMA9_SOLLC		Uncharacterized protein
T3	Up	Solyc12g049030.1	K4DFI4_SOLLC	GO:0006629; GO:0016717	Uncharacterized protein
T3	Up	Solyc07g008210.2	K4CBU0_SOLLC	GO:0016020; GO:0006979	Uncharacterized protein
T3	Up	Solyc01g010230.2	K4ATL8_SOLLC		Uncharacterized protein
T3	Up	Solyc08g076730.2	K4CN34_SOLLC		Uncharacterized protein
T3	Up	Solyc10g084960.1	K4D3T0_SOLLC		Uncharacterized protein

Table A.10 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Up	Solyc02g082740.1	K4BAE4_SOLLC		Uncharacterized protein
T3	Up	Solyc12g096960.1	K4DHG9_SOLLC	GO:0006952; GO:0009607	Uncharacterized protein
T3	Up	Solyc04g007380.1	K4BNP5_SOLLC	GO:0005524; GO:0004674	Uncharacterized protein
T3	Up	Solyc08g077480.2	K4CNA7_SOLLC		Uncharacterized protein
T3	Up	Solyc12g100270.1	K4DI48_SOLLC	GO:0006633; GO:0016021; GO:0005506; GO:0016491	Uncharacterized protein
T3	Up	Solyc01g088660.2	K4AYQ6_SOLLC		Uncharacterized protein
T3	Up	Solyc09g063150.2	K4CU45_SOLLC		Uncharacterized protein
T3	Up	Solyc03g034370.1	K4BFV7_SOLLC		Uncharacterized protein
T3	Up	Solyc09g097810.2	K4CWV3_SOLLC		Uncharacterized protein
T3	Up	Solyc03g033800.1	K4BFQ2_SOLLC		Uncharacterized protein
T3	Up	Solyc01g008620.2	K4AT60_SOLLC	GO:0005975; GO:0004553	Uncharacterized protein
T3	Up	Solyc02g014030.1	K4B4K3_SOLLC	GO:0005524; GO:0004674	Uncharacterized protein
T3	Up	Solyc04g040130.1	K4BRF1_SOLLC	GO:0006629; GO:0016717	Uncharacterized protein
T3	Up	Solyc04g051690.2	K4BSC8_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T3	Up	Solyc12g011150.1	K4DCK1_SOLLC		Uncharacterized protein
T3	Up	pip1	K4B8T1_SOLLC	GO:0008234	Uncharacterized protein
T3	Up	Solyc01g089880.2	K4AYS9_SOLLC		Uncharacterized protein
T3	Up	Solyc05g050130.2	K4C145_SOLLC	GO:0006032; GO:0004568; GO:0005615; GO:0050665; GO:0000272; GO:0016926; GO:0010228	Uncharacterized protein
T3	Up	Solyc03g095770.2	K4BIZ9_SOLLC	GO:0043565; GO:0003700	Uncharacterized protein
T3	Up	Solyc09g097760.2	K4CWU8_SOLLC		Uncharacterized protein
T3	Up	Solyc08g074490.2	K4CMG8_SOLLC		Uncharacterized protein
T3	Up	Solyc01g086670.2	K4AY60_SOLLC		Uncharacterized protein
T3	Up	Solyc07g009230.2	K4CC42_SOLLC	GO:0006952	Uncharacterized protein
T3	Up	Solyc03g005980.2	K4BE21_SOLLC	GO:0016021; GO:0005215	Uncharacterized protein
T3	Up	Solyc02g080510.1	K4B9S2_SOLLC		Uncharacterized protein
T3	Up	Solyc08g068710.1	K4CM93_SOLLC	GO:0008080	Uncharacterized protein
T3	Up	Solyc03g122350.2	K4BN33_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T3	Up	ail	K4CKN7_SOLLC		Uncharacterized protein
T3	Up	Solyc03g119590.1	K4BMA8_SOLLC		Uncharacterized protein

