# Identification of regulatory factors in the signal transduction pathway in herbivore-induced maize

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## Summary

In order to survive in a changing environment, plants are able to communicate with other organisms. One aspect of chemical communication is the production of complex mixtures of volatile organic compounds (VOC) after the plants are attacked by an herbivore enemy. Those volatiles can be used as cues by parasitic wasps to locate their hosts. Therefore, this tritrophic interaction has been termed “indirect defense”.

The ecological aspects of the indirect defense and the biosynthesis of the terpene volatiles are well studied in maize (*Zea mays*). Two terpene synthases, TPS10 and TPS23, are responsible for the biosynthesis of the major sesquiterpene volatiles produced after attack by the larvae of the lepidopteran herbivore *Spodoptera littoralis*. TPS10 converts the precursor farnesyl diphosphate (FPP) into the sesquiterpenes (*E*)-ß-farnesene and (*E*)-α-bergamotene. The enzyme TPS23 synthesizes (*E*)-ß-caryophyllene from the same substrate. The signal transduction pathways responsible for the regulation of volatile induced defenses remain mostly unclear. However, damage by different types of herbivores results in specific volatile signals, which suggests a complex regulatory network.

This work focused on the identification of transcription factors involved in the signaling cascade between herbivore damage and volatile emission. Microarray hybridization identified several transcription factors affected by herbivory, mechanical damage, and mechanical damage plus caterpillar regurgitate. Also, the effects of herbivore-damaged roots upon leaves and vice versa (systemic effects) were assayed. The majority of transcription factors reacted in a similar fashion to several types of induction which included caterpillar feeding and mechanical damage. Nevertheless, maize plants responded to mechanical damage by emitting only ~50 % of sesquiterpenes found in herbivore-induced plants, indicating a separate recognition of caterpillar regurgitate.

The analysis of plant hormones after herbivore damage confirmed their roles in specific signal transduction pathways. While an increase of jasmonic acid (JA) concentration was observed after all types of mechanical damage to the plant, salicylic acid (SA) concentrations were only increased when plants were treated with caterpillar regurgitate. Therefore, SA might have a role in maize herbivore signal transduction pathways that is different from its role in signal transduction after pathogen attack.

The expression patterns and product formation of the terpene synthases TPS10 and TPS23 were investigated in response to herbivory. Transgenic Arabidopsis plants with promoter::reporter gene constructs of both terpene synthases displayed an herbivore-regulated activity similar to the expression patterns in maize. This heterologous expression system was utilized to further characterize the promoters of both genes. The promoter of *tps10* was only induced when plants were treated with both mechanical damage and JA. The promoter of *tps23* was induced by either treatment alone. A promoter deletion analysis revealed an essential area with a WUN-motif in the promoter of *tps10*. An area with the same motif in the promoter of *tps23* was not crucial for gene expression. Overall, this study indicated that maize is able to respond to a variety of cues of herbivory and contribute to the formation of herbivore-specific volatile signals via several signal transduction pathways. The exact components involved in each of the signal transduction cascades and their functions still need to be determined.

## Zusammenfassung

Um in einer sich veränderten Umwelt zu überleben, nutzen Pflanzen unterschiedliche Arten der Kommunikation. Die Produktion von komplexen Gemischen volatiler organischer Verbindungen ist ein Aspekt der chemischen Kommunikation. Diese flüchtigen Substanzen werden von Pflanzen nach Fraßbefall abgegeben und können als Lockstoffe für parasitäre Schädlinge der Fraßfeinde genutzt werden. Diese tritrophische Interaktion kann der indirekten Verteidigung der Pflanze dienen.

Die ökologischen Gesichtspunkte der indirekten Verteidigung und die Biosynthese der flüchtigen Terpene sind in Mais (*Zea mays*) gut untersucht. Zwei Terpensynthasen synthetisieren die Mehrheit der Sesquiterpene, die durch den Befall mit der Larve eines Eulenfalters (*Spodoptera littoralis)* gebildet werden. Die Terpensynthase TPS10 katalysiert die Umsetzung des Substrates Farnesyldiphosphat (FPP) zu den Sesquiterpenen (*E*)-ß-Farnesen und (*E*)-α-Bergamoten. (*E*)-ß-Caryophyllen wird aus dem gleichen Ausgangsprodukt von der Terpensynthase TPS23 gebildet. Die Signalkaskade, die nach der Verletzung der Pflanze zur Bildung der flüchtigen Terpene führt, ist weitgehend unbekannt. Die Abhängigkeit der Zusammensetzung der volatilen Signale vom Typ des angreifenden Herbivoren deutet auf ein komplexes regulatorisches Netzwerk hin.

Der Fokus dieser Arbeit lag in der Identifizierung von Transkriptionsfaktoren, die an diesen Signalwegen beteiligt sein könnten. Durch die Hybridisierung von Microarrays wurden mehrere Transkriptionsfaktoren gefunden, deren Genexpression durch Raupenfraß, mechanische Verwundung und Elizitoren differenziell reguliert wurde. Der systemische Effekt eines Herbivorenbefalls der Wurzeln auf die Genexpression der Blätter und umgekehrt wurde ebenfalls untersucht. Die Mehrzahl der Transkriptionsfaktoren zeigte eine ähnliche Genexpression nach unterschiedlichen Induktionsmethoden. Dennoch wurden aber nur etwa 50 % der Sesquiterpene von der Maispflanze abgegeben, nachdem diese nur mechanisch verwundet wurde. Das deutet auf separate Signalwege für die mechanische Verwundung und für die Reaktion auf Elizitoren von Insekten hin. Eine Analyse der Pflanzenhormone bestätigte deren Rolle bei der Signaltransduktion nach Herbivorie. Während Jasmonsäure auch in mechanisch verwundeten Pflanzen gefunden wurde, war Salicylsäure nur nach Zugabe von Elizitoren aus dem Regurgitat von *S. littoralis* messbar. Daher scheint sich die

Funktion der Salicylsäure in Mais nach Herbivorenbefall von der Funktion bei der Pathogenabwehr, die in anderen Pflanzen charakterisiert wurde, zu unterscheiden.

Die Genexpression und die Synthese der volatilen Produkte von TPS10 und TPS23 nach Insektenfraß wurden ebenfalls untersucht. Transgene Arabidopsispflanzen mit Promotor::Reportergenkonstrukten beider Terpensynthasen zeigten dieselbe herbivorie-regulierte Aktivität wie in Mais. Dieses heterologe Expressionssystem wurde zur weiteren Charakterisierung der Promotoren genutzt. Während der Promotor von *tps10* sowohl die mechanische Verwundung als auch Jasmonsäure für die Aktivierung benötigte, konnte der Promotor von *tps23* jeweils einzeln durch mechanische Verwundung und Jasmonsäure aktiviert werden. Promoter-Deletionsstudien von *tps10* deuteten auf einen essentiellen Promotorbereich hin, der ein WUN-Motiv enthält. Das WUN-Motiv ist ebenfalls im Promotor von *tps23* vorhanden, allerdings scheint dieser Bereich hier keine exklusive Rolle bei der Genexpression zu spielen. Insgesamt zeigen die Ergebnisse, dass die Verletzung der Maispflanze durch Herbivoren verschiedene fraßbedingte Signale erzeugt, die durch mehrere Signalkaskaden zur Bildung von herbivor-spezifischen Volatilen führt. Die Funktion der identifizierten Komponenten in den jeweiligen herbivor-spezifischen Signalkaskaden benötigt eine weitere Aufklärung.

# Abbreviations

| | |
|---|---|
| aa | amino acid |
| ABA | abscic acid |
| ABRE | abscic acid responsive element |
| *a.dest.* | destilled water |
| $Amp^r$ | ampicillin resistance |
| Amu | atomic mass unit |
| AP2/EREBP | apetala2/ethylene responsive element binding protein |
| APS | ammonium persulfate |
| ARF | auxin responsive factor |
| BCIP | 5-bromo-4-chloro-3-indolyl phosphate |
| bHLH | basic helix loop helix |
| BLAST | basic local alignment search tool |
| BSA | bovine serum albumin |
| CAF1 | CCR4-associated factor 1 |
| CAPS | N-cyclohexyl-3-aminopropansulfonacid |
| CCR4 | carbon catabolite repressor 4 |
| cDNA | copy DNA |
| $Cm^r$ | chloramphenicol resistance |
| CoA | coenzyme A |
| cpm | counts per minute |
| cps | counts per second |
| CTR1 | constitutive triple response 1 |
| DAPI | 4',6-diamidino-2-phenylindol |
| DMNT | (3,*E*)-4,8-dimethyl-1,3,7-nonatrien |
| DNA | deoxyribonucleic acid |
| dNTP | deoxynucleotide triphosphate |
| DMAPP | dimethylallyl pyrophosphate |
| DRE | drought responsive element |
| dsDNA | double stranded DNA |

| | |
|---|---|
| DTT | dithiothreitol |
| EDTA | ethylene diamine tetraactic acid |
| EIN | ethylene insensitive |
| EMSA | electrophoretic mobility shift assay |
| ERE | ethylene responsive element |
| ERF | ethylene response factor |
| FPLC | fast protein liquid chromatography |
| FPP | farnesyl diphosphate |
| GC-MS | gas chromatography-mass spectrometry |
| $Gent^r$ | gentamycin resistance |
| GGPP | geranylgeranyl diphosphate |
| GLV | green leaf volatiles |
| GO | Gene Ontology |
| GPP | geranyl diphosphate |
| GUS | ß-glucuronidase |
| IPP | isopentenyl diphosphate |
| IPTG | isopropyl-1-thio-β-D-galactoside |
| JA | jasmonic acid |
| JAI3 | jasmonate insensitive 3 |
| JA-Ile | jasmonic acid isoleucin |
| JAR | JA amino acid conjugate synthase |
| JAZ | jasmonate-ZIM-domain proteins |
| JERE | JA- and elicitor responsive element |
| $k_{cat}$ | turn over number |
| kDa | kilodalton |
| $Km^r$ | kanamycin resistance |
| LB | Luria-Bertani |
| LHY | late elongated hypocotyl |
| LTR | long terminal repeat |
| MeJA | methyl jasmonate |
| MEP | 2C-methyl-D-erythritol-4-phosphate |

| | |
|---|---|
| MES | (2-N-morpholino)ethanesulphonic acid |
| MeSA | methyl salicylate |
| MPK | mitogen-activated protein kinase |
| mRNA | messenger RNA |
| MTTF | membrane-tethered transcription factor |
| MU | 4-methylumbelliferone |
| MUG | 4-methylumbelliferyl-beta-D-glucuronide |
| NAC | no apical meristem (NAM), ATAF1,2 and cup-shaped cotyledon (CUC2) |
| NBT | nitro-blue tetrazolium |
| NLS | nuclear localization signal |
| NPR1 | nonexpressor of pathogenesis-related genes 1 |
| Nt | nucleotide |
| NTA | nitrilotriacetic acid |
| OD | optical density |
| ORF | open reading frame |
| PAGE | polyacrylamide gel electrophoresis |
| PCR | polymerase chain reaction |
| PEG | polyethylenglycol |
| phi | phosphate induced |
| RACE | rapid amplification of cDNA ends |
| RNA | ribonucleic acid |
| rRNA | ribosomal RNA |
| SA | salicylic acid |
| SAR | systemic acquired resistance |
| SARE | salicylic acid responsive element |
| $SCF^{COI1}$ | skip-cullin-F-box |
| SDS | sodium dodecyl sulfate |
| $Sm/Sp^{r}$ | streptomycin/spectinomycin resistance |
| SPME | solid phase micro extraction |
| TAE | tris-acetate-EDTA |

| | |
|---|---|
| TF | transcription factor |
| TEMED | N,N,N’,N’-tetramethylethylenediamine |
| TIC | total ion chromatogram |
| TMV | *tobacco mosaic virus* |
| TPS | terpene synthase |
| Tris | tris(hydroxymethyl)aminomethane |
| UV | ultra-violet |
| VOC | volatile organic compound |

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# 1. Introduction

## 1.1 The role of volatiles in plant defense

Organisms have evolved a way of communication with other organisms in order to survive in their environment. The chemical nature of plant communication has recently developed into a subject for intense research.

Plants are able to produce a complex mixture of volatile organic compounds (VOC) which are means to exchange information with its environment. These VOCs can be grouped into several chemical families: phenylpropanoid/benzenoids, fatty acid derivatives, amino acid derivates, sulfur-containing compounds, and terpenes (Dudareva *et al.* 2006). Most volatile terpenes belong to mono- ($C_{10}$) and sesqui- ($C_{15}$) terpenes and can be released from flowers and vegetative organs. Since the production of volatiles is cost-intensive for plants (Wright *et al.* 1979), these compounds were suspected to play an important role. Volatile compounds that are emitted from flowers can attract pollinators and seed dispersers to provide a reproductive advantage (Raguso and Pichersky 1995; Pichersky and Gershenzon 2002; Reinhard *et al.* 2004). Also, vegetative organs can emit volatiles. Sharkey and coworkers showed that isoprene, a simple $C_5$- terpene volatile, is released from the foliage of many tree species. Isoprene facilitates the photosynthetic apparatus to recover from brief episodes of temperatures over 40°C (Sharkey *et al.* 2001). The function of volatiles emitted from herbivore-attacked plants, has been well studied. Sometimes, these compounds are released when feeding ruptures pre-existing internal or external secretory structures in which the volatiles are synthesized and stored (Franceschi *et al.* 2005). In this case, the volatiles can directly repel or otherwise kill the invader (microbes, animals) due to their toxic nature (De Moraes *et al.* 2001; Kessler and Baldwin 2001; Vancanneyt *et al.* 2001). In other cases, airborne volatiles are produced from herbivore-damaged plants several hours after plant damage (Paré and Tumlinson 1997). Here, the volatiles serve as a chemical signal that attracts the enemies of the herbivore (Dicke 1994; Degenhardt *et al.* 2003; Howe and Jander 2008), thereby reducing the number of attacking herbivores (Kessler and Baldwin 2001). Belowground, the volatiles released from roots can act as antimicrobial and antiherbivore substances. They can also recruit enemies of root-feeding herbivores (Rasmann *et al.* 2005). Interestingly, plant volatiles do not only have the potential to affect animals but also other

plants in the direct proximity (Pichersky and Gershenzon 2002). It was shown that tobacco (*Nicotiana attenuata*) plants growing next to wounded sagebrush (*Artemisia tridentata*) suffered reduced levels of herbivore damage and exhibited increased levels of transcriptional responses (Kessler *et al.* 2006). In a different experiment, undamaged bean plants (*Phaseolus vulgaris*) exposed to volatiles from herbivore-infested neighbors showed an elevated expression of several genes involved in defense metabolism (Arimura *et al.* 2000). This so called "priming" was also found in poplar (Frost *et al.* 2008) and maize (Engelberth *et al.* 2004) when plants were exposed to green leaf volatiles, methyl jasmonate (MeJA), or volatile terpenes. An overview of the functional aspects of plant volatiles is depicted in Fig.1.1.

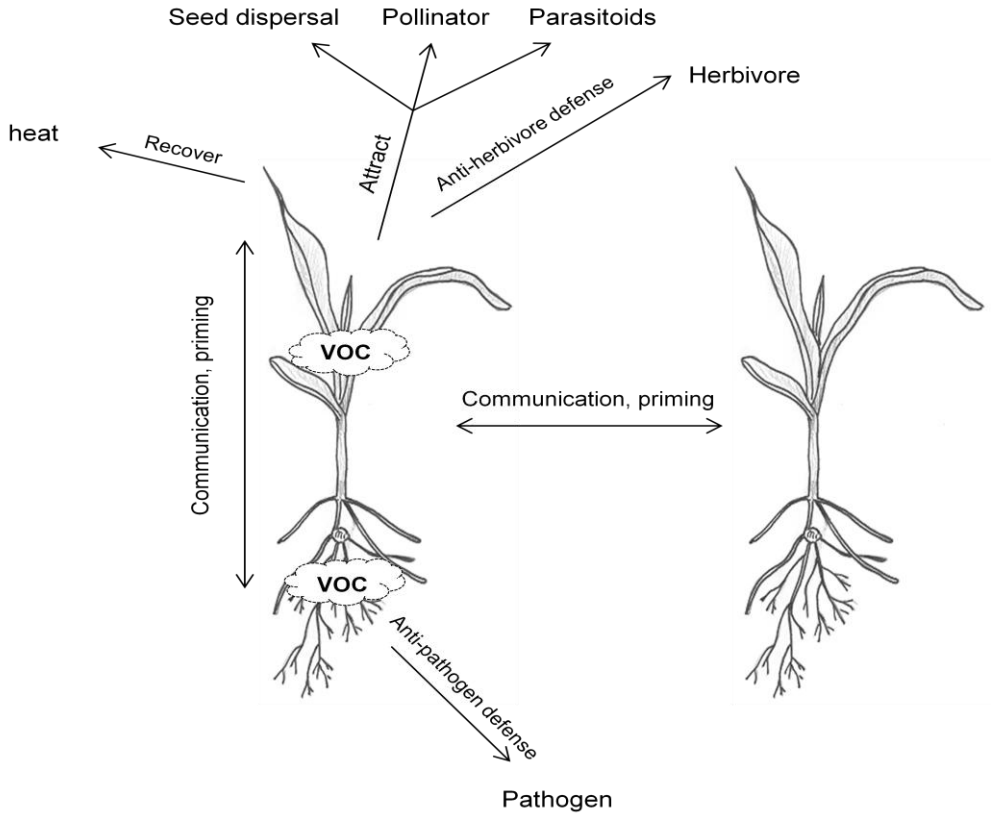



**Fig.1.1: Volatile-mediated plant interactions with its environment.** VOCs emitted from the plant can attract pollinators, seed disseminators, and parasitoids. Defense against herbivore attackers takes place above- and belowground. Communication between different organs of the plant and in between plants (priming, allelopathy) can be mediated by VOCs. The volatile terpene isoprene has a function in photoprotection and thermotolerance.

Systemic signaling has been described in several plant species (Howe and Jander 2008). Within hours, inducible defenses are found in undamaged parts of herbivore-attacked plant, providing a better resistance to future insect attacks (Karban and Baldwin 1997; Bostock 2005). These defenses include increased leaf concentration of terpenoids in cotton (*Gossypium herbaceum*) and *Zea mays* (Bezemer *et al.* 2003; Bezemer *et al.* 2004; Rasmann *et al.* 2005), certain glucosinolates in *Brassica spp.* (Van Dam et al. 2004; Van Dam and Raaijmakers 2006), and phytoectosteroids in *Spinacia oleracea* (Schmelz *et al.* 1998) upon root attack. Also, increased defenses in roots have been observed after leaf herbivory (Baldwin *et al.* 1994; Van Dam *et al.* 2001). These interactions indicate a possible effect of root herbivory upon defenses in the leaves by changing the performance of leaf herbivores (Wäckers and Bezemer 2003; Van Dam *et al.* 2005).