Table A.10 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Up	Solyc09g091000.2	K4CWC6_SOLLC	GO:0006952; GO:0009607	Uncharacterized protein
T3	Up	Solyc04g016040.1	K4BQA5_SOLLC		Uncharacterized protein
T3	Up	Solyc09g011560.2	K4CRI2_SOLLC		Uncharacterized protein
T3	Up	Solyc05g009520.1	K4BXC6_SOLLC		Uncharacterized protein
T3	Up	Solyc04g054760.2	K4BSM4_SOLLC		Uncharacterized protein
T3	Up	Solyc11g030730.1	K4D7K8_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T3	Up	Solyc04g005100.2	K4BNB6_SOLLC	GO:0003677; GO:0003682	Uncharacterized protein
T3	Up	Solyc03g114100.1	K4BKR2_SOLLC		Uncharacterized protein
T3	Up	GGPS1	K4D5T0_SOLLC	GO:0008299; GO:0016740	Uncharacterized protein
T3	Up	Solyc04g076010.2	K4BU40_SOLLC		Uncharacterized protein
T3	Up	Solyc08g007460.2	K4CIN3_SOLLC		Uncharacterized protein
T3	Up	Solyc12g042480.1	K4DF40_SOLLC	GO:0020037; GO:0005506; GO:0004497; GO:0016705	Uncharacterized protein
T3	Up	Solyc05g006850.2	K4BWL1_SOLLC	GO:0045454; GO:0006662; GO:0015035	Uncharacterized protein
T3	Up	XTH6	K4D9N5_SOLLC	GO:0048046; GO:0005618; GO:0042546; GO:0016998; GO:0071555; GO:0006073; GO:0033946; GO:0016762	Xyloglucan endotransglucosylase/hydrolase (EC 2.4.1.207)
T3	Down	Solyc06g072350.2	K4C8V5_SOLLC	GO:0016021; GO:0005886	CASP-like protein
T3	Down	Solyc06g069730.2	Q7M1K8_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0046872; GO:0009765; GO:0009522; GO:0009523; GO:0018298	Chlorophyll a/b-binding protein (cab-12) (Uncharacterized protein)
T3	Down	LOC100191137	B2MW87_SOLLC	GO:0005622; GO:0008270	CONSTANS-like protein (Hop-interacting protein THI010) (Uncharacterized protein)
T3	Down	Solyc11g006250.1	G1DEX3_SOLLC	GO:0005576; GO:0016788; GO:0016042	Cutin-deficient 1 protein (Uncharacterized protein)
T3	Down	Cel1	Q42871_SOLLC	GO:0008810; GO:0030245	Endoglucanase (EC 3.2.1.4)
T3	Down	ER5	P93220_SOLLC	GO:0009269	Ethylene-responsive late embryogenesis-like protein (Uncharacterized protein)
T3	Down	Solyc04g014510.2	K4BPV5_SOLLC	GO:0005524; GO:0004356; GO:0006542	Glutamine synthetase (EC 6.3.1.2)