## 1.2 The indirect defense in *Zea mays*

Maize is one of the major crop plants, a nutrition base for many cultures and used as a source for bioethanol (Wheals *et al.* 1999). Therefore, pests damaging maize fields can cause major economical losses. Consequently, many researchers investigated the natural defense mechanisms in *Zea mays*. It was found that maize is able to defend itself by releasing a complex mixture of volatiles after herbivore damage through the larvae of the Egyptian cotton leaf worm (*Spodoptera littoralis*, (Turlings *et al.* 1990)). These volatiles can be used as cues by the parasitic wasp *Cotesia marginiventris* to locate its host for oviposition (Turlings *et al.* 1990; Turlings *et al.* 2005). Upon parasitization, the lepidopteran larvae feed less and die eventually due to the growing parasitic larvae within. This can result in a significant reduction in the damage to the plant (Hoballah *et al.* 2002; Hoballah *et al.* 2004). This tritrophic interaction, termed “indirect defense”, was recognized in the 1980s and studied since (Fig 1.2). Similar interactions were also found belowground. Parasitic nematodes locate their host through the volatiles released by herbivore-damaged maize roots (Rasmann *et al.* 2005). Maize volatiles consist mainly of terpenoids and products of the lipoxygenase pathway as well as some minor aromatic compounds (Turlings *et al.* 1990; Degen *et al.* 2004; Köllner *et al.* 2004).

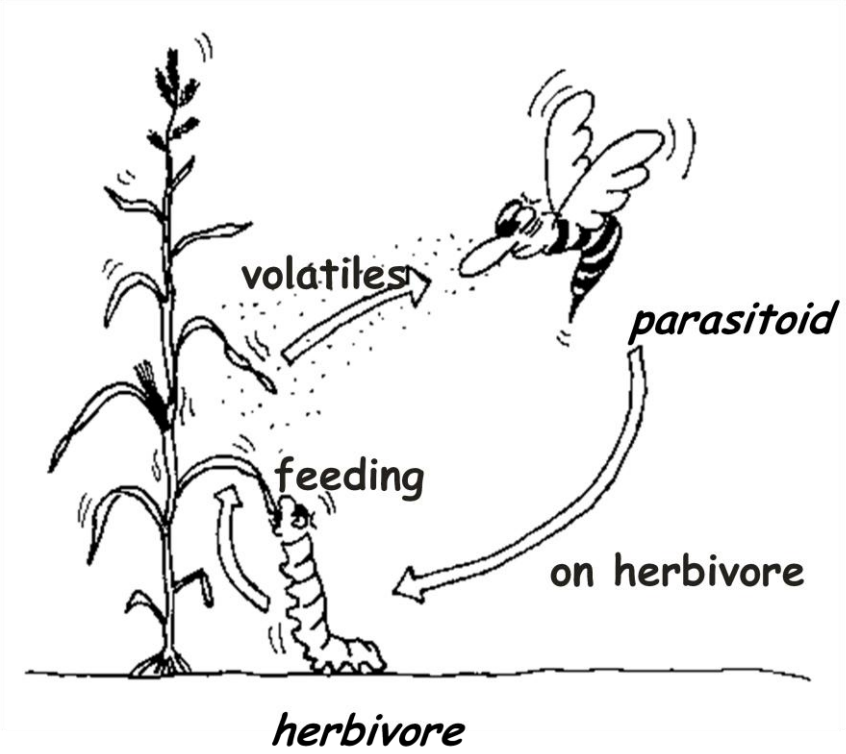



**Fig 1.2: Schematic overview of the tritrophic interaction in maize.** When maize is fed upon by the larvae of *S. littoralis*, it releases a complex mixture of volatiles which act as cues for the parasitic wasp *C. marginiventris* to locate its host (picture by Tobias Köllner).

Overall, there are more than 100 terpene synthase genes identified today (Tholl 2006; Degenhardt *et al.* 2009). All of them appear to have evolved from an ancestral diterpene synthase (Trapp and Croteau 2001; Martin *et al.* 2004). Furthermore, hemi-, mono-, sesqui-, and diterpene synthases from plants are more related to each other than to tri-, and tetraterpene synthases (Wu *et al.* 2005). All terpenoids originate from the precursor isopentenyl diphosphate (IPP) and its isomer dimethylallyl diphosphate (DMAPP, (Dudareva *et al.* 2006). Synthesis of these compounds occurs via the MEP pathway in plastids or the mevalonate pathway in the cytosol and mitochondria (Gershenzon and Croteau 1993; Rodríguez-Concepción and Boronat 2002). The enzymes responsible for the production of the maize terpenes, especially (*E*)-ß-caryophyllene, (*E*)-α-bergamotene, and (*E*)-ß-farnesene, have been identified and characterized. The terpene synthase TPS23 uses the substrate farnesyl diphosphate (FPP) to produce (*E*)-ß-caryophyllene as major product, and δ-elemene and α-humulene as minor products (Fig.1.3, (Köllner *et al.* 2008)).

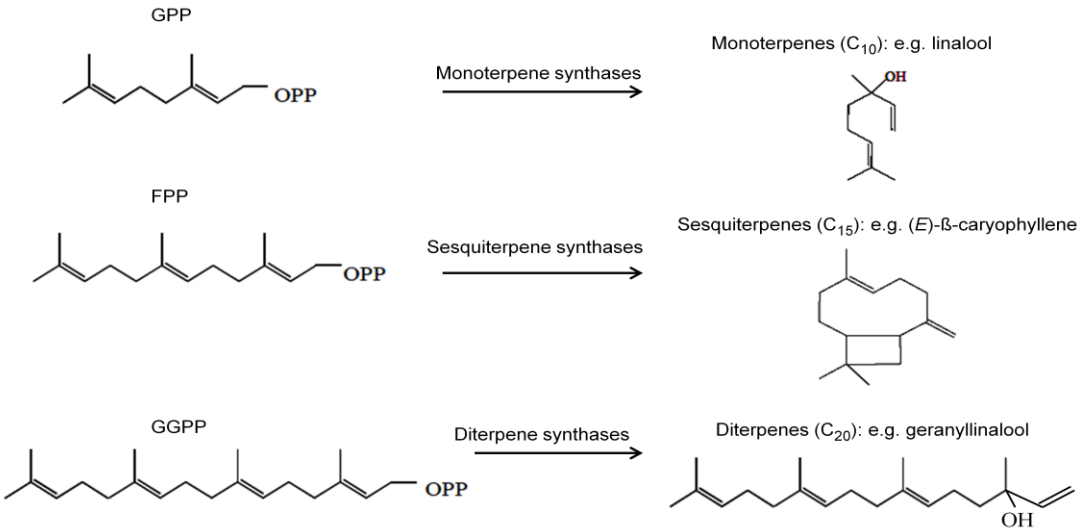



**Fig.1.3: The production of terpenes is mediated by different kinds of terpene synthases.** Monoterpene synthases use the substrate GPP to produce monoterpenes. The substrate FPP is the starting point for the synthesis of sesquiterpenes and is converted by sesquiterpene synthases. Diterpenes are produced by diterpene synthases using the precursor GGPP.

The terpene synthase TPS23 is induced after damage by the larvae of *S. littoralis* in the leaves and attack by larvae of the Western corn rootworm (*Diabrotica virgifera virgifera*) at the roots. The terpene synthase TPS10 which converts FPP into (*E*)-α-bergamotene and (*E*)-ß-farnesene (Schnee *et al.* 2006) is only induced after aboveground herbivory. In herbivore-induced roots, the terpenes specific for TPS10 were not found. This observation suggested differences in the signaling pathways that regulate the activity of both terpene synthases.

The composition of emitted volatiles differs between organs, developmental stages, and maize lines (Köllner *et al.* 2004). While the maize variety Delprim produces not only the sesquiterpenes (*E*)-α-bergamotene and (*E*)-ß-farnesene, but also (*E*)-ß-caryophyllene, the maize cultivar B73 does not produce (*E*)-ß-caryophyllene. This behavior is not only present in the leaves but also in infested roots (Rasmann *et al.* 2005). Roots of the maize line Delprim produce (*E*)-ß-caryophyllene after root attack by the larvae *D. virgifera*, but B73 does not. Since (*E*)-ß-caryophyllene can act belowground as a signal for pathogenic nematodes which feed upon the *D. virgifera* larvae, the production of (*E*)-ß-caryophyllene might be an important defense mechanism (Degenhardt *et al.* 2009).

## 1.3 Plant signal transduction in response to herbivory

### 1.3.1 The function of plant hormones in signal transduction after herbivore attack

Plant hormones such as jasmonic acid (JA), salicylic acid (SA), ethylene, and abscisic acid (ABA) not only regulate plant growth and development, but the responses to abiotic and biotic stresses with considerable signaling cross talk (Walley et al. 2007). ABA, a sesquiterpenoid with one asymmetric carbon at C-1 (Rock and Zeevaart 1991), is known for the control of germination, seedling growth and development (Fig.1.4). It plays a key role in the adaptive responses to abiotic stresses such as drought (Davies and Zhang 1991), high salinity, and cold. It also mediates adaptive responses like stomata closure (Tardieu and Davies 1992). The functional aspects of ABA, calcium, and the signaling cascade leading to the closing of the guard cells have been studied intensively. There are two signaling cascades leading to stomata closure, one via $Ca^{2+}$ and one via ABA which are both interconnected. Both cascades lead to the activation of anion channels and thereby reduce the osmotic potential of the cell (Marten *et al.* 2007). ABA might also play a role in herbivore defense (Anderson *et al.* 2004). ABA deficiency in tomato (*Solanum lycopersicum*) and *Arabidopsis thaliana* leads to an enhanced performance of larvae of the beat armyworm (*Spodoptera exigua*) and the Egyptian cotton leaf worm (*Spodoptera littoralis,* (Thaler and Bostock 2004; Bodenhausen and Reymond 2007). However, upon root attack ABA and ABA-induced signaling do not play an exclusive role in leaf defense. It is rather the ABA-independent hydraulic changes upon herbivory that induces plant defenses. Overall, the increase of ABA concentration after belowground attack might be a plant response to reduce the negative effects of water loss (Erb *et al.* 2011).

Ethylene, the only volatile phytohormone, has many biological functions (Fig.1.4). It triggers fruit ripening, influences senescence and the abscission of plant organs, plays a role in seed germination, root formation, pollination, cell elongation, sex determination, and flowering (Abeles *et al.* 1992). It also regulates responses to biotic and abiotic stresses. The importance of ethylene to biotic stress on aboveground parts of the plants after attack by arthropod herbivores has also been demonstrated (Kendall and Bjostad 1990; von Dahl and Baldwin 2007). Because of its volatility, ethylene is highly transportable by either direct diffusion

through the vascular tissue or diffusion from the rhizosphere to the phyllosphere (Jackson and Campbell 1975). Ethylene might also be involved in volatile defense signaling within and between plants (Ruther and Kleier 2005).

The plant hormone most strongly associated with defense against pathogen attack is salicylic acid (SA, Fig.1.4). This hormone modulates plant responses to pathogen infection and regulates responses to abiotic stresses through signaling crosstalk with other plant hormones (Achard *et al.* 2006; Horváth *et al.* 2007; Spoel and Dong 2008; Vlot *et al.* 2009). Additionally, SA plays a role in plant adaptive responses to osmotic stress (Singh and Usha 2003), chilling, drought (Senaratna *et al.* 2000), heat stress (Clarke *et al.* 2004), and salt stress (Khodary 2004). Through the interactions with gibberellins, ABA, JA, and ethylene, SA exerts a role in a variety of plant development processes (Yasuda *et al.* 2008; Alonso-Ramírez *et al.* 2009; Leon-Reyes *et al.* 2009). The importance of SA for the induction of systemic acquired resistance (SAR) has been well studied (Ross 1961; Kuc 1982). However, SA-responsive genes were also found to be up-regulated after herbivore attack (Zarate *et al.* 2007). The methylated form of salicylic acid, methyl salicylate (MeSA) is released after pathogen infection and might be a potential signal for the induction of defense-related genes in neighboring plants (Shulaev *et al.* 1997).

Jasmonic acid is synthesized via the octadecanoid pathway (Vick and Zimmerman 1984; Feussner and Wasternack 2002) from α-linolenic acid or hexadecatrieonic acid (Ishiguro *et al.* 2001; Hyun *et al.* 2008). This hormone is a key regulator for stress-induced genes in all plants (Reymond and Farmer 1998; Schaller 2001). It is implicated in systemic plant responses against herbivory aboveground (Farmer and Ryan 1992; Howe *et al.* 1996) and likely also belowground (Schmelz *et al.* 1999; Puthoff and Smigocki 2007). Jasmonic acid is also induced in the tissue surrounding the site of wounding (Felix and Boller 1995; O'Donnell *et al.* 1996) and is actively transported or diffuses from its site of synthesis (Farmer *et al.* 1992). Its role in long-distance wound signaling (Stratmann 2003; Wasternack *et al.* 2006) is supported by the fact that exogenous JA moves easily through the phloem (Zhang and Baldwin 1997). Experiments in tomato showed that jasmonate signaling is required for a functional recognition of a long distance wound signal while jasmonate biosynthesis is required for the generation of such a long distance wound signal (Li *et al.* 2002). Thus, Li and coworkers demonstrated that jasmonate is a essential component of the

transmissible wound signal and may act as intercellular signal or trigger for the production of such signal (Li *et al.* 2002). An overview of structures of the major hormones found in plants is shown in Fig.1.4.

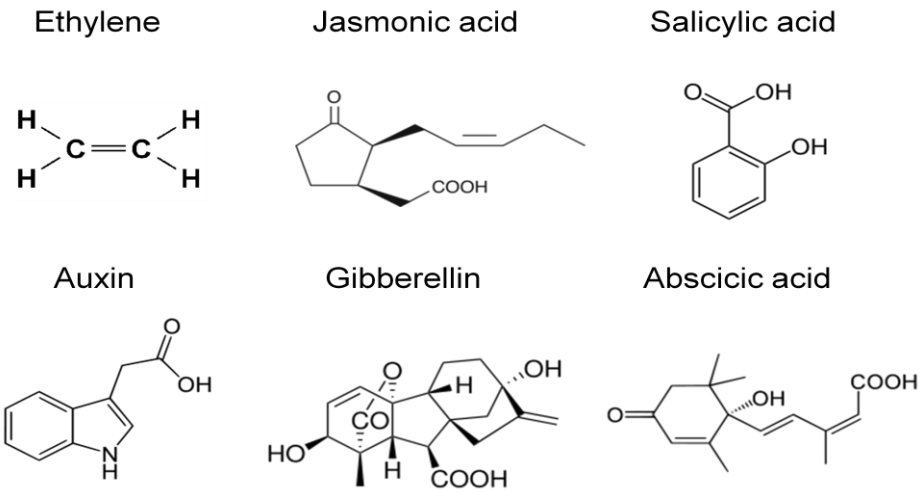



**Fig.1.4: Overview of major plant hormones: ethylene, jasmonic acid, salicylic acid, auxin, gibberellins, and abscisic acid with the regarding chemical structure, respectively.**

The production of plant hormones varies greatly depending on the nature of the attacking pathogen or insect (Mur *et al.* 2006). In addition to JA, SA, ET, and ABA, further plant hormones seem to have a function in the immune response of plants. Unfortunately, the role of brassinosteroids (Nakashita *et al.* 2003), gibberellins (Navarro *et al.* 2008) and auxin (Navarro *et al.* 2006; Wang *et al.* 2007) in plant defense is less studied. Since hormone-dependent pathways are differentially effective against specific types of attackers (Thomma *et al.* 2001; Glazebrook 2005; Thatcher *et al.* 2005), there has to be a cross talk between the signaling pathways that induces plant defense (Reymond and Farmer 1998; Koornneef and Pieterse 2008; Spoel and Dong 2008). This cross talk can be either antagonistic or synergistic in order to fine tune the response to the invading attacker (Reymond and Farmer 1998; Pieterse *et al.* 2001; Kunkel and Brooks 2002; Bostock 2005). JA and ethylene are both required for the activation of wound responses and induce each other's synthesis (Ross 1961), while SA inhibits the synthesis and the signaling pathway of JA and ET (Dong 1998).

### 1.3.2 Components of the signaling transduction pathways of plant defenses

The signal transduction pathway from herbivore attack to the production of volatile terpenes is mostly unknown. It is evident that a defense response depends on the developmental stage of a plant as well as on the strategy of the invading attacker (De Vos *et al.* 2005). Also, the quantity, composition and timing of a phytohormonal blend produced by the plant varies among different attackers (De Vos *et al.* 2005). For the primary defense response to a pathogen, plants must be able to recognize common features of microbial pathogens, such as flagellin, chitin, glycoproteins and lipopolysaccharides, so-called PAMPs (Göhre and Robatzek 2008; Nürnberger and Kemmerling 2009). The positive outcome of a immune reaction to pathogen invasion results in a hypersensitive response (De Wit 1995; De Wit 1997) and leads to a SAR which is dependent on a SA signaling (Durner *et al.* 1997). This SAR is induced throughout the plant and is relevant for an enhanced and long-lasting resistance to secondary challenges by the same or unrelated pathogen (Wobbe and Klessig 1996). While the receptor type for SA is unknown (Santner and Estelle 2009), one key regulator of SA-mediated signaling has been characterized. NPR1 (nonexpressor of pathogenesis-related genes 1) is an ankyrin repeat-containing protein (Cao *et al.* 1997) that interacts with TGA transcription factors to activate pathogen-related gene expression (Fan and Dong 2002; Després *et al.* 2003). Its nuclear localization has been implicated in the activation of SA-responsive genes (Kinkema *et al.* 2000; Dong 2004). For the antagonistic effect of SA on the JA-signaling pathway, NPR1 has to be localized in the cytosol (Spoel *et al.* 2003; Yuan *et al.* 2007). The picture becomes even more complicated since the cytosolic function of NPR1 can be bypassed by ethylene (Leon-Reyes *et al.* 2009).

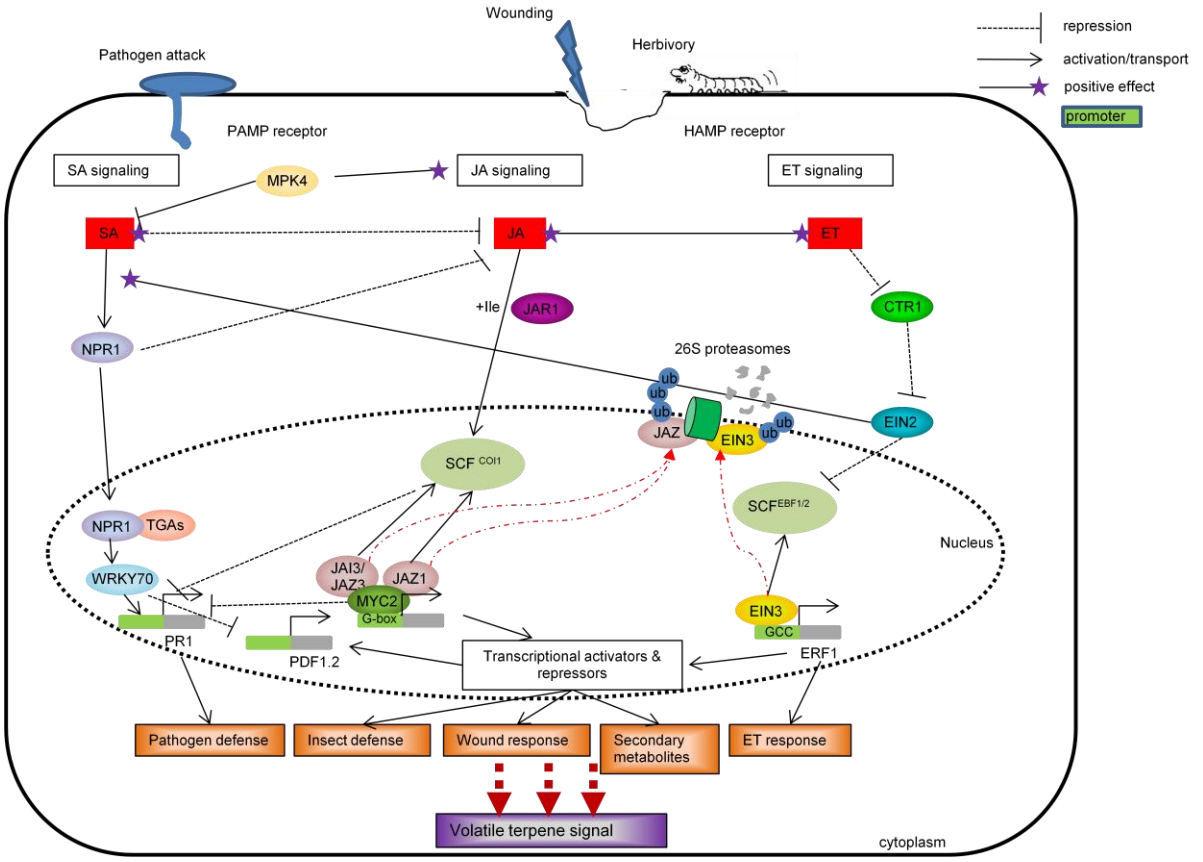



**Fig.1.5: Overview of the jasmonate signaling pathway and the connection to salicylic acid and ethylene in Arabidopsis.** Several stress signals can activate a phosphorylation cascade that induces jasmonate signaling. Jasmonic acid is further modified in the cytosol to produce several jasmonic acid derivates (MeJA, JA-Ile). In the presence of JA, the JAZ protein that acts as transcriptional regulator of MYC2 is degraded via $SCF^{COI1}$ and releases MYC2 from repression. The transcription factor MYC2 probably binds to the conserved G-box elements in the promoters of other transcriptional activators and repressors from AP2/ERF, WRKY, and MYBs, which modulate distinct JA-dependent functions. There are several factors that act as a signaling cross point between different pathways. NPR1, MPK4, WRKY70, $SCF^{COI1}$, and MYC2 are involved in the interactions between SA and JA. It is also known that SA and JA act antagonistically and synergistically in a dose-dependent manner. The JA and ET pathways positively influence each other, but ET also has a positive effect on SA. The negative role of CTR1 is suppressed upon perception of ET. Downstream signaling through EIN2 is mediated by repression the E3 ubiquitin ligase SCFEBF1/2-dependent 26S proteasome degradation of EIN3. EIN3-like transcription factors activate transcription factors such as ERF1, resulting in the expression of downstream ET-responsive genes. Only major key players are shown. Altered after Kazan and Pieterse (Kazan and Manners 2008; Pieterse *et al.* 2009).

The jasmonate signaling pathway has been investigated intensively and some of the key elements are known. Jasmonic acid is induced after wounding or herbivore feeding (Farmer and Ryan 1992). After JA formation, the JAR1 (JA amino acid conjugate synthase) protein binds isoleucin to jasmonic acid (Staswick and Tiryaki 2004), which represents the biologically active signal. In the presence of jasmonic-isoleucin (JA-Ile), the $SCF^{COI1}$ (skip-cullin-F-box) complex promotes the ubiquitination of JAI3 (jasmonate insensitive3) and JAZ (jasmonate-ZIM-domain proteins) which leads to their degradation by the 26S proteasome (Chini *et al.* 2007; Thines *et al.* 2007). Without the JAZ3 protein, the transcription factor MYC2 is de-repressed and can activate the transcription of jasmonate-responding genes including JAZ3 (Lorenzo *et al.* 2004). Therefore, jasmonic acid signaling contains a negative self-regulation. Jasmonate-inducible genes include proteinase inhibitors such as insect antifeedants (Ryan 1990), antifungal proteins like Thi (thionins), and PDF1.2 (defensin) (Penninckx *et al.* 1998; Vignutelli *et al.* 1998) that is often used as molecular marker for herbivory. Interestingly, the signaling pathways of ethylene, gibberellin, and auxin are also mediated via SCF complexes (Devoto and Turner 2005). An overview of the signaling pathway of JA and the crosstalk with SA and ET is depicted in Fig.1.5.

## 1.4 Regulatory elements of wound-inducible promoters

Promoters contain sequence elements that regulate gene activity in response to environmental cues. Those regulatory elements are bound by transcription factors which control the activation of gene expression. Several *cis*-acting elements have been identified in connection with the regulation of defense genes. A methyl jasmonate-responsive element was identified in the promoter of lipoxygenase in barley with the sequence TGACT (Rouster *et al.* 1997). Table 1.1 gives some examples of further *cis*-elements involved in plant defense.

**Tab.1.1: Examples of identified regulatory elements induced by hormones or wounding.**

| Name | Sequence | Response to | Reference |
|---|---|---|---|
| **ABRE** | ACGTG | ABA | (Hattori *et al.* 1995) |
| **as-1** | TGACG | SA/pathogen | (Strompen *et al.* 1998) |
| **ATMYC2** | CAYRTG | ABA | (Abe *et al.* 2003) |
| **ERE** | ATTTCAAA | Ethylene | (Itzhaki *et al.* 1994) |
| **G-box** | CACGTG | JA | (Chini *et al.* 2007) |
| **G-box** | AGCCGCC | Ethylene | (Ohme-Takagi and Shinshi 1995) |
| **GT-1 motif** | GAAAAA | Pathogen/salt | (Park *et al.* 2004) |
| **JERE** | GCC core | JA/MeJA | (Menke *et al.* 1999) |
| **MYBR** | TGGTTAG | ABA | (Abe *et al.* 2003) |
| **MYCR** | CACATG | ABA | (Abe *et al.* 2003) |
| **S-box** | AGCCACC | Fungal elicitor | (Kirsch *et al.* 2000) |
| **W-box** | TGACY | Wound | (Nishiuchi *et al.* 2004) |
| **WUN-box** | TCATTACGAA | Wound | (Matton *et al.* 1993; Pastuglia *et al.* 1997) |
| **SARE** | TTCGATC | SA | (Hayashi *et al.* 2003) |

In addition, Hayashi and colleagues presented several inducible elements found in the promoters of *ngr1* and *ngr3*, two enzymes encoding S-like ribonucleases. Here, a tobacco mosaic virus (TMV)-responsible element, the GT1 binding site, is described. The same promoter also contains many elicitor-responsive elements like ERE, TC-rich repeats, an ELI-box, and an EIR-element (Hayashi *et al.* 2003).

Two additionally jasmonate-responsive elements, JASE1 and JASE2, have been reported. Both elements have been found in the promoter of the *opr1* gene in Arabidopsis (He and Gan

2001). The LTR (long terminal repeat) promoter of the tobacco retrotransposon element *Tto1* contains a L/AC-I or H-box-like motif, which is responsive to MeJA (Takeda *et al.* 1999). Overall, a number of jasmonate-responsive elements exist. Well-studied promoter elements are the G-box and motifs with a GCC-core. Promoters containing a G-box (e.g. *PDF1* (Lorenzo *et al.* 2003)) respond to jasmonates while they are negatively influenced by ethylene. On the other hand, promoters with a GCC-motif (e.g. vegetative storage protein (Benedetti *et al.* 1995)) are activated by JA with a synergistic effect of ET (Memelink 2009).
In several studies, inducible promoters have been used to generate transgenic plants that are more resistant to various diseases. Moreno and colleagues used the promoter of a fungal-induced class II chitinase fused to the antifungal protein of *Aspergillus giganteus* to create rice plants with resistance to the blast fungus *Magnaporthe grisea* (Moreno *et al.* 2005).

## 1.5 Transcription factors involved in the regulation of plant defense

An important part of plant stress responses is the regulation of specific stress genes that primarily occurs at the level of transcription (Rushton and Somssich 1998). Transcription factors regulate early steps of gene expression. They are defined as proteins that contain a specific DNA-binding domain (Mitsuda and Ohme-Takagi 2009). A genome-wide analysis identified over 2000 putative transcription factors in the Arabidopsis genome (Davuluri *et al.* 2003; Mitsuda and Ohme-Takagi 2009) while the fruit fly (*Drosophila melanogaster*) only contained 600 transcription factors. This suggests that transcriptional regulation plays a more important role in plants than in animals (Riechmann *et al.* 2000). Even between different organs of the same plant, there are differences in the activation of transcription factors. Roots of Arabidopsis express more stress-related transcription factor genes than leaves (Chen *et al.* 2002).
Different families of transcription factors have been identified in Arabidopsis: AP2/EREBP, bZIP/HD-ZIP, MYB, and zinc finger domain proteins. The expression of these factors is often induced or repressed under stress conditions and therefore has most likely a role in plant stress responses (Shinozaki and Yamaguchi-Shinozaki 2000). Transcription factors can activate or repress gene expression depending on the structure of their activation domain (Mitsuda and Ohme-Takagi 2009). Members of the AP2/EREBP (apetala2/ethylene

responsive element binding protein) family are induced after abiotic stress, bacterial infection, infection with different pathogens including bacteria, fungi, oomycetes, and viruses (Chen *et al.* 2002). BZIP/HD-ZIP transcription factors are induced after abiotic stress like cold, salt, osmoticum, and JA, and abiotic stress plus bacterial infection (Chen *et al.* 2002). These basic leucine zipper proteins play a role in phytomorphogenic development and hormone signaling (Jakoby *et al.* 2002) and show similar features to other bZIP proteins of plants (Cheong *et al.* 1998). The bZIP transcription factors recognize C-boxes and C/T or C/A-boxes over G-boxes in the promoters of their target genes (Song *et al.* 2008).

The expression of MYB transcription factors can be up-regulated after abiotic stress, abiotic stress plus bacterial infection, bacterial infection, as well as infection with different pathogens (e.g. fungi, oomycetes, viruses) (Chen *et al.* 2002). Also, MYB transcription factors were implicated as key regulators in aliphatic glucosinolate biosynthesis in Arabidopsis (Hirai *et al.* 2007). Since the MYB domain consists of up to 3 imperfect repeats forming a helix-turn-helix structure (Frampton *et al.* 1991), it is thought that MYB proteins interact with basic helix loop helix proteins (bHLH) to form complexes through the conserved amino acid sequence $[DE]Lx_2[RK]x_3Lx_6Lx_3R$ (Zimmermann *et al.* 2004). In maize, two R2R3-MYB proteins interact with bHLH transcriptions factors that are required for the production of the purple anthocyanin pigments (Petroni *et al.* 2000). bHLH proteins form a ubiquitous family of regulators in eukaryotes. Functional analyses predicted different roles in plant cell, tissue development, and plant metabolism (Heim *et al.* 2003).

Transcription factors that have a strictly conserved amino acid sequence and bind to the W-box motif belong to the group of WRKY transcription factors (Eulgem *et al.* 1999). They contribute to the control of some of the stress responses and are up-regulated after pathogen infection or wounding (Eulgem *et al.* 2000). Several studies indicate a role of WRKY factors from *Arabidopsis thaliana* during senescence (Eulgem *et al.* 2000). Interestingly, all WRKY factors contain an intron within the region encoding the C-terminal region, and share a zinc-finger-like motif (Eulgem *et al.* 2000). In tobacco plants, WRKY transcription factors are involved in the early events of the hypersensitive response against tobacco mosaic virus (Yoda *et al.* 2002). Members of the WRKY group III transcription factors in Arabidopsis are induced after salicylic acid treatment (Kalde *et al.* 2003) and have a functional role in the cross talk between SA and JA pathway (Li *et al.* 2004). In this regard, it was published that

NPR1 is controlled by WRKY factors (Yu *et al.* 2001) and that those transcription factors are downstream components of the MAPK pathway (Petersen *et al.* 2000; Miao *et al.* 2007). WKRY transcription factors are the substrates for MAP kinases, which can regulate activation of SA-dependent resistance as well as block the induction of PDF1.2 by JA (Petersen *et al.* 2000). A further example of WRKY factors is OsWRKY from rice that is regulated by multiple factors to achieve disease resistance (Cai *et al.* 2008).

Another group of transcription factors are zinc-finger transcription proteins which are implicated after abiotic stress, bacterial infection, and infection with pathogens (Chen *et al.* 2002). An important example for this group is the CaZFP, an $Cys_2/His_2$-type zinc-finger transcription factor suggested in early defense of pepper plants against pathogens and abiotic stress (Kim *et al.* 2004). It binds to two *cis*-acting elements, AGT core motifs, separated by 13 bp (Takatsuji and Matsumoto 1996).

Transcription factors with an implicated role in the JA-ET crosstalk are AtMYC2, a helix-loop-helix-leucine zipper, and the ERF1 ethylene responsive factor (Felton and Korth 2000; Lorenzo *et al.* 2004). ERF1 binds to GCC-box in the promoter of target genes (Fujimoto *et al.* 2000) and is induced after infection with pathogens (Solano *et al.* 1998). An essential transcription factor in the signaling pathway of JA and ET that can activate PDF1.2 gene expression is ORA59 which belongs to the AP2/ERF domain transcription factors (Pré *et al.* 2008).

SA biosynthesis is influenced by the transcription factor NtWIF (Waller *et al.* 2006) that is activated upon phosphorylation by wound-induced protein kinase (WIPK) in tobacco (Maffei *et al.* 2007). Also, the CaRAV1 transcription factor from pepper (*Capsicum annum* L.) is involved in the SA-dependent signaling pathway (Sohn *et al.* 2006) and contains two or more distinct types of DNA-binding domains (Kagaya *et al.* 1999). This transcription factor belongs also to the family of AP2/EREBP. In pepper, the important transcription factor CaATL1 was found. CaATL1 contains an AT-hook motif and increases in response to SA and/or ethephone treatment. Therefore, it has been implicated in the response against pathogen attack (Kim *et al.* 2007). GBF3 (G-box factor 3) belongs to the family of bZIP transcription factors and functions downstream of SA and NPR1 in the SA dependent signaling pathway (Chen *et al.* 2002). Additionally, NPR1 is known to respond to ABA (Lu

*et al.* 1996). Therefore, it was thought that the signaling pathway activated by senescence may overlap with stress signaling pathway (Chen *et al.* 2002).

The activity of transcriptions factors is not only regulated at the level of transcription but by proteolytic activation. Some transcription factors were found to be anchored in the ER or golgi membranes in a dormant state and are activated upon proteolysis (Chen *et al.* 2008). This group of MTTFs (membrane-tethered transcription factors) contains some bZIP and NAC transcription factor, but only one was found in response to ABA (Chen *et al.* 2008).

## 1.6 Objectives of this work

The crop plant *Zea mays* is known to respond to herbivore attack with the emission of terpene volatiles. The composition of the volatile blend is specific for the type of herbivore and the site of attack, suggesting a complex signal transduction network that is involved in the formation of the volatile signal. Since terpene biosynthesis and its key enzymes, the terpene synthases, have already been investigated in maize, we chose this plant as a model system to investigate the signal transduction pathway for herbivore-induced genes and elucidate their temporal and spatial patterns. The project starts with a transcriptome analysis to identify genes that are altered in their expression patterns after herbivore attack. The analysis focuses on transcription factors which may play an important role in the regulation of plant defense genes. An investigation of the spatial and temporal expression pattern in response to several herbivore-related stimuli provides insight into the major cues and nature of the plant regulatory networks for volatile terpene biosynthesis.

A second approach to elucidate the regulation of volatile terpene biosynthesis focuses on the regulation of the terpene synthases *tps10* and *tps23.* A promoter deletion analysis will be performed to identify important regulatory *cis*-elements for both genes. Heterologous expression of promoter::reporter gene constructs in *Arabidopsis thaliana* provides a method to overcome the limitations of maize transformation.

# 2. Materials and methods

## 2.1 Cultivation and treatment of *Zea mays* L.

Seeds of the four maize lines B73, Delprim, W22, and UFMu-02709 were grown in climate-controlled chambers (York Int., York, USA) under the following conditions: 16 h photoperiod, 1 mmol $m^{-2}$ $s^{-1}$ of photosynthetic active radiation, a temperature cycle of 22°C/18°C (day/night), and 65 % relative humidity (Tab.2.1). Clay substrate potting soil (Klasmann, Gross-Hesepe, Germany) with Osmocote fertilizer (Scotts, Nordhorn, Germany) in seed flats (400x600x60 mm) or pots (160 mm in diameter) were used to cultivate plants.

**Tab.2.1: Description of maize lines used in this work**

| **Name** | **Description** | **Origin** |
|---|---|---|
| **B73** | Inbred line [Reid Yellow Dent] | KWS (Einbeck, Germany) |
| **Delprim** | Hybrid line ([DSP1387C[Dent] x DSP1743A[Flint]) | DSP AG (Delley, Switzerland) |
| **W22** | NSL 30053 - NC7, inbred line | US National Plant Germplasm System (Beltsville, USA) |
| **UFMu-02709** | Mu transposon insertion line with W22 as background | US National Plant Germplasm System (Urbana, USA) |

Twelve to fourteen day-old plants with 3 to 4 expanded leaves were used in all experiments. For herbivore treatment, three third instar larvae (*Spodoptera littoralis*) were enclosed in the lower part of the middle leaf of each plant in a clipped cage. The larvae were able to feed at least 12 h or according to the time course experiment: 0.5 h, 1 h, 2 h, and 4 h, respectively.
For mechanical damage, the upper side of 2 young leaves was scraped with a razor blade on each side of the midvein in an area of about 5x10 mm. For elicitor treatment, 10 µl of *S. littoralis* regurgitate (1:2 diluted with sterile water and boiled for 5 min at 95°C) or jasmonic acid (in 0.05 % DMSO) as an aqueous solution was applied to the wounded area. Additionally, plants were damaged with the mechanical caterpillar Mecworm (MPI for Chemical Ecology, Jena, Germany) for the same time points and induced again with 10 µl

regurgitate (Fig.2.1). The metal punch (Ø=0.5 mm) of this unit was programmed to damage 30 mm² of the leaf material (Mithöfer *et al.* 2005).

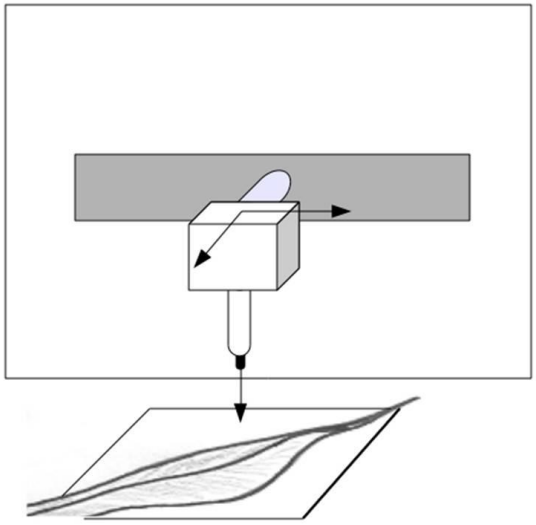


**Fig.2.1: Schematic design of the Mecworm.** The punching unit can be moved in two dimensions and results in a damaged area according to the programmed instructions.