Table A.10 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Down	Solyc01g008420.2	K4AT40_SOLLC	GO:0015297; GO:0015238; GO:0016021	MATE efflux family protein
T3	Down	Solyc10g080690.1	K4D2V9_SOLLC	GO:0016787; GO:0016042	Patatin (EC 3.1.1.-)
T3	Down	Solyc06g071320.2	Q53J17_SOLLC		T10O24.15, related (Uncharacterized protein)
T3	Down	Solyc06g072710.2	K4C8Z1_SOLLC	GO:0003677; GO:0006352; GO:0003700; GO:0016987	Uncharacterized protein
T3	Down	Solyc03g121900.1	K4BMY8_SOLLC		Uncharacterized protein
T3	Down	Solyc04g015620.2	K4BQ64_SOLLC		Uncharacterized protein
T3	Down	Solyc09g009420.1	K4CQX1_SOLLC	GO:0009813; GO:0010224; GO:0009744	Uncharacterized protein
T3	Down	Solyc04g008040.2	K4BNW0_SOLLC	GO:0007010	Uncharacterized protein
T3	Down	Solyc01g087710.2	K4AYG1_SOLLC		Uncharacterized protein
T3	Down	Solyc06g084140.2	K4CAR9_SOLLC	GO:0009507; GO:0016021; GO:0008271	Uncharacterized protein
T3	Down	Solyc03g005900.2	K4BE13_SOLLC	GO:0016788; GO:0006629	Uncharacterized protein
T3	Down	Solyc05g051850.2	K4C1L6_SOLLC	GO:0006021; GO:0004512; GO:0008654	Uncharacterized protein
T3	Down	Solyc12g011010.1	K4DCI7_SOLLC		Uncharacterized protein
T3	Down	Solyc07g007550.2	K4CBM5_SOLLC	GO:0004566; GO:0005975; GO:0005576; GO:0005765; GO:0009505	Uncharacterized protein
T3	Down	Solyc01g086920.2	K4AY85_SOLLC	GO:0006281; GO:0009507; GO:0016301; GO:0000166; GO:0009411; GO:0042493	Uncharacterized protein
T3	Down	Solyc10g005030.2	K4CX37_SOLLC	GO:0000160	Uncharacterized protein
T3	Down	Solyc04g076880.2	K4BUC5_SOLLC	GO:0005524; GO:0006094; GO:0004612	Uncharacterized protein
T3	Down	Solyc06g060310.2	K4C6L2_SOLLC	GO:0051537; GO:0010277; GO:0005506; GO:0016705	Uncharacterized protein
T3	Down	Solyc01g090970.2	K4AZ37_SOLLC	GO:0005576	Uncharacterized protein
T3	Down	Solyc07g055950.2	K4CGC8_SOLLC		Uncharacterized protein
T3	Down	Solyc10g076940.1	K4D236_SOLLC	GO:0016021; GO:0055085	Uncharacterized protein

Table A.10 continued.

Time	Group	Gene names	Uniprot ID	Gene ontology IDs	Protein names
T3	Down	Solyc08g067330.1	K4CLV9_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0009765; GO:0009523; GO:0018298	Uncharacterized protein
T3	Down	Solyc03g005790.2	K4BE02_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0009765; GO:0009523; GO:0018298	Uncharacterized protein
T3	Down	Solyc01g079830.2	K4AXM8_SOLLC		Uncharacterized protein
T3	Down	Solyc08g075490.2	K4CMR6_SOLLC		Uncharacterized protein
T3	Down	Solyc03g118310.2	K4BLY2_SOLLC		Uncharacterized protein
T3	Down	Solyc02g070990.1	K4B877_SOLLC	GO:0016168; GO:0009507; GO:0016021; GO:0046872; GO:0009765; GO:0009522; GO:0009523; GO:0018298	Uncharacterized protein
T3	Down	Solyc06g069790.2	K4C8F1_SOLLC		Uncharacterized protein
T3	Down	Solyc03g006490.2	K4BE72_SOLLC		Uncharacterized protein
T3	Down	Solyc03g111550.2	K4BK18_SOLLC	GO:0005576; GO:0016788; GO:0016042	Uncharacterized protein
T3	Down	Solyc02g077330.2	K4B8W0_SOLLC	GO:0042335; GO:0005576; GO:0016788; GO:0016042; GO:0000038	Uncharacterized protein
T3	Down	Solyc08g078870.1	K4CNP6_SOLLC		Uncharacterized protein
T3	Down	Solyc09g075750.1	K4CVF2_SOLLC	GO:0009742; GO:0019210; GO:0006629; GO:0005886	Uncharacterized protein

T1, T2, and T3 represent one, two, and four weeks after infestation, respectively.