## 2.2 Cultivation of *Spodoptera littoralis* (Boisd.) [Lepidoptera: Noctuidae]

Eggs of the Egyptian cotton worm (*Spodoptera littoralis)* were obtained from Syngenta (Basel, Switzerland) and raised on an artificial wheat germ diet (Heliothis mix, Stonefly Industries, Bryan, USA) for about 10-15 days at 22°C under an illumination of 750 µmol $m^{-2}$ $s^{-1}$. Third instar larvae were used for herbivore induction experiments.

## 2.3 Cultivation, treatment and transformation of *Arabidopsis thaliana* L.

*Arabidopsis thaliana* variety Columbia was used for all experiments. Transformed Arabidopsis plants were used in the T2 generation and were grown like wild type plants under standard conditions, including a 3 day cold period to obtain a simultaneous germination of the seeds. Plants were sown in a 100x100x110 mm pots in clay substrate potting soil (Klasmann, Gross-Hesepe, Germany) with Osmocote fertilizer (Scotts, Nordhorn,

Germany) in a climate controlled room at 150 µmol $(m^2)^{-1}$ $s^{-1}$ of photosynthetic active radiation at 22ºC and 65 % relative humidity at long-day conditions (16 h light). After starting to develop basal leaves, plants were separated into 60x60x80 mm pots.

Five week-old plants were induced by scratching the upper leaf with a razor blade and application of 10 µl 250 µM jasmonic acid (in 0.05 % DMSO) or by adding 2 ml 250 µM jasmonic acid to the plant soil over 3 days.

Arabidopsis was transformed using the floral dip method (Clough and Bent 1998; Zhang *et al.* 2006). The transformed *Agrobacterium tumefaciens* (2.4.4) were inoculated in a LB medium with spectinomycin, gentamycin and rifampicin for 48 h at 25°C. 25 ml of the pre-cultures cells were shaken in 500 ml LB medium containing the three antibiotics for 24 h at 27°C ($OD_{600}$=0.9). After centrifugation at 5500 g for 20 min at room temperature, the pellet was redisolved in 400 ml infiltration medium and $OD_{600}$ was adjusted to around 9.0 by adding infiltration medium.

The inflorescence of *A. thaliana* variety Columbia was transformed by dipping the whole upper parts of the plants for 10 s into the infiltration suspension. Plants were then wrapped in blue plastic hoods and kept overnight without direct sunlight. The transformed seeds were harvested and dried for several days. Positive transformed seeds were selected using a 1:3000 dilution of Basta® herbicide (Bayer Cropscience, Monheim am Rhein, Germany). The herbicide was applied every second day after the plants had reached a size of about 5 mm.

| | |
|---|---|
| Infiltration medium: | 5 % [w/v] sucrose |
| | 0.005 % [v/v] Silwet L-77 |

## 2.4 Microbiological methods

### 2.4.1 Bacterial strains and cultivation

*Escherichia coli* and *Agrobacterium tumefaciens* were cultured in LB medium in a shaker or grown on LB-agar plates in an incubator at 37°C, unless noted otherwise (Tab.2.2). Stock cultures were obtained by adding 300 µl 100 % sterile glycerol to 1 ml liquid culture and frozen at -80°C.

**Tab.2.2: Bacterial strains and their application**

| **Strains** | **Genotype** | **Application** |
|---|---|---|
| ***E. coli* Bl21 (DE3) (Novagen, Madison, USA)** | F$^-$ *omp*T *gal dcm lon hsd*$S_B$ ($r_B^-$ $m_B^-$) (DE3) | protein overexpression in pHIS8-3 (T7 promoter) |
| ***E. coli* TOP10 (Invitrogen, Carlsbad, USA)** | F$^-$ *mcr*A Δ(*mrr-hsd*RMS-*mcr*BC) Φ80*lac*ZΔM15 Δ*lac*X74 *deo*R *rec*A1 *ara*D139 Δ (*ara-leu*)7697 *gal*U *gal*K *rps*L ($Str^R$) *end*A1 *nup*G | general cloning of PCR products for sequencing and subcloning |
| ***A. tumefaciens* GV3101 (van Larebeke et al., 1974)** | with nopaline vir helper plasmid pMP90 | introduction of *tps* promoter constructs into *Arabidopsis thaliana* |

LB culture: 25 g LB medium (AppliChem, Darmstadt, Germany) in 1 l *a.dest.*

LB agar: 32 g LB-medium (AppliChem, Darmstadt, Germany) in 1 l *a.dest.*

### 2.4.2 Antibiotics

**Tab.2.3: Concentrations of applied antibiotics**

| **Antibiotic** | **Stock solution (mg ml$^{-1}$ in *a.dest*)** | **End concentration (µg ml$^{-1}$ media)** |
|---|---|---|
| **Kanamycin** | 50 | 50 |
| **Ampicillin** | 100 | 100 |
| **Gentamycin** | 50 | 50 |
| **Rifampicin** | 30 (in methanol) | 30 |
| **Spectinomycin** | 100 | 100 |

### 2.4.3 Transformation of *Escherichia coli*

50 µl of chemically competent *E. coli* cells were thawed on ice and mixed with 3 µl ligation solution. After 30 min incubation on ice, the transformation mixture was heat-shocked for 45 s at 42°C and transferred to ice again for 1 min. Subsequently, 150 ml SOC medium was added and the cultures were shaken for 1 h at 37°C. Half of the transformed culture was spread on a prewarmed agar plate with the corresponding antibiotic and incubated at 37°C over night (B6120 Kendro, Heraeus). Colonies where picked and checked for successful transformation with vector or insert specific PCR primers.

SOC-medium: 2 % Trypton [g/v] (Sigma-Aldrich, St. Louis, USA)
0.5 % yeast extract [g/v] (Sigma-Aldrich, Munich, Germany)
0.5 % glucose [g/v]
10 mM NaCl
2.55 mM KCl
21.6 mM $MgCl_2$
20 mM $Mg_2SO_4$

LB-agar: 32 g LB-medium (AppliChem, Darmstadt, Germany) in 1 l *a.dest.*

### 2.4.4 Transformation of *Agrobacterium tumefaciens*

The freeze-thaw method (Hofgen and Willmitzer 1988) was used to transform *Agrobacterium tumefaciens* with the destination vector containing the reporter gene GUS and a promoter fragment of *tps10* and *tps23*. 200 µl chemo-competent cells were thawed on ice and incubated with 0.5-1 µg plasmid DNA for 5 min on ice, in liquid nitrogen, and at 37°C, respectively. One ml LB medium was added, the reaction incubated for 30 min on ice, and then transferred to 28°C and shaken for 3 h. After centrifugation for 1 min at 7000 g, the cells were resuspended in 100 µl LB medium and 30 or 70 µl were plated on an agar plate containing spectinomycin, gentamycin and rifampicin. The agar plates were incubated at 28°C for 3 days.

LB-agar: 32 g LB-Agar (AppliChem, Darmstadt, Germany) in 1 l *a.dest.*

## 2.5 Nucleic acid techniques

### 2.5.1 Isolation of total RNA from maize

RNA for cDNA synthesis and QRT-PCR was extracted from leaves and roots with the RNeasy Plant Mini kit from Qiagen (Hilden, Germany) according to the manufacturer's protocol. Tissue was disrupted in liquid nitrogen, lysed in the presence of a denaturing guanidine isothiocyanate containing buffer and homogenized by centrifugation through a shredder column. Ethanol was added and samples were applied to silica-gel membrane columns which selectively bind the RNA. After several washing steps with ethanol-containing buffers, total RNA was eluted in 40 µl nuclease free water. Quantification of the total RNA was measured by UV spectrophotometers Ultrospec 2100pro (Amersham Biosciences, Uppsala, Sweden) and Infinite 200 Nano Quant (Tecan Group Ldt, Männedorf, Switzerland) and on an agarose gel.

RNA extraction for microarray experiments was also performed using the RNeasy Plant Mini kit from Qiagen with the following protocol. 50-80 mg frozen plant material was mixed with 450 µl RLT buffer, vortexed vigorously for 5 min and incubated at 21°C for 15 min in an Eppendorf Thermomixer (Eppendorf, Hamburg, Germany) at 1400 rpm. The extract was

transferred to a QiaShredder Column and centrifuged for 2 min at 16000 g. The supernatant was mixed with 225 µl 100 % ethanol, transferred to the RNeasy mini Column and centrifuged for 25 s at 8000 g. Flow through was discarded, 350 µl RW1 buffer was added to the column and again centrifuged for 15 s at 8000 g. DNA digestion was performed on column by adding 90 µl DNase buffer (Promega, Madison, USA) and 10 µl DNase (Promega, Madison, USA). After the incubation of 15 min at room temperature, 350 µl RW1 buffer was added and centrifuged for 15 s at 11000 g. The flow-through was discarded and 500 µl RPE buffer was added. After the centrifugation (15 s at 11000 g) the flow through was discarded and the washing step was repeated. The column was dried for 2 min at 11000 g and RNA was eluted with 40 µl 70°C preheated nuclease free water and centrifuged at 9000 g for 1 min.

### 2.5.2 Isolation of genomic DNA from plant material

Plant material was frozen in liquid nitrogen and ground into a fine powder. Genomic DNA was isolated with the DNeasy Plant kit from Qiagen (Hilden, Germany) according to the manufacturer's instruction.

### 2.5.3 Isolation of plasmid DNA from bacteria

For the isolation of plasmid DNA from bacteria, the Nucleo Spin Plasmid kit from Macherey&Nagel (Düren, Germany) was used following manufacturer's instruction.

### 2.5.4 DNA Digestion

DNA was digested using Promega DNase (Promega, USA) according to the manufacturer's protocol unless noted otherwise. 2.75 µg RNA was incubated for 30 min at 37°C with the appropriate buffer and DNase. The reaction was stopped by adding 1 µl stop solution and incubation for 10 min at 65°C.

### 2.5.5 Oligonucleotides

Oligonucleotide primers used in this work were purchased from MWG-Biotech (Ebersbach, Germany) and are listed in Tab.2.4.

**Tab.2.4: Oligonucleotide Primers used in this work**

| Name | Sequence | Application |
|---|---|---|
| **HG 3** | GGTCAGGATAGAGAAGGGAGAGC | Housekeeping gene: RNA polymerase II large subunit fwd |
| **HG 4** | GAAGAAGCCAGTAGTTTACAAGCC | Housekeeping gene: RNA polymerase II large subunit rev |
| **HG 5** | AGGCGTTCCGTGACACCATC | Housekeeping gene: putative APT1A fwd |
| **HG 6** | CTGGCAACTTCTTCGGCTTCC | Housekeeping gene: putative APT1A rev |
| **S53** | CCGGGTCGAGATCACCAAGATA | TPS2 QRT-PCR |
| **S54** | GGGAAGTGAATCAGCAGCCA | TPS2 QRT-PCR |
| **S57** | GGCAGCACTCCAAGGATCTTCT | TPS3 QRT-PCR |
| **S58** | TGGGAAGTGAATCAGCAGCCG | TPS3 QRT-PCR |
| **AM120** | AGGGAACTTCGTGGTGGATGATAC | TPS10 QRT-PCR fwd |
| **AM121** | TGGCGTCTGGTGAAGGTAATGG | TPS10 QRT-PCR rev |
| **BH51** | TCTGGATGATGGGAGTCTTCTTTG | TPS23 QRT-PCR fwd |
| **BH52** | GCGTTGCCTTCCTCTGTGG | TPS23 QRT-PCR rev |
| **SF9** | CCGACTTAGGCTGCTCATCA | ZmOMT1 QRT-PCR fwd |
| **SF10** | GCTGCATCTCCCTTGTGTGTC | ZmOMT1 QRT-PCR rev |
| **SK10** | GATGTTGTGCATAACAGTATTAGGAGC | ZmOMT3 QRT-PCR fwd |
| **SK11** | ATGCCAAGCGAGATAGTGAGAAAC | ZmOMT3 QRT-PCR rev |
| **SM1** | CCGACTTAGGCTGCTCATCG | ZmOMT4 QRT-PCR fwd |
| **SM2** | GCCTCACCCTTGTGGTTTCTT | ZmOMT4 QRT-PCR rev |
| **TF3** | CCACAGGACAGGACACACAGAG | TF1 QRT-PCR fwd |
| **TF4** | CTGGATTGCTGGCGATGAACC | TF1 QRT-PCR rev |
| **TF5** | TGAGCGTGGAGTGGTGGAC | TF2 QRT-PCR fwd |
| **TF7** | GGGAGGGTGGTGGATGACG | TF2 QRT-PCR rev |
| **TF13** | AGATGAACAGGAAGCCAGGAGAC | TF4 QRT-PCR fwd |
| **TF14** | AAGCCACCGCCGAAGGAG | TF4 QRT-PCR rev |
| **TF17** | ACACCCGCCAGATTTGAAGTAAG | TF5 QRT-PCR fwd |
| **TF18** | CAGTGGAGTGGATACAGTGATGAG | TF5 QRT-PCR rev |
| **TF23** | CTACCGCCGCCGTTGTTC | TF7 QRT-PCR fwd |
| **TF24** | TGCCTTCCTGCTTGCTTGC | TF7 QRT-PCR rev |
| **TF25** | ATGGAGTTTGACCTGCTGAATTAC | TF8 QRT-PCR fwd |
| **TF26** | CGGCGTGTACTGCTCTGG | TF8 QRT-PCR rev |
| **TF31** | CACTACCCGCCCGTCCTC | TF9 QRT-PCR fwd |
| **TF32** | TGCCGTCGCCCAGAATCG | TF9 QRT-PCR rev |
| **TF40** | TTCACAGAGGAGGAAGAAGAGC | TF12 QRT-PCR fwd |
| **TF41** | TGGACGGCGAGGAGGATG | TF12 QRT-PCR rev |
| **TF42** | ACAGCGATACAAGATTAGCATACG | TF13 QRT-PCR fwd |
| **TF43** | CAACTACACAAGCAGCGATGG | TF13 QRT-PCR rev |
| **TF46** | TGCGGTTGGTGGCTCATAAG | TF14 QRT-PCR fwd |
| **TF47** | AAGGTTCTCAGGCTTCAAGTCC | TF14 QRT-PCR rev |
| **TF50** | GAAGGGCAAGAAGAAGAAGAAGTC | TF15 QRT-PCR fwd |
| **TF51** | GGTGAAGCAGGCGGATGG | TF15 QRT_PCR rev |
| **TF53** | ACTGCTCTGTCCTACTTGGC | TF16 QRT-PCR fwd |
| **TF54** | AGTCCTCTCGGTCCTTGGC | TF16 QRT-PCR rev |
| **TF55** | GGAAGCCTTAGTGGAAGCAGTAG | TF17 QRT-PCR fwd |
| **TF56** | CGTAGTTGATGGAAGCAAGTTGTG | TF17 QRT-PCR rev |
| **TF65** | GCAGTCTGTCCCATTTGATAGGC | TF20 QRT-PCR fwd |
| **TF66** | ACTCAGGCTCATAGGTCACTTCC | TF20 QRT-PCR rev |
| **TF70** | CTCTGGATGATGGATGGCGAAGG | TF21 QRT_PCR fwd |
| **TF71** | ACAAGGGAAGCACGGCACTG | TF21 QRT-PCR rev |
| **TF72** | ACTCCCACTCCCAATCACACTC | TF22 QRT-PCR fwd |
| **TF73** | GCCGTCCACCTGCTCCTC | TF22 QRT-PCR rev |
| **TF78** | TGGACGGAGATGAATGTGGAGAC | TF23 QRT-PCR fwd |
| **TF79** | CCCAGGACGACAAGAGGAACC | TF23 QRT-PCR rev |
| **TF94** | GCCTCGTCTCGTCTCGTCTTC | TF28 QRT-PCR fwd |
| **TF95** | GGTCAGCCTTCGTCCTCTTCC | TF28 QRT-PCR rev |
| **TF96** | GCAGAGCAGAAGCCCAGCAG | TF29 QRT-PCR fwd |
| **TF97** | GGTGGAGATGGTGAGGAGGAAC | TF29 QRT-PCR rev |
| **TF100** | GACGCTTCCTCACGCCTCTG | TF30 QRT-PCR rev |
| **TF101** | CCACACCACCTCGCTGAACC | TF30 QRT-PCR fwd |
| **TF104** | GGCAGCGGTGGAGGAGAC | TF31 QRT-PCR fwd |

| | | |
|---|---|---|
| **TF105** | TCACAAGTTCAGAAGAGCAGAAGC | TF31 QRT-PCR rev |
| **TF108** | CATCTGCTCCAACCTCTCCTTCTC | TF32 QRT-PCR fwd |
| **TF109** | GCTGCCCGTCTCCTGAACC | TF32 QRT-PCR rev |
| **TF118** | CACGCCGCCGGAGGAGTTG | TF34 QRT-PCR rev |
| **TF119** | GCGCAAGTACGGGCAGAAGCAGG | TF34 QRT-PCR fwd |
| **TF122** | CGGTGGGCTCAAGACAAAACA | TF35 QRT-PCR rev |
| **TF123** | TTCCAAAGCAAACAGGCAGAT | TF35 QRT-PCR fwd |
| **TF141** | TCACTGGGGCAAGTGGGTGG | TF40 QRT-PCR fwd |
| **TF142** | TTGGCATCGCCTTGCTCTTGG | TF40 QRT-PCR rev |
| **TF147** | GATGTTGATCACCATGCCGTCC | TF42 QRT-PCR fwd |
| **TF148** | CAACTCCGCCTCGCAGTGCC | TF42 QRT- PCR rev |
| **TF161** | TCAAGCTGCCGACCCCTCC | TF46 QRT-PCR fwd |
| **TF162** | CGCCTCCGTCATAGTGCTTCC | TF46 QRT-PCR rev |
| **TF169** | ATGACGCCCGGGAACTCCGT | TF2 RACE rev |
| **TF170** | ACCGCCACCACCACCATCCC | TF2 RACE fwd |
| **TF171** | GCATACTCCGATCCACGCAGG | TF35 RACE fwd |
| **TF172** | AAGCATGGGAGTTGGGCATC | TF35 RACE rev |
| **TF173** | GCTTGAGCTGATGACCACGATG | TF8 RACE fwd |
| **TF174** | GTACCCGGTGGTGGTGGTCGT | TF8 RACE rev |
| **TF175** | GGAAGACCCGCACACACACGC | TF30 RACE fwd |
| **TF176** | CCCATGCCCACGCCTCCGAC | TF30 RACE rev |
| **TF177** | CAGGTTAAGGGGAGCGAGAAC | TF34 RACE fwd |
| **TF178** | GGCGCGTGGACAGCGGCTTGG | TF34 RACE rev |
| **TF179** | ACGGTGAGCAGCACTCTCGCC | TF23 RACE fwd |
| **TF180** | CCGCGTGGTTTAGCTCCAGTGTTG | TF23 RACE rev |
| **TF181** | CAGCTGAGCTGATAGTGACCC | TF29 RACE fwd |
| **TF182** | GGAACCAAAAAAGAAAAGAAAAC | TF29 RACE rev |
| **TG1** | GTCGACGCATGGGTCCTGAA | TF1 cloning fwd |
| **TG2** | TCAATGACAGCGCAGAACC | TF1 cloning fwd |
| **TG3** | CTAAAAAATTCCTCGTTCA | TF1 cloning rev |
| **TG4** | TGAGCTCACTCAGAAGGG | TF1 cloning rev |
| **TG5** | AGAAGAATTCAGTTTGGGAG | TF2 cloning rev |
| **TG6** | TATTCTTGATCATCTCAGCA | TF2 cloning rev |
| **TG7** | TCGCGTTACATGTCGCCGT | TF8 cloning rev |
| **TG8** | ATGAGTTTTAGGACTCGTC | TF20 cloning fwd |
| **TG9** | AAGTAGCATCACATTCCAA | TF20 cloning rev |
| **TG10** | ATGCAGCTGGGGAAGACCGC | TF22 cloning fwd |
| **TG11** | CCTCGCCTCAGCTCAGAACT | TF22 cloning rev |
| **TG12** | GACCTCCCGCCTGGCTGCTCC | TF34 cloning fwd |
| **TG13** | AGCAGCGGACATGGTAGGAG | TF34 cloning fwd |
| **TG14** | ATGTCGCCCTCCTCCTACTTCT | TF34 cloning fwd |
| **TG15** | AGTAGCTGACAGTGGTCGT | TF34 cloning fwd |
| **TG16** | AGATTGGGTGCGTGCGTCA | TF34 cloning rev |
| **TG17** | TCGCCAGCTCTAGCAGAGGA | TF34 cloning rev |
| **TG18** | AAATGCAGATGGACTCCTA | TF23 cloning fwd |
| **TG19** | ATGCCGGCCTCGTTCCAG | TF23 cloning fwd |
| **TG20** | GAAGTGGATCAGTCATTGTCA | TF23 cloning rev |
| **TG21** | TTGTTTGAGTCGACGGGCAT | TF35 cloning fwd |
| **TG22** | CCTGCCTAGTTCTCTGCC | TF30 cloning rev |
| **TG23** | CGATCATGCGCTAGCTAGTTCAC | TF8 cloning rev |
| **TG24** | ATGGGACAGCCGGTGACGAG | TF1 cloning fwd |
| **TG25** | TCAGAAGGGGCCCAACCCC | TF1 cloning rev |
| **TG26** | ATGGGTCTGCCGATGAGGAG | TF1 cloning fwd |
| **TG27** | TCAGAACTGTCCCAACCCG | TF1 cloning rev |
| **TG28** | ATGCCTTCAGTCGAGGTCG | TF2 cloning fwd |
| **TG29** | TCAGTTTGGGAGCTCGAGG | TF2 cloning rev |
| **TG30** | ATGGAGTTTGACCTGCTG | TF8 cloning fwd |
| **TG31** | TTACATGTCGCCGTGGGG | TF8 cloning rev |
| **TG32** | ATGTTCCAAGGAATGATGT | TF20 cloning fwd |
| **TG33** | TCACATTCCAAAGGGGGCA | TF20 cloning rev |
| **TG34** | ATGGGTCTGCCGATGAGGA | TF22 cloning fwd |
| **TG35** | TCAGAACTGTCCCAACCC | TF22 cloning rev |
| **TG36** | ATGCAGATGGACTCCTAC | TF23 cloning fwd |
| **TG37** | GGAGGATCGCGTGTCAAAAC | TF23 cloning fwd |
| **TG38** | TCAGTCATTGTCAGCAAAG | TF23 cloning rev |
| **TG39** | ATGGCGCCCCGGGTGGCGGA | TF30 cloning fwd |

| | | |
|---|---|---|
| **TG40** | CTAGTTCTCTGCCGGCGG | TF30 cloning rev |
| **TG41** | ATGAGCTGCGCGGGGCAG | TF32 cloning fwd |
| **TG42** | ATGGTCGACGACCCGGCC | TF32 cloning fwd |
| **TG43** | CTAGGCGACCGGCGGCCAGT | TF32 cloning rev |
| **TG44** | ATGGCGTCCTCGACGGGGA | TF34 cloning fwd |
| **TG45** | TCACCGGTAGAGGGGCGCC | TF34 cloning rev |
| **TG46** | ATGGACTTCCACCACAGCA | TF35 cloning fwd |
| **TG47** | TCAAGGGGTGGTGATGTC | TF35 cloning rev |
| **TG48** | ATGGGTCATGATGAAGCTGTAG | TF21 cloning fwd |
| **TG49** | GGCACAAGGGAAGCACGGCAC | TF21 cloning rev |
| **TH1** | TCCGAATTCATGACAGCGCAGAACCC | TF1 expression fwd |
| **TH2** | GCGGCCGCCTAAAAAATTCCTCGTTCACC | TF1 expression rev |
| **TH3** | AGCTTGCGGCCGCCTAAAAAATTCCTCGTTCACC | TF1 expression rev |
| **TH4** | TCCGAAATTCATGCAGCTGGGGAAGACCGCCGTC | TF22 expression fwd |
| **TH5** | TCCGAATTCATGCAGCTGGGGAAGACCGCCGTC | TF22 expression fwd |
| **TH6** | GCGGCCGCTAGATCAGAACTGTCCCAACCC | TF22 expression rev |
| **TH7** | AGCTTGCGGCCGCTAGATCAGAACTGTCCCAACCC | TF22 expression rev |
| **TH8** | TCCGAATTCATGTTCCAAGGAATGATGT | TF20 expression fwd |
| **TH9** | GCGGCCGCAAGTAGCATCACATTCCAAAGGG | TF20 expression rev |
| **TH10** | AGCTTGCGGCCGCAAGTAGCATCACATTCCAAAGGG | TF20 expression rev |
| **TH11** | TCCGAATTCATGAGTTTTAGGACTCGTCATGTTCC | TF20 expression fwd |
| **TH12** | TCCGAATTCATGAGCTGCGCGGGGCAG | TF32 expression fwd |
| **TH13** | AGCTTGCGGCCGCCTAGGCGACCGGCGGCCAGT | TF32 expression rev |
| **TH14** | TCCGAATTCATGGAGTTTGACCTGCTG | TF8 expression fwd |
| **TH15** | AGCTTGCGGCCGCTTACATGTCGCCGTGGGG | TF8 expression rev |
| **TP1** | CATCAGCTGCCATGAAAGTATA | TPS23 promoter studies 1651-1800 rev |
| **TP2** | GCTGGCTACCTATATTAAGAAC | TPS23 promoter studies 1651-1800fwd |
| **TP3** | CAAGCACCTGGATCCTATGGT | TPS23 promoter studies 1511-1693 rev |
| **TP4** | TGTGTTGCACATGCCTGTCG | TPS23 promoter studies 1511-1693 fwd |
| **TP5** | GATCTGCCGACAGGCATGTG | TPS23 promoter studies 1378-1537 rev |
| **TP6** | AACATTTGAGGTGTATGGTTG | TPSS23 promoter studies 1378-1537 fwd |
| **TP7** | GCATTTTCATGCATACAACC | TPS23 promoter studies 1260-1413 rev |
| **TP8** | ACGAGTCACGGGTGGCGGTC | TPS23 promoter studies 1260-1413 fwd |
| **TP9** | CATCGATCCTTGCATTAGACC | TPS23 promoter studies 1136-1296 rev |
| **TP10** | CTATACATGTGATCTTTAGAGGT | TPS23 promoter studies 1136-1296 fwd |
| **TP11** | CTCTAAAATGTGAACAATATGTAC | TPS23 promoter studies 1026-1180 rev |
| **TP12** | CAAAGGTTGTATGCACAAAAGGC | TPS23 promoter studies 1026-1180 fwd |
| **TP13** | GAGTATCAAAATCTGATTAATTTC | TPS10A promoter studies 8-161 fwd |
| **TP14** | CAAATGGTCTGATCGGTTAATG | TPS10A promoter studies 8-161 rev |
| **TP15** | AACATACACCGCGTTAGCATC | TPS10A promoter studies 115-291 fwd |
| **TP16** | TGTGTTGATCGTTTTGTCTTG | TPS10A promoter studies 115-291 rev |
| **TP17** | CAAGACAAAACGATCAACACACC | TPS10A promoter studies 271-421 fwd |
| **TP18** | ATGCAATGAACAACCATTCGGG | TPS10A promoter studies 271-421 rev |
| **TP19** | CATATCCCGAATGGTTGTTC | TPS10A promoter studies 395-566 fwd |
| **TP20** | GCTGAGACAAAATGGAGTTGC | TPS10A promoter studies 395-566 rev |
| **TP21** | GTCTCAGCTAGGATAAATACTGG | TPS10A promoter studies 559-718 fwd |
| **TP22** | GTACTTCCTCTCAACTATTACTTC | TPS10A promoter studies 559-718 rev |
| **TP23** | GAAGTAATAGTTGAGAGGAAGTACCA | TPS10A promoter studies 712-855 fwd |
| **TP24** | CTTCTGATTGTTTCAGTGTGTTG | TPS10A promoter studies 712-855 rev |
| **TP25** | GAAACAATCAGAAGCTGTAGACG | TPS10A promoter studies 842-1005 fwd |
| **TP26** | CTTGGGTGGAAGGCGGTGGCAT | TPS10A promoter studies 842-1005 rev |
| **TP27** | ACCACAACCTTAATTAATATACACC | TPS10B promoter studies 1-174 fwd |
| **TP28** | AGAATCTCTTAGGAATCTACTTC | TPS10B promoter studies 1-174 rev |
| **TP29** | AACCATATATATACGGAGCGG | TPS10B promoter studies 458- fwd |
| **TP30** | ATTACCAGACTTGTGAGCTTGTGG | TPS10A promoter studies 622 fwd |
| **TPG1** | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCAAAATTAAT ACTGGGAAAAGG | TPS23 promoter Gateway cloning1.8 kb |
| **TPG2** | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCTGCAGATGG AAGAAACACAAC | TPS23 promoter Gateway cloning 600 bp |
| **TPG3** | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCTTAAGCTTG TAGAATGGCAG | TPS23 promoter Gateway cloning 1.2 kb |
| **TPG4** | GGGGACCACTTTGTACAAGAAAGCTGGGTCGAAAGTATAG TATACTAGCTA | TPS23 promoter Gateway cloning rev |
| **TPG5** | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCCTTTGCCTA GTGTCAAAAAAAACACTC | TPS10 promoter Gateway cloning 1.5 kb |
| **TPG6** | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCCTAGTGTCA | TPS10 promoter Gateway cloning 1.5 kb-b |

| | | |
|---|---|---|
| | AAAAAAACACTCGGC | |
| **TPG7** | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCAAAGAAGCTCTTTGGCGAGTG | TPS10 promoter Gateway cloning 1.5 kb-c |
| **TPG8** | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGAGTATCAAAATCTGATTAATTTC | TPS10 promoter Gateway cloning 800 bp |
| **TPG9** | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCCATTGCATAATGTGACTCC | TPS10 promoter Gateway cloning 500 bp |
| **TPG10** | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGAAGTAATAGTTGAGAGGAAGTACCA | TPS10 promoter Gateway cloning 200 bp |
| **TPG11** | GGGGACCACTTTGTACAAGAAAGCTGGGTCTTGCAGCAGCCCCTGCACATC | TPS10 promoter Gateway cloning rev |
| **TPG12** | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCTGCACGCAGAAGTAATAGTTGAGAG | TPS10 promoter Gateway cloning 200 bp new |
| **TPG13** | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGGATGATGTAACATTTGAGGTG | TPS23 promoter Gateway cloning 400 bp |
| **TPG14** | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCAATATAATGCAAATTGAGTAC | TPS23 promoter Gateway cloning 200 bp |

### 2.5.6 Amplification of DNA

DNA was amplified by "polymerase chain reaction" (PCR) in a thermocycler Primus 96 (MWG Biotech, Ebersberg, Germany) or Peclab (Peclab, Germany). Standard PCR was performed using Go Taq-DNA polymerase (Promega, Madison, USA). Amplification reactions of inserts for cloning experiments were carried out with Advantage2 Polymerase Mix (BD Biosciences Clontech, Palo Alto, USA) or with *Pfu*Turbo DNA Polymerase (Stratagene, La Jolla, USA). A 50 µl standard PCR mix contained 1 µl primer 1, 1 µl primer 2 (10 pmol $\mu l^{-1}$ each), 1 µl dNTP (10 mM), 5 µl reaction buffer, 0.5 µl polymerase (0.1-2.5 U) and 5-200 ng DNA template. Cycling conditions were as follows:

| | | |
|---|---|---|
| | 94°C for 3 min | |
| Denaturation | 94°C for 30 s | 25-35 cycles |
| Annealing | 50-68°C for 30 s | |
| Extension | 72°C for 30 s - 3 min | |
| | 72°C for 5 min | |

Denaturation conditions remained constant in all PCRs, however annealing temperatures and extension times were adapted depending on the melting temperatures of primers (annealing temperature = melting temperature of primers minus 2-5 °C) and the expected fragment sizes (extension time = 1 min per 1 kb).

### 2.5.7 RACE-PCR

A 5'- and 3'-RACE cDNA library were constructed from mRNA using the SMARTer RACE cDNA amplification kit (BD Biosciences Clontech, Palo Alto, USA) according to the instructions provided by the manufacturer. The procedure forms first-strand cDNA with specific adaptor sequences either at the 5'- or at the 3'-end of the cDNA that allows for RACE- (rapid amplification of cDNA-ends) PCR. Following RACE PCR, nested PCR was conducted to obtain specific single bands using inner primers.

### 2.5.8 cDNA synthesis

cDNA for applications in QRT-PCR reactions was synthesized with the reverse transcriptase Superscript III (Invitrogen, Carlsbad, USA). 0.75 µg of DNA digested RNA (2.5.4) was mixed with 4 µl dNTPs, 0.5 µl oligo(dT)primers and 0.5 µl random primers, and filled to a volume of 13 µl with *a. dest.* The reaction was incubated for 5 min at 65°C and shortly cooled down on ice. Four µl reaction buffer, 1 µl DTT, as well as, 1 µl RNase and 1 µl SuperscriptIII was added to the sample and incubated at room temperature for 5 min and afterwards transferred to 50°C for 1 h. Reverse transcription was terminated by an 70°C incubation period of 15 min and the cDNA was stored in aliquots at -20°C.

### 2.5.9 Quantitative RT-PCR

Quantitative real time PCR was performed to analyze transcript accumulation of specific genes in different samples. In order to observe the accumulation of our DNA fragments, 10 µl Brilliant Sybr Green QPCR Master Mix (Stratagene, La Jolla, USA) was added to 1 µl cDNA and 0.5 µl of each primer (0.25 mM). Since Sybr Green is a chemical compound that fluoresces when unspecifically bound into the minor groove of double-stranded DNA, it can be measured by its fluorescence after excitation at 497 nm. The signal intensity depends on the initial concentration of target present in the PCR reaction and is therefore a tool to calculate the present mRNA amount of one specific gene.

QRT-PCR reactions were carried out in an Mx3000P (Stratagene, La Jolla, USA) or the CFX96 (Bio-Rad, Munich, Germany) with the following reaction scheme:

| | | |
|---|---|---|
| | 95°C for 10 min | |
| Denaturation | 95°C for 30 s | 40 cycles |
| Annealing | 56-68°C for 30 s | |
| Extension | 72°C for 1 min | |
| Melting Curve: | 95°C for 1 min | |
| | 56°C to 95°C for 30 s each | |

Gene expression levels were quantified using the standard curve method. The standard curve for each gene was generated using pooled cDNA in equal amounts from all samples. Two reference genes, a putative adenine phosphoribosyltransferase 1 (TA172777_4577) and a maize RNA polymerase II largest subunit (AF519538), were used to quantify the cDNA in each sample. The expression level of both genes was similar in control and herbivore-induced plants, with a cycle threshold value difference from 1 to 2. Using the automated threshold determination given by the Mx3000P software, the starting amount of cDNA was calculated for each sample. Relative expression levels were calculated as the expression level of the respective gene divided by the geometric mean of the expression levels of the two reference genes.

### 2.5.10 Restriction of DNA, plasmids and PCR products

Restriction of DNA with restriction endonucleases was applied to produce compatible inserts and vectors for ligation and to screen vectors for successful insertion of PCR products. Enzymes and the appropriate buffers (10x) were purchased from NEB (Schwalbach, Germany) or Fermentas (St. Leon-Rot, Germany). Reactions were carried out with 2-20 U enzyme and 0.5-3 µg DNA with the suitable amount of buffer in reaction volumes of 20 to 60 µl and incubated for 1-2 h at 37°C.

### 2.5.11 Isolation of DNA fragments from agarose gels and PCR reactions

The DNA fragments of interest were cut under UV illumination (260 nm) and extracted with the NucleoSpin Extract kit from Macherey&Nagel (Düren, Germany). The pieces of agarose were dissolved in a buffer containing chaotropic salts which promotes the binding of DNA to the silica membrane of a column. After washing the column with ethanol-containing buffers,

purified DNA was eluted with 35 µl 5 mM Tris-HCl (pH8.5). The same kit was used to purify PCR products from reaction solutions.

### 2.5.12 Ligation of DNA fragments

DNA fragments with compatible or blunt ends were ligated using 1 U T4-DNA-Ligase from Fermentas (St. Leon-Rot, Germany) with the provided 10x ligase buffer. Vector and inserts were mixed in an estimated molecule ratio of 1:5 and incubated at 37°C for 1 h or at 16°C over night.

### 2.5.13 Cloning and transformation of DNA fragments

DNA fragments were cloned with the TOPO TA Cloning® kit from Invitrogen (Carlsbad, USA) or the CloneJET™ PCR Cloning kit from Fermentas (St. Leon-Rot, Germany) according to the manufacturer's instructions. For expression analysis, DNA fragments and corresponding vectors (Tab.2.5) were digested with the specific restriction enzyme to produce compatible overhangs (2.5.10), and ligated as described above.

**Tab.2.5: Vectors and their application in this work**

| Vector | Characteristics | Application |
|---|---|---|
| **pHIS8-3 (Joseph P.Noel, The Salk Institute, La Jolla, USA)** | Bacterial expression vector with N-terminal His(8)-tag, $Km^r$, T7-promoter | Overexpression of His-tagged proteins in *E. coli* |
| **pJet1.2/blunt (Fermentas, St. Leon-Rot, Germany)** | Bacterial cloning vector, 2974 bp, $Amp^r$, $P_{lac}$-promoter, T7 RNA-promoter | Cloning of PCR products |
| **pCR®4-TOPO® (Invitrogen, Carlsbad, USA)** | Bacterial cloning vector, 3900 bp, $Amp^r$, $Km^r$, $P_{lac}$-promoter, T7 RNA-promoter | Cloning of PCR products |
| **pDONR™ vector 207 (Invitrogen, Carlsbad, USA)** | Transformation vector, 5585 bp, $Gent^r$, $Cm^r$, pUC origin | Donor vector for Gateway cloning system |
| **pBGWFS7.0 (Invitrogen, Carlsbad, USA)** | Transformation vector, 12451 bp, GUS gene, GFP gene, $Sm/Sp^r$, CoIE1, pVS1 | Destination vector for Gateway cloning system (Karimi *et al.* 2002) |

### 2.5.14 Sequencing and sequence analysis

Sequencing of plasmids and DNA fragments was performed by either Eurofins MWG (Ebersberg, Germany) or GATC (Konstanz, Germany). Samples were diluted to the concentrations and volumes specified by these companies and send via mail.

DNA and protein sequence data were evaluated with the software DNAStar (Madison, USA) and the web-based software Multalin at http://multalin.toulouse.inra.fr/multalin/multalin.html. Data bank searches were performed using BLAST (basic local alignment search tool) at http://www.ncbi.nlm.nih.gov/, maizesequence database at http://www.maizesequence.org/index.html and TIGR at http://www.tigr.org/ as well as the plantGDB database at http://www.plantgdb.org/. Analysis of regulatory elements was performed using PLACE (http://www.dna.affrc.go.jp/PLACE/) and plant CARE (http://bioinformatics.psb.ugent.be/webtools/plantcare/html/).

### 2.5.15 Gateway Cloning System

The Gateway® Technology is a universal cloning method based on the site-specific recombination properties of bacteriophage lambda (Invitrogen, http://www.invitrogen.com, (Landy 1989)). This method was used to clone the promoter fragments of *tps10* and *tps23* fused to the GUS gene into the destination vector in order to transform the resulting vector into *Agrobacterium tumefaciens*.

The promoter fragments were cut into sizes starting from 1.5 kb for *tps10* and 1.8 kb for *tps23* using PCR (Tab.2.6) and cloned according to the manufacturer's instructions via BP reaction into the donor vector pDONR™ vector 207. After selection on a kanamycin containing LB plate and colony PCR, the resulting entry clone was cloned using the LR reaction in the destination vector pBGWFS7.0. This destination vector contained the reporter gene ß-glucuronidase. The resulting expression clone was used for transformation into *A. tumefaciens*.

The promoter constructs were cloned and transformed with support by Kurt Stampniok and Ulschan Scheler (AG Degenhardt).

**Tab.2.6: Overview of the promoter sizes of *tps10* and *tps23* used for the Gateway cloning system.**

| Name of the construct | Size in [nt] | Primers used |
|---|---|---|
| **tps10 1.5 kb::GUS** | 1297 | TPG5, 6, 7; TPG11 |
| **tps10 800 bp::GUS** | 965 | TPG8; TPG11 |
| **tps10 500 bp::GUS** | 559 | TPG9; TPG11 |
| **tps10 200 bp::GUS** | 293 | TPG10, 12 ; TPG11 |
| **tps23 1.8 kb::GUS** | 1779 | TPG1; TPG4 |
| **tps23 1.2 kb::GUS** | 1186 | TPG2; TPG4 |
| **tps23 600 bp::GUS** | 602 | TPG3; TPG4 |
| **tps23 400 bp::GUS** | 397 | TPG13, TPG4 |
| **tps23 200 bp::GUS** | 172 | TPG14, TPG4 |

### 2.5.16 Microarray hybridization

The Maize Long Oligonucleotide 46k Array (version 1) provided by the University of Arizona was used for global expression profiling.

Material from plants treated according to the time course experiment (2.1) was ground in liquid nitrogen into a fine powder and total RNA was extracted as described above. A DNA digestion using Promega DNase (Promega, Madison, USA) was performed on-column according to the manufacturer's instructions.

Utilizing the Amino Allyl MessageAmp$^{TM}$II aRNA Amplification Kit (Ambion, Carlsbad, USA), amplified RNA was produced and labeled with Cy3/Cy5 Mono-Reactive Dye Pack (GE Healthcare, Freiburg, Germany) according to the instruction of the manufacturer's. The labeled RNA probes were purified (RNeasy MinElute Cleanup, Qiagen, Hilden, Germany), mixed and hybridized with the Long Oligonucleotide Microarray with the protocols provided by the University of Arizona (http://ag.arizona.edu/microarray/methods.html). Reverse labeling experiments were performed to eliminate dye-specific bias. For each treatment, the RNA was labeled with Cy3 and Cy5 in the reverse experiment. Considering the reverse labeling experiments, a total of 4 biological replicates and 2 technical replicates were included. After hybridization, the microarray slides were washed and scanned immediately with the DNA microarray scanner (system: G2565AA/BA from Agilent, Santa Clara, USA) and images were processed by Feature Extraction software (Agilent, Santa Clara, USA).

The R-based open source software Bioconducter (http://www.bioconductor.org) was used to analyze the resulting data files. Local background subtraction and Lowess normalization was applied for each microarray slide (Yang 2002). The p-values and $log_2$-ration between arrays were calculated using the linear model and empirical Bayes methods from the limma package of Bioconductor. Genes with a ratio cut-off of two and a p-value <0.05 were used for further analysis.

## 2.6 Electrophoresis and transfer techniques

### 2.6.1 Electrophoresis

DNA fragments were separated by electrophoresis in 1.5x TAE agarose gels (1.5 % agarose [g/v]; Bio-Rad Laboratories, Hercules, USA, 1 µg $ml^{-1}$ ethidium bromide). DNA probes were mixed with 1/4 volume loading buffer and separated at a constant voltage of 100 V in an *i*-Mupid mini electrophoresis unit (Helixx, Ontario, Canada) containing 0.5x TAE buffer. Nucleic acid was visualized under UV-light due to the intercalation of ethidium bromide into the DNA. To characterize the fragment sizes, an additional 3 µl of a 1 kb or 100 bp marker was applied to the gel (Invitrogen, Carlsbad, USA).

| | |
|---|---|
| Loading buffer: | 50 % glycerin [v/v] |
| | 0.05 % bromphenol blue [g/v] |
| | 100 mM EDTA |
| 0.5x TAE-Puffer: | 40 mM Tris-acetate pH8.0 |
| | 20 mM sodium acetate |
| | 1 ml EDTA |

### 2.6.2 SDS-PAGE

Proteins were separated under denaturing conditions using the polyacrylamide electrophoresis with sodium dodecyl sulfate (SDS) on 12 % polyacrylamide gels. The production of the gels was carried out after Laemmli (1970).

Protein probes were mixed with 2x buffer and denaturated for 10 min at 90°C and concentrated in the stacking gel at a constant voltage of 100 V. In the separation gel, protein samples were separated at 200 V. Following electrophoresis, proteins were either blotted on a nitrocellulose membrane (Western blot 2.6.3) or directly stained for 30 min with Coomassie Brilliant Blue solution. Destaining of the gel was obtained by incubation with destaining solution for several hours. For the estimation of the protein sizes fragments were compared to the “Pre-Stained” protein marker (Invitrogen, Carlsbad, USA).

| | |
|---|---|
| 2x buffer: | 100 mM Tris-HCl pH6.0 |
| | 4 % SDS [g/v] |
| | 10 % 2-mercaptoethanol [v/v] |
| | 20 % glycerol [v/v] |
| | 0.1 % bromphenol blue [g/v] |
| Stacking gel 4 %: | 0.125 M Tris-HCl pH6.8 |
| | 4 % acrylamide/bisacrylamide (29:1) Roth (Karlsruhe) |
| | 0.1 % SDS [g/v] |
| | 0.075 % APS [g/v] |
| | 0.05 % TEMED [v/v] |
| Separation gel 12 %: | 0.375 M Tris-HCl pH8.8 |
| | 12 % acrylamide/bisacrylamide (29:1) |
| | 0.1 % SDS [g/v] |
| | 0.075 % APS [g/v] |
| | 0.05 % TEMED [v/v] |
| 10x SDS-buffer: | 200 mM Tris |
| | 1.9 M glycine |
| | 10 % SDS [g/v] |

Coomassie Brilliant

Blue solution: 45 % methanol [v/v]
7 % acetic acid [v/v]
0.1% Coomassie Brilliant Blue R250® [g/v] (Sigma-Aldrich, St. Louise, USA)

Destaining solution: 5 % methanol [v/v]
7 % acetic acid [v/v]

### 2.6.3 Western-Blot

#### 2.6.3.1 Transfer of proteins

Proteins were transferred from the polyacrylamide gels onto nitrocellulose membranes (Millipore Corporation, Bedford, USA) using a tank blotting system („Mini Trans-Blot Cell“, Bio-Rad Laboratories, Hercules, USA). Therefore, membranes were washed with ethanol and equilibrated for 15 min in blotting buffer with filter paper and pads. The setup is shown in Fig.2.2. The transfer was carried out by constant voltage of 100 V for 3 h.

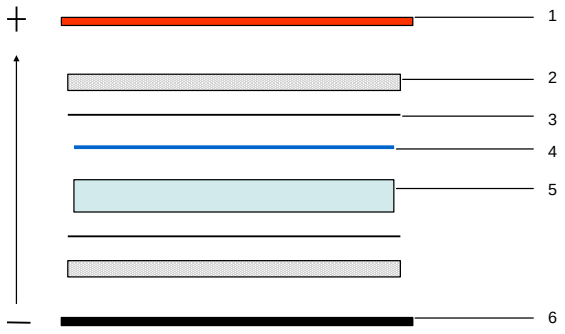



**Fig.2.2: Western-Blot setup.** 1: cathode; 2: pads; 3: filter paper; 4: nitrocellulose membrane; 5: SDS-Gel; 6: anode.

Blot-buffer: 25 mM Tris
192 mM glycine
20 % methanol [v/v]

### 2.6.3.2 Protein detection

To block unspecific binding of the antibody, the nitrocellulose membrane was incubated with the protein-side facing up for 30 min at room temperature in blocking solution.

A specific monoclonal anti-polyhistidine antibody from mouse (Sigma-Aldrich, St. Louis, USA) was used as primary antibody in a dilution 1:6000 in blocking solution. The membrane was incubated over night with constant shaking and then rinsed 3 times 5 min each in TBST-buffer. The secondary antibody anti-mouse IgG from goat which is conjugated to alkaline phosphatase (Sigma-Aldrich, St. Louis, USA) was added to the membrane with a working dilution of 1:30000. After an incubation of 1 h, the membrane was washed 3 times for 5 min in TBST-buffer. The colored precipitate was obtained by adding NBT/BCIP solution („BCIP/NBT Liquid Substrate System“, Sigma-Aldrich, St. Louis, USA). This reaction, where the alkaline phosphatase converts the NBT/BCIP solution into a blue pigment, was carried out in darkness and was stopped by adding $H_2O$.

Blocking solution: 2 % BSA [g/v] in TBST-Puffer

TBST-Puffer: 10 mM Tris-HCl pH8.0
150 mM NaCl
0.05 % Tween 20 [v/v]

### 2.6.4 Band shift assays (EMSA)

EMSA was performed using the Gel Shift Assay System from Promega (Madison, USA) according to the manufacturer's instruction. Ten mCi $ml^{-1}$ [$\gamma^{32}$-P] ATP was attached to 1.75 pmol $\mu l^{-1}$ of the truncated promoter fragments during incubation with the T4 Polynucleotide Kinase 10x buffer and T4 polynucleotide kinase for 10 min at 37°C. The specific concentration of the oligonucleotide-fragments was calculated after this formula:

$$c(pmol) = \frac{c(\frac{ng}{ml}) * 10^6}{MW}$$

$$MW\ of\ dsDNA = (length\ in\ nt * 667.4) + 157.9$$

c(pmol) = concentration of the oligofragment in pmol
c(ng/ml) = concentration of the oligofragment in mg/ml
MW = molecular weight of the oligofragment

The reaction was stopped by adding 1 µl of 0.5 M EDTA. To remove unincorporated label from the oligonucleotide, 89 µl of TE buffer was added to the sample and purified using a G-25 spin column (GE Healthcare, Buckinghamshire, UK) according to the manufacturer's instructions. One µl of the purified oligofragments was measured using a scintillation counter. A binding reaction was set up using 250 ng of the purified transcription factor (2.7.1) and 2 µl Gel Shift Binding 5x buffer. After 10 min incubation at room temperature, 2 µl of the labeled promoter fragment were added and incubated again for 20 min at room temperature. One µl gel loading buffer was added to the negative control only because this buffer might inhibit the *in vitro* binding ability between DNA and proteins. Before loading 10 µl of each probe, the 3.8 % 0.5x TBE nondenaturating polyacrylamide gel was pre-run for 10 min at 250 V. The gel was run at 200 V for 20 min, removed from the cassette, placed on a filter paper, sealed in a plastic film and exposed to a phosphor sensitive screen for 90 min. Pictures were developed using a phosphor imager. Unlabeled promoter fragments were used as specific competitor and SP1 consensus oligo, provided from the kit, as unspecific competitor.

| | |
|---|---|
| TE buffer: | 10 mM Tris-HCl pH8.0 |
| | 1 mM EDTA |
| 10x TBE buffer: | 0.9 M Tris base |
| | 0.9 M boric acid |
| | 0.02 M disodium EDTA·$2H_2O$ |
| | pH8.3 |
| 3.8 % gel: | 1x TBE buffer |
| | 3.8 % acrylamide/bisacrylamide (19:1) |
| | 3 % glycerin |
| | 0.005 % TEMED [g/v] |
| | 0.075 % APS [v/v] |

## 2.7 Protein techniques

### 2.7.1 Heterologous expression of transcription factors in *E. coli* and purification of recombinant protein

The open reading frames (ORFs) of the identified transcription factors were cloned into the bacterial expression vector pHIS8-3 with an N-terminal His-tag (Tab.2.5) and expressed in *E. coli* BL21 (DE3). 400 ml LB-medium were inoculated with a 3 ml overnight culture of *E. coli* containing the expression constructs and incubated at 37°C with constant shaking to an $OD_{600}$ of 0.7. The vector-mediated expression was induced by adding IPTG to a final concentration of 2 mM to the medium. Cultures were shaken for 3 h at 37°C and harvested by centrifugation (20 min at 5000 g, 4°C). The pellet was resuspended in 10 ml chilled lysis buffer and disrupted by a 5 x 30 s treatment with a sonicator (Branson sonifier 250, Schwäbisch Gmünd). 15 mg lysozyme (Appli Chem, Darmstadt) was added and incubated for 1 h at 4°C. The *E. coli* cell fragments were removed by centrifugation at 14000 g for 20 min, 4°C, 1 ml Ni-NTA-Agarose (50 %, Qiagen, Hilden) was added to the supernatant and shaken for 2 h at 4°C. The supernatant was added to an equilibrated column (Poly-Prep® Chromatography column, BioRad (Munich) and washed twice with 3 ml washing buffer. His-tagged proteins bound to the Ni-NTA-matrix were eluted with 3 ml elution buffer. One ml fractions were collected. The protein-containing elution fractions were combined after the protein quantification (2.7.2) and used as probes in the band shift assays (2.6.4).

| | |
|---|---|
| LB-culture: | 25 g LB -medium (AppliChem, Darmstadt) in 1 l *a.dest.* |
| Lysis buffer in PBS: | 500 mM NaCl |
| | 2.7 mM KCl |
| | 1.7 mM $KH_2PO_4$ |
| | 10.1 mM $Na_2HPO_4$ |
| | 20 mM imidazol |
| | 1 % Tween 20 |
| | 10 % glycerol |
| | 10 mM ß-mercaptoethanol |

Washing buffer
in PBS: 500 mM NaCl
2.7 mM KCl
1.7 mM $KH_2PO_4$
10.1 mM $Na_2HPO_4$
20 mM imidazol
10 % glycerol
10 mM ß-mercaptoethanol

Elution buffer in PBS: 500 mM NaCl
2.7 mM KCl
1.7 mM $KH_2PO_4$
10.1 mM $Na_2HPO_4$
250 mM imidazol
10 % glycerol
10 mM ß-mercaptoethanol

PBS-buffer: 137 mM NaCl
2.7 mM KCl
7 mM $Na_2HPO_4 \cdot 2\ H_2O$
1.5 mM $KH_2PO_4$
pH7.4 with HCl

### 2.7.2 Protein quantification

Purified protein was quantified according to Bradford (1976). Protein samples were diluted 1:20 and added with 200 µl 1.8x Roti®-Quant (Roth, Karlsruhe) to 250 µl and incubated for 5 min at room temperature. OD was measured at 590 nm (NanoQuant, Tecan, Crailsheim) and compared with the standard curve prepared with 0, 20, 30, 40, 50, 60, 80 and 100 µg $ml^{-1}$ bovine serum albumin (Sigma-Aldrich, St. Louis, USA), respectively.

## 2.8 Chromatographic analysis

### 2.8.1 Volatile collection

For the analysis of volatile terpenes, plant material was frozen in liquid nitrogen and ground into a fine powder using a mortar and pistil. 200 mg of the ground material was transferred to a glass vial with a septum in the lid. A 100 µm PDMS SPME fiber was inserted through the

septum and incubated for 30 min at 40°C. The volatile spectrum was analyzed by gas chromatography-mass spectrometry.

### 2.8.2 Gas chromatography – mass spectrometry (GC-MS)

GC-MS was performed on a Shimatsu GC-MS2010Plus gas chromatograph (Duisburg, Germany) with $H_2$ as carrier gas at 1 ml $min^{-1}$. The injection temperature was set to 220°C and samples were added directly using a SPME fiber without split. The temperature on the column was raised from 60°C (constant for 3 min) to 200°C with a rate of 7°C per minute and then finally raised to 300°C with a rate of 100°C per minute. The mass spectrometer was run with the following settings: interface temperature: 250°C, ion source temperature: 200°C, ionization potential: 70 V, and a scan range of 46-350 amu. An EC-5 column (length: 30.0 m, diameter: 0.25 mm and film thickness: 0.25 µm (Grace, Deerfield, USA)) was used as chromatographic column.

The data were analyzed with Shimatsu Labsolution software and the mass spectrum libraries "Wiley8" (Hewlett-Packard) and "Shim2205" (Shimatsu).

### 2.8.3 Identification of plant hormones

Approximately 200 mg of leaf material was used for hormone extraction and mixed with 1 ml ethyl acetate spiked with 40 ng $ml^{-1}$ labeled phytohormones, $D_6$-abscisic acid (ABA), $D_4$-salicylic acid (SA), jasmonic acid-$^{13}C_6$ isoleucin (JA-Ile) and 200 ng $ml^{-1}$ $D_2$-jasmonic acid (JA), respectively. The mixture was vortexed for 10 min and then centrifuged at 4°C for 20 min at 16000 g. Extraction was repeated with 500 µl ethyl acetate without internal standard and supernatants were combined and dried in the speedvac at 30°C. The pellet was dissolved in 500 µl 70 % methanol and centrifuged at 16000 g to remove precipitates. Ten µl supernatant was used for the analysis on the Varian 1200L Triple-Quadrupol-MS (Palo Alto, USA). Hormones were separated on a ProntoSil C18-ace-EPS column (50x2 mm, 5 µm, 120 Å) with 0.05 % formic acid and methanol as solvent solutions with a flow rate of 0.4 ml/min in a gradient mode. The compounds were detected in the ESI negative mode. Molecular ions (M-H) with *m/z* 137, 209, 263 and 322 for SA, JA, ABA and JA-Ile and 141, 213, 269 and 328 for the respective internal standards were fragmented. Daughter ions 93, 59, 153 and 130 for the compounds and 97, 59, 159 and 136 for the internal standards were recorded for

quantification. Collision energy was 15 V for SA, 12 V for JA, 9 V for ABA and 19 V for JA-Ile. Needle, shield and detector were set at 4500 V, 600 V and 1800 V, respectively.

## 2.9 Histochemical methods

### 2.9.1 GUS staining

GUS staining was used to analyze the activity of promoter fragments of *tps10* and *tps23*. The ß-glucuronidase gene was fused to the promoter fragments using the Gateway cloning system (2.5.15) into an expression vector. The promoter containing plasmid was stable transformed into *Arabidopsis thaliana* using Agrobacterium (2.4.4).

The GUS enzyme converts its substrate, X-Gluc (5-bromo-4-chloro-3-indolyl-beta-D-glucononic acid, cyclohexylammonium salt), into glucuronic acid and the colorless 5-bromo-4-chloro-indoxyl intermediate which spontaneously undergoes an oxidative dimerization to from the insoluble and highly colored indigo dye (5,5'-dibromo-4,4'-dicholor-indigo).

Arabidopsis material was harvested after different induction treatments (2.3) and transferred to glass tubes containing sufficient GUS-staining solution to cover the whole leaf. Vacuum was applied to the vials to ensure complete exposure of the plant cells to the X-Gluc substrate. Leaves were incubated in this solution at 37°C over night.

To remove the chorophyll from the plant material, the leaves were transferred to 80 % ethanol for several hours at 37°C until all chlorophyll was extracted. Leaves were than washed and scanned.

GUS-staining solution:
- 50 mM sodium dihydrogene phosphate (pH7.0)
- 10 mM EDTA
- 0.1 % Triton [v/v]
- 0.1 % N-lauryl-sarcosine [g/v]
- 0.7 µg $ml^{-1}$ ß-mercaptoethanol
- 1 mg $ml^{-1}$ X-Gluc (added freshly)

### 2.9.2 Quantitative GUS assay

The ß-glucuronidase activity was measured quantitatively using 4-methylumbelliferyl-beta-D-glucuronide (MUG) as its substrate (Kay *et al.* 2007). MUG is converted by the ß-glucuronidase to 4-methylumbelliferone (4-MU) which has an excitation wavelength at 365 nm and an emission wavelength at 345 nm and can therefore be used in fluorescence measurements.

20 mg of frozen plant material was ground in liquid nitrogen, placed in 300 µl GUS-extraction buffer, and redissolved. After centrifugation for 5 min at 20000 g at 4°C, 200 µl of the supernatant was transferred to a 96-well plate and centrifuged again for 10 min at 1610 g and 4°C. 100 µl of the supernatant were kept for a Bradford assay (2.7.2). Another 20 µl were transferred to a new 96-well plate and 180 µl 5 mM MUG (dissolved in fresh GUS-extraction buffer) was added and incubated in the dark for 90 min at 37°C. 20 µl of this reaction was transferred to a black 96-well PCR plate (Greiner, Frickenhausen, Germany) and stopped by adding 180 µl 0.2 M sodium carbonate. The fluorometric endpoint measurement was conducted using the infinite 200 Pro (Tecan, Crailsheim, Germany).

For each measurement, a standard curve with 4-MU with the concentrations of: 0.1 µM; 1 µM; 10 µM and 100 µM was prepared. GUS activity was calculated in pmol MU µg protein$^{-1}$ min$^{-1}$ according to the formula below (Boch *et al.* 2009).

$$A_{GUS}\left[\frac{pmol\ MU}{\mu g\ protein * min}\right] = \frac{F * dF * 2000\ pmol\ MU}{90\ min * protein\ [\mu g] * F_{2000\ pmol\ MU}}$$

| | |
|---|---|
| $A_{GUS}$ | GUS activity |
| F | fluorescence of sample |
| dF | dilution factor of sample |
| $F_{2000\ pmol\ MU}$ | fluorescence of standard |
| GUS extraction buffer: | 50 mM sodium dihydrogene phosphate (pH7.0) |
| | 10 mM EDTA |
| | 0.1 % SDS [g/v] |
| | 0.1 % Triton [v/v] |
| | 10 mM MUG (added freshly) |

## 2.10 Statistical analyses

To calculate the statistical relevance of the given data, the appropriate statistical methods were used dependent on the experimental setup. In most cases, a two way ANOVA was performed and Post-Hoc tests were conducted with the Holm-Sidak method to calculate pairwise comparisons. Normal distribution of the data and equality of variances was verified. In case of no normality, data were transformed if possible or analyzed by an ANOVA based on ranks. Significant differences of the data are indicated for $p<0.05$. The respective method for each experiment is provided in the text.

# 3. Results

## 3.1 Identification of genes regulated by herbivore treatment

Maize plants produce a complex mixture of terpene volatiles upon herbivory (Turlings *et al.* 1990; De Moraes *et al.* 1998), but the regulatory mechanisms and signaling cascade leading to the production of volatile terpenes is mainly unknown. In this work, the identification of essential signaling compounds involved in defense responses in *Zea mays* was one main focus.

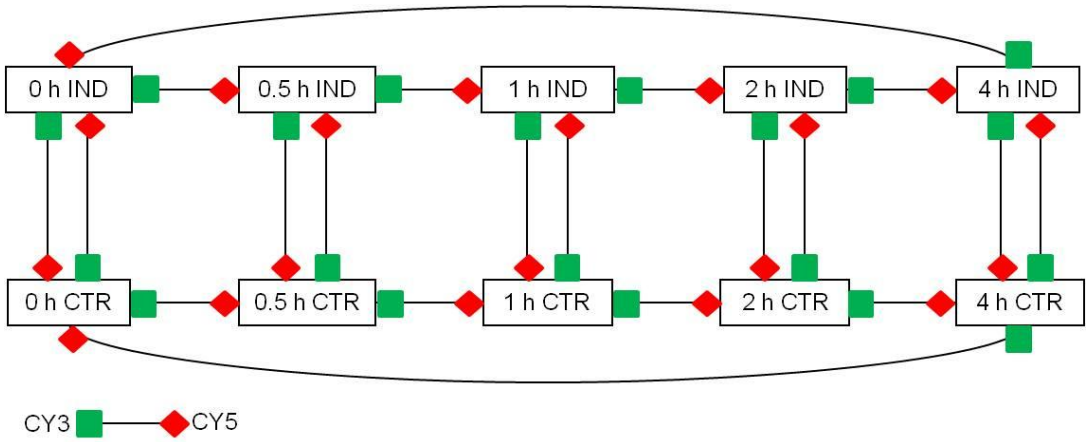



**Fig.3.1: Experimental setup for the microarray hybridization experiment used in this work.** Maize plants were left unharmed (CTR) or treated for 30 min with larvae of *S. littoralis* (IND). Leaves were harvested after 0.5 h, 1 h, 2 h, and 4 h. Additionally, a 0 h time point was included. Four biological replicates were included for each measurement. RNA was obtained from all plants and for all time points and labeled with the fluorescent dyes CY3 and CY5 according to the setup. Each line represents one microarray hybridization experiment using two RNA probes. Thereby, one probe was labeled with CY3 and one with CY5. Dye swaps were performed to guarantee minimal effects of different dye incorporations.

To detect genes regulated by herbivore feeding, we conducted a microarray hybridization experiment with a 46k oligo microarray from the University of Arizona. This microarray was printed by the Maize Oligonucleotide Project Team (http://www.maizearray.org/) on a glass slide and contains 46128 70mer oligos based on cDNA and EST sequence information from *Zea mays* var. B73. Therefore, the chip represents a large fraction of the transcriptome of the maize line B73. The experimental design chosen, described as “loop-design”, included 4

biological replicates and dye swaps for each sample (Fig.3.1). Dye swaps minimize the effect of different incorporations of fluorescent molecules into RNA, whereas the loop design provides a higher statistical power than a simple reference design (Churchill 2002).

To induce *Zea mays* var. Delprim, two second instar larvae of *S. littoralis* were placed on the lower part of maize leaves for 30 min. Both the herbivore-damaged and the undamaged plants were harvested after 0 h, 0.5 h, 1 h, 2 h, and 4 h to determine the transcriptional changes. The undamaged plants were harvested at each time point to account for circadian changes and other factors that might affect plant gene expression throughout the 4 h experiment. A reliable test for the successful herbivore induction of the plant material is the expression of the terpene synthases TPS10 and TPS23, since those enzymes produce the main volatiles released after herbivore attack in maize (Köllner *et al.* 2004). To check for efficient herbivore induction in damaged plants, terpene production was determined by GC-MS in induced leaf material at 4 h after induction (Fig.3.2).

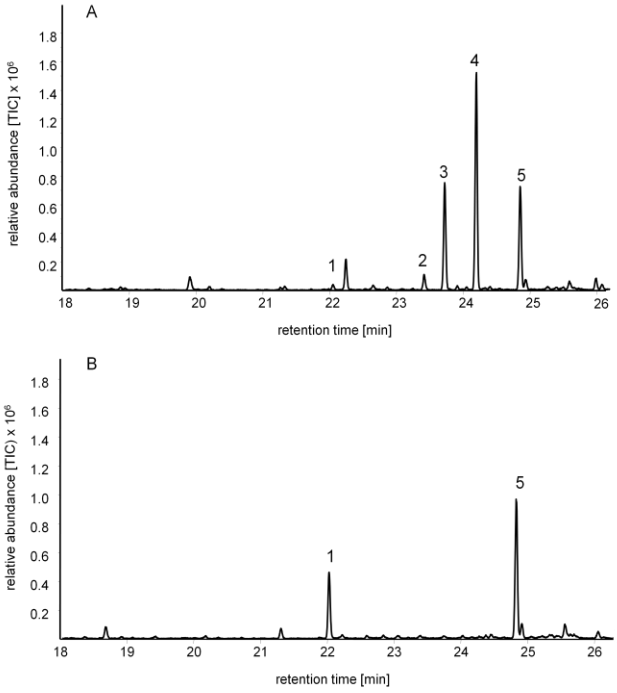



**Fig.3.2: Gas chromatographic analysis of herbivore-damaged and undamaged maize leaves.** (A) Maize leaves were induced by herbivore feeding for 30 min and material was harvested after 4 h or (B) undamaged material harvested after 4 h. Plant material was ground into a fine powder and 200 mg were incubated for 30 min with a SPME fiber. Peaks were identified as 1: unknown, 2: (*E*)-ß-caryophyllene, 3: (*E*)-α-bergamotene, 4: (*E*)-ß-farnesene and 5: ß-Ionone, respectively.

The sesquiterpenes (*E*)-ß-caryophyllene, (*E*)-α-bergamotene and (*E*)-ß-farnesene were emitted after the herbivore induction period while no sesquiterpenes were visible in the control plants. This result confirmed the induction of the maize plants was appropriate for microarray analysis.

To evaluate the up- and down-regulated genes, the raw data from the microarray were analyzed using the statistical program R as described in section 2.5.16. Only genes with a relative induction higher than 2-fold were chosen for further analysis. Induced oligo fragments were run through different databases to find a putative gene function. A list of all genes differentially regulated after herbivory can be found in the appendix (7.6). To generate a simple overview of the molecular function and cell processes the affected genes were involved in, the program Blast2GO (Conesa *et al.* 2005) was used.

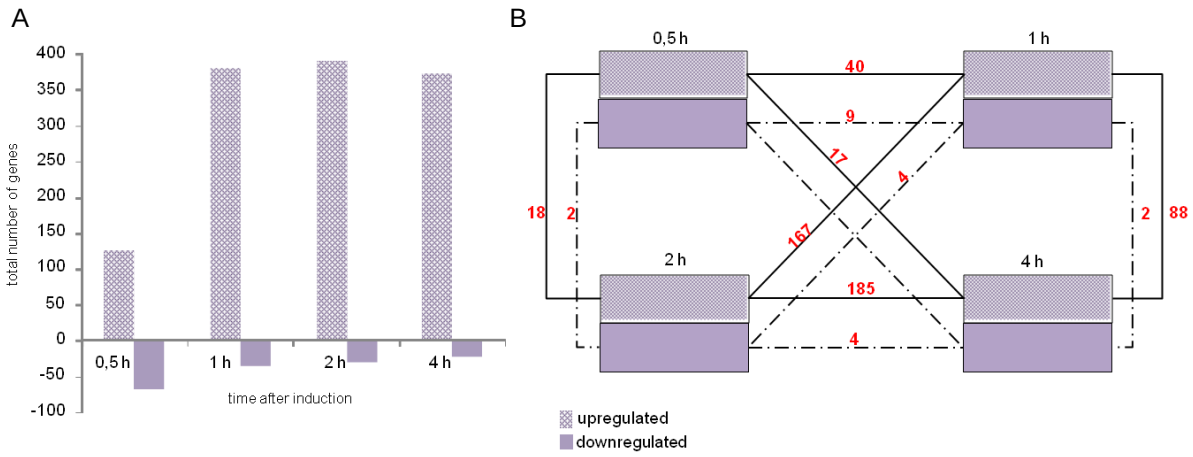



**Fig.3.3: Overview of all differential regulated genes by herbivory.** Plants were treated with *S. littoralis* for 30 min and harvested at 0.5 h, 1 h, 2h, and 4 h. A: The total number of genes that showed a differential fold of ≥ 2 are displayed. B: The number of genes that shared a same regulation pattern is displayed.

An overview of all positive- and negative-regulated genes found after herbivore treatment is shown in Fig.3.3. Half an hour after the caterpillar treatment, 125 transcripts displayed increased expression within the leaves while 68 genes showed a reduced expression. After one hour, the number of up-regulated genes increased to 381 and did not drop dramatically at 2 h and 4 h. Overall, the majority of differentially regulated genes showed an increased expression level. Only 12% of the genes displayed a decreased expression. For better

visualization, identified genes were displayed regarding their biological process (Fig.3.4). The functional annotation of the sequences was given by Gene Ontology.

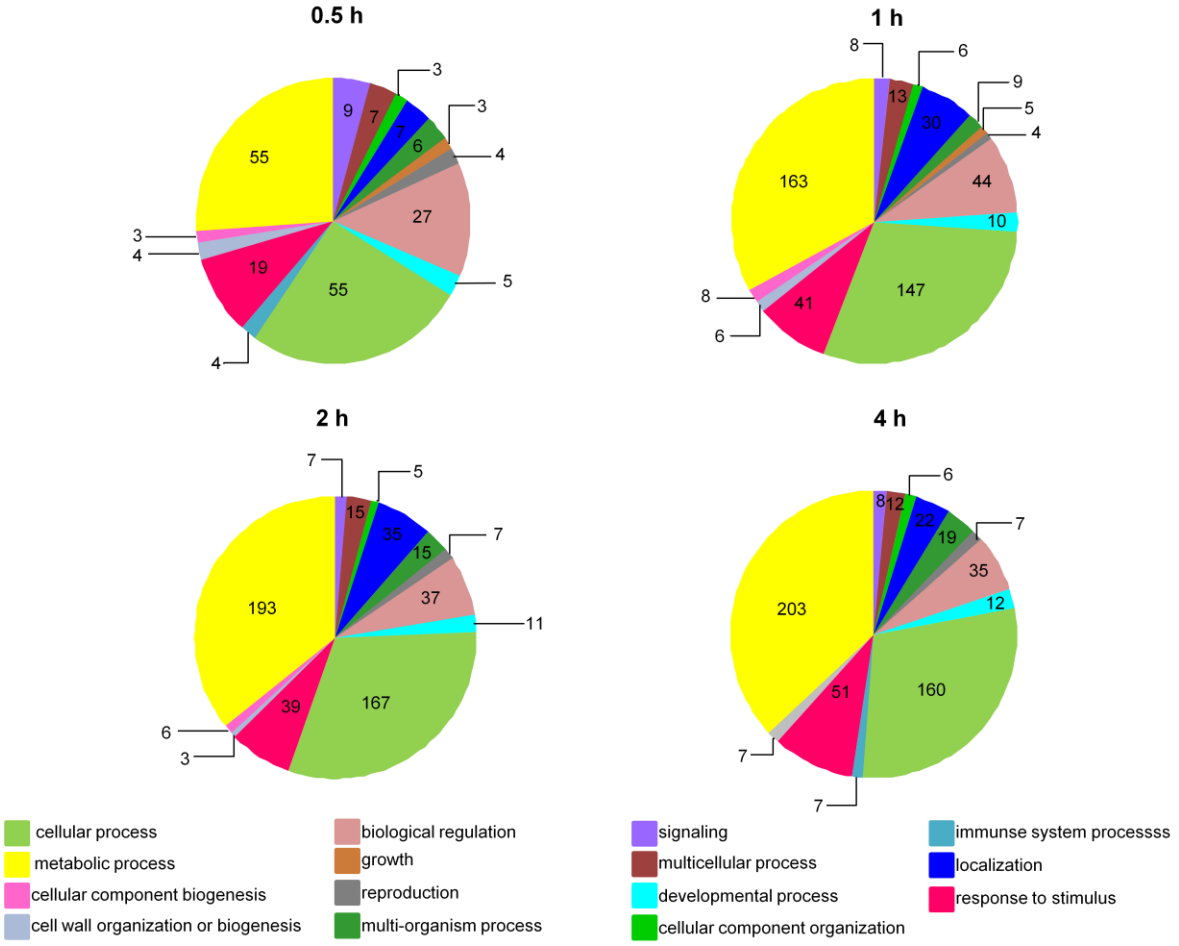



**Fig.3.4: Classification of herbivore-regulated genes in regard to the biological processes of the plant.** Genes regulated by herbivory and identified with the Long Oligo Microarray, were mapped and associated with their biological role within the plant using Blast2Go (sequence filter = 2; level = 2). Plants were treated with *S. littoralis* for 30 min and harvested at 0.5 h, 1 h, 2 h, and 4 h. The numbers indicate the number of associated sequences.

At the four time points, the majority of the identified genes belonged to the group of "metabolic and cellular processes". The genes belonging to the group "response to stimulus" increased over the 4 h period from 19 to 51 sequences, while genes with a function in plant growth were completely missing after 1 h.

Next to the biological function, the identified transcripts were compared regarding their molecular function. Within this analysis, the sequences could be grouped into: binding activity, enzyme regulator activity, transporter activity, transcription regulator activity, etc. Fig.3.5 shows an overview of the genes which were differentially regulated within the microarray hybridization experiment. The graphs were obtained from Blast2Go with a sequence filter setting of 2, level 2. At the four time points, genes belonging to the group of "catalytic activity" and "binding" took up the major portion. It is noteworthy that genes can belong to more than one functional group, depending on the Gene Ontology numbers provided by Blast2Go. The figure shows that genes having a binding function were doubled from 0.5 h to one hour after herbivore attack. Genes mapped to "transcription regulator activity" showed the highest amount after 0.5 h after the treatment and were then limited to 3 genes. This suggests that the plant was able to respond very quickly to the herbivore damage by activating a specific set of transcription factors.

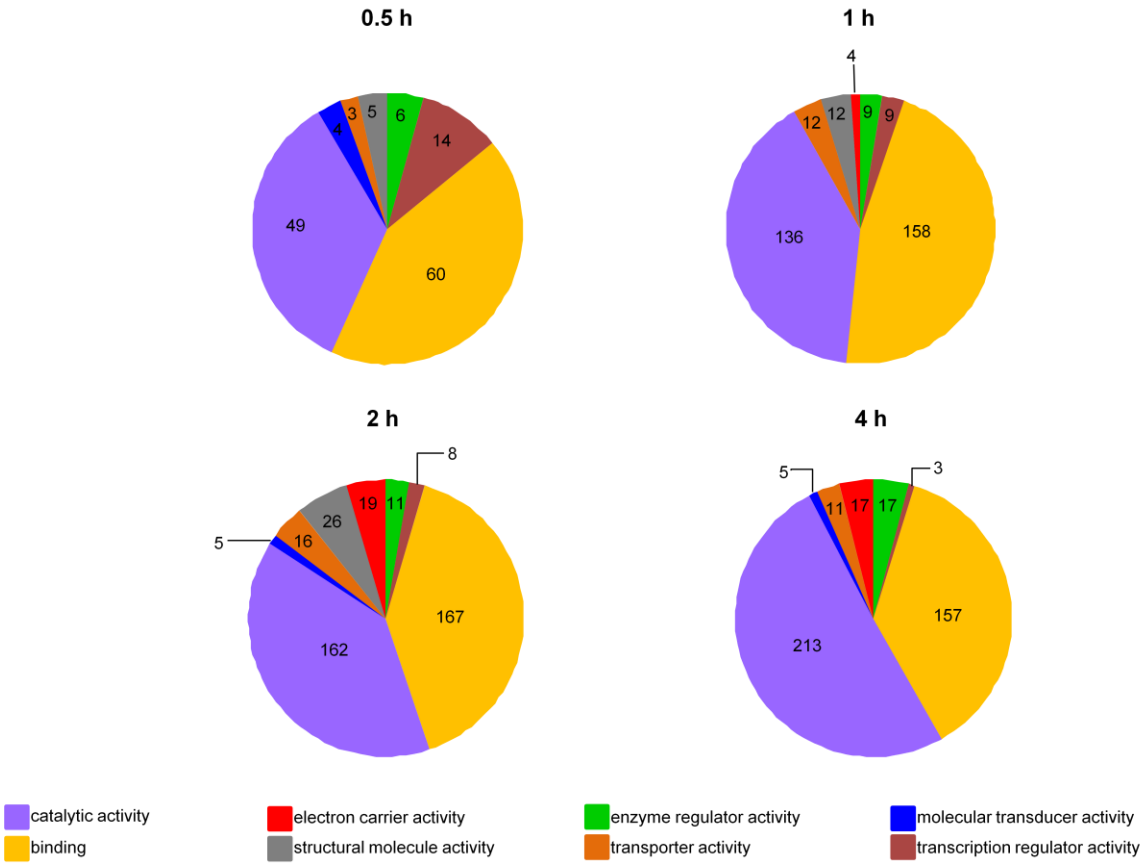



**Fig.3.5: Classification of herbivore-regulated genes in regard to the molecular function of the plant.** Plant material was harvested at 0.5 h, 1 h, 2 h, and 4 h after a 30 min treatment with *S. littoralis*. Transcripts with concentration differences (>2 fold) were detected after herbivory and assembled into molecular functional groups. Figures were obtained from Blast2GO (Sequence filter = 2, level = 2). The numbers indicate the number of associated sequences.

To analyze the functional distribution of the herbivore-induced genes more specifically, several biological processes were investigated for positive and negative-regulated genes. The functional classifications chosen were transport, transcription, signaling, cell wall metabolism, secondary metabolism, photosynthesis, stress response, amino acid metabolism, carbon metabolism, nucleotide metabolism, plant development, and hormone metabolism (Fig.3.6). While the total numbers of herbivore-regulated genes increased strongly between the 0.5 h and 1 h time points, the highest number of negatively regulated genes were present at 0.5 h. Nine transcripts with a putative function in stress response were negatively regulated and ten transcripts were up-regulated. Among the genes with putative functions in gene

transcription, seven transcripts were down-regulated and 13 were up-regulated. One hour after herbivore induction, the total number of genes induced by herbivory increased dramatically, while only few genes were still reduced. 39 genes functioning as regulatory factors showed an increased transcript accumulation, also 17 genes of hormone metabolism were differentially expressed. Genes of this group were not involved 0.5 h after induction. There are only few changes between 1 h and 2 h after herbivore induction, mainly the number of transcripts involved in the amino acid metabolism rose. This could be explained with the need of amino acids for the translation of proteins necessary for defense. The main difference between 2 and 4 h after the herbivore treatment was the suppression of genes having a role in transcriptional activity and the negative-regulation of transcripts playing a role in the photosynthesis of the plant. While a plant is attacked by an herbivore, resources may rather be put into defense than into photosynthesis.

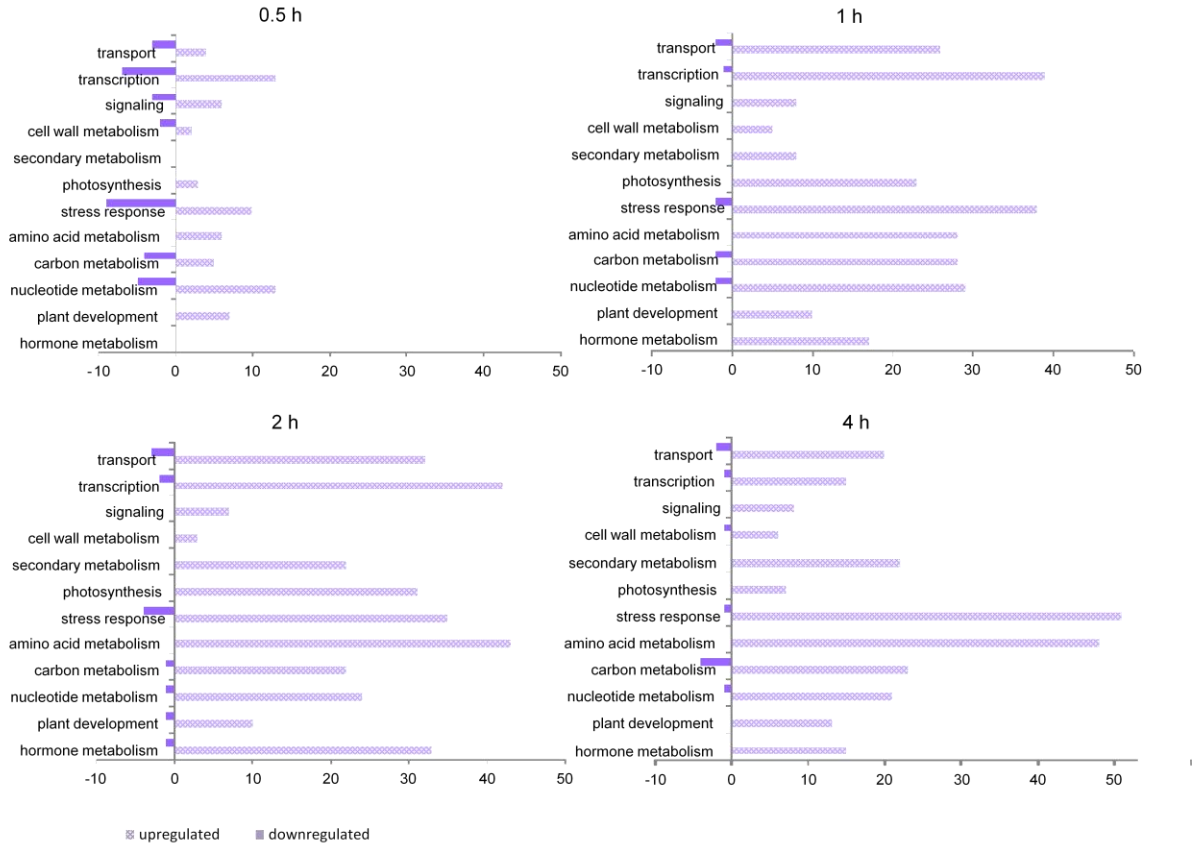



**Fig.3.6: Functional classification of genes with herbivore-regulated transcript levels.** Plants were treated with *S. littoralis* for 30 min and harvested at 0.5 h, 1 h, 2 h, and 4 h. Total numbers of genes with enhanced and repressed transcript accumulation were distributed into functional groups.

Transcription factors affected by herbivore treatment were the main focus of this study, assuming that those play a critical role in the induction of plant defense. Transcription factors are small proteins which regulate the gene expression through binding of the promoter of specific target genes, either by itself or in co-operation with other regulatory proteins. The Long Oligonucleotide chip was based on the ESTs of the maize inbred line B73 for which the genome sequence is available in genomic databases like TIGR, PlantGDB, NCBI and Maizesequence. Oligofragments of putative transcription factors on the microarray chip were aligned to the genomic sequence in the databases to obtain the full length sequences. Unfortunately, this method was not successful for all putative transcription factors. Thus, RACE PCR had to be performed where the information from those databases could not solve the genomic sequence of the transcription factors of interest. Table 3.1 gives an overview of annotated transcription factors identified by the Long Oligonucleotide Microarray, their accession number and their putative genomic annotation.

**Tab.3.1: Putative transcription factors (TF) and their annotation.**

| Synonyms | Accession number | Annotation |
|---|---|---|
| **TF1** | MZ00026661 / TC280937 | putative NAC-domain protein |
| **TF2** | MZ00031423 / TC314449 | CAF1 like protein |
| **TF3** | MZ00044429 / TC326357 | MYB-like DNA binding |
| **TF4** | MZ00006968 / TC297179 | Zn-finger protein |
| **TF5** | MZ00014652 / TC284178 | CHY Zn-finger protein |
| **TF6** | MZ00017631 / TC298582 | putative transcription factor |
| **TF7** | MZ00018761/ AZM5_85107 | MYB-like DNA binding protein |
| **TF8** | MZ00017826/ AZM5_89531 | bHLH-like protein |
| **TF12** | MZ00056923/ AZM5_18508 | MYB-like protein |
| **TF15** | MZ00031032/ AZM5_10006 | putative PRLI-interacting factor |
| **TF18** | MZ00029591/ AZM5_14769 | DNA binding protein |
| **TF19** | MZ00024627/AZM5_32315 | ETTIN-like auxin response factor |
| **TF20** | MZ00024626/ AZM5_31563 | ETTIN-like auxin response factor |
| **TF21** | MZ00049092 /AZM5_95253 | G-Box binding protein |
| **TF22** | MZ00035947/ AZM5_27326 | NAC-domain protein |
| **TF23** | MZ00005265/ AZM5_98744 | helix-loop-helix DNA-binding protein |

| | | |
|---|---|---|
| **TF24** | MZ00003819/ AZM5_142343 | ethylene responsive transcriptional coactivator |
| **TF25** | MZ00035924/ AZM5_43253_1 | response regulator Cip1 |
| **TF26** | MZ00042739/ AZM5_152884, AZM5_108687 | WRKY transcription factor |
| **TF27** | MZ00017310/ AZM5_31855, AZM5_24906 | Zn-finger protein |
| **TF28** | MZ00048444/ AZM5_15878 | MYB factor protein |
| **TF29** | MZ00041804/ AZM5_5103 | ZN-finger protein |
| **TF30** | MZ00026596/ AZM5_13093 | ethylene responsive element binding factor3 |
| **TF31** | MZ00025601/ AZM5_10813 | putative leucine zipper protein |
| **TF32** | MZ00025832/ AZM5_7677 | bHLH transcription factor |
| **TF33** | MZ00025058/ AZM5_85092 | transcription factor like protein |
| **TF34** | MZ00020619/ AZM5_6856 | transcription factor WRKY12 |
| **TF35** | MZ00023008/ AZM5_416 | putative I-box binding factor |
| **TF36** | MZ00028957/ AZM5_14321 | calmodulin-binding protein-like |
| **TF37** | MZ00041802/ AZM5_5103 | Zn-finger protein |
| **TF38** | MZ00018541/ AZM5_87053 | Putative EREBP-like protein |
| **TF39** | MZ00032877/ AZM5_50726 | putative phi-1 |
| **TF40** | MZ00015673/ AZM5_90421 | DRE binding factor 1 |
| **TF41** | MZ00001133/ AZM5_93171 | putative LHY-protein |
| **TF42** | MZ00056523/ AZM5_37193 | putative phi-1 |
| **TF43** | MZ00029551/ AZM5_16115 | Zn-finger protein 1 |
| **TF44** | MZ00004193/ AZM5_107126 | putative bZIP protein HY5 |
| **TF45** | MZ00014137/ AZM5_98313 | transcription factor-like |
| **TF46** | MZ00056566/ AZM5_16172 | Zn-finger transcription factor ZF1 |
| **TF47** | MZ00035095/ AZM5_18076 | putative nucleoid DNA-binding protein cnd41 |
| **TF48** | MZ00037615/TC329977 | putative NLI interacting factor |
| **TF49** | MZ00016101/TC295701 | putative RAB7A protein |
| **TF50** | MZ00000664/TC308252 | RING finger-like protein |
| **TF51** | MZ00036019/TC280937 | putative NAC-domain protein |

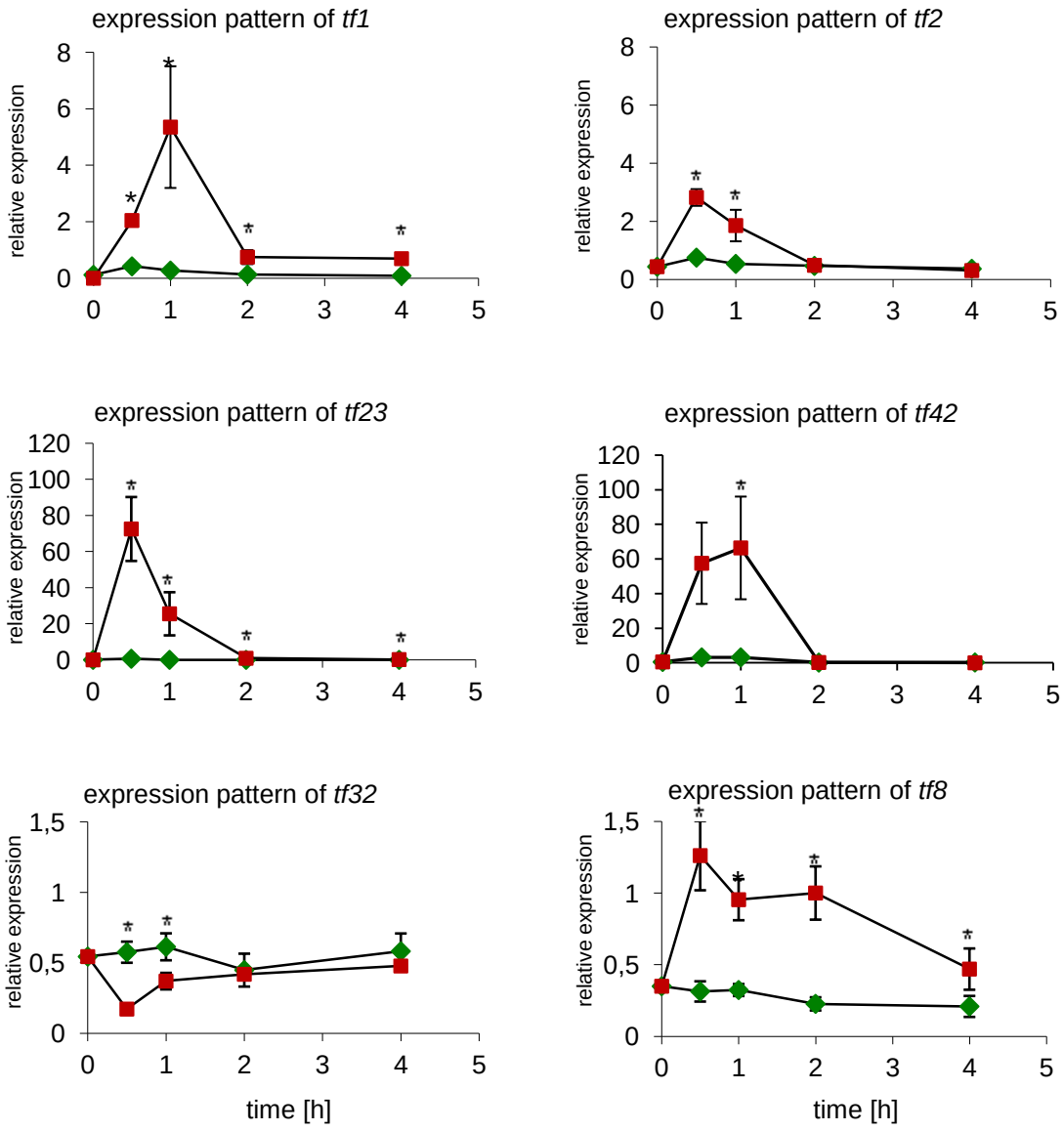
## 3.2 The induction of transcription factors depends on environmental cues

### 3.2.1 The transcript patterns of transcription factors respond to herbivore feeding

To confirm the expression patterns of the identified transcription factors and investigate their spatial distribution, primers for the chosen transcription factors were designed from the oligonucleotide fragments given by the microarray and the genome databases. Results from the microarray experiment were verified with QRT-PCR using plant material that was also harvested at 0 h, 0.5 h, 1 h, 2 h, and 4 h after herbivore damage. Verification of this data was important due to the low threshold of 2 used for statistical analysis. This low threshold was necessary to identify a large fraction of the transcription factors involved in plant defenses. Compared to enzymes, transcription factors are usually present in a low amount to regulate gene expression and therefore do not rise that strongly. On the other hand, the chance of false positives rises. Only for 18 of the selected transcription factors, the microarray results could be affirmed. To test for successful induction of the plant material, five additional herbivore-regulated genes, the terpene synthases *tps10* and *tps23,* and the O-methyl transferases: *omt1*, *omt3* and *omt4* were analyzed with QRT-PCR.

Transcription factors of several classes were affected by herbivore feeding in the leaf: MYB-like binding proteins, WRKY binding proteins, I-Box binding proteins, G-Box binding proteins, zinc-finger protein, bHLH binding proteins and bZIP binding proteins. Most of the herbivore-induced transcription factors exhibited a transient increase in transcript levels. The kinetics of this increase differed between the factors and was used to classify them into early and late responding factors. The transcript accumulation profiles of six transcription factors and two terpene synthases are shown in Fig.3.7. Transcription factors *tf1, tf2, tf8* and *tf23* showed a significant expression maximum already after half an hour of induction, indicating a fast response after herbivory. *Tf42* also had a highly induced expression at 30 min after induction but reached its maximum at 1 h after the onset of treatment. In contrast, *tf32* demonstrated a negative regulation pattern. In this case, the expression level between control plants and induced plants showed a significant down-regulation of gene expression for the time points half an hour and 1 h after treatment. Overall, transcription factors were induced from half an hour to two hours after the treatment, while the expression of the terpene

synthases started at around 2 h after herbivore feeding and then slowly increased. This correlated with the volatile measurement which was detected at 4 h after herbivore treatment (Fig.3.2). The results for all further investigated transcription factors are in the appendix (7.1).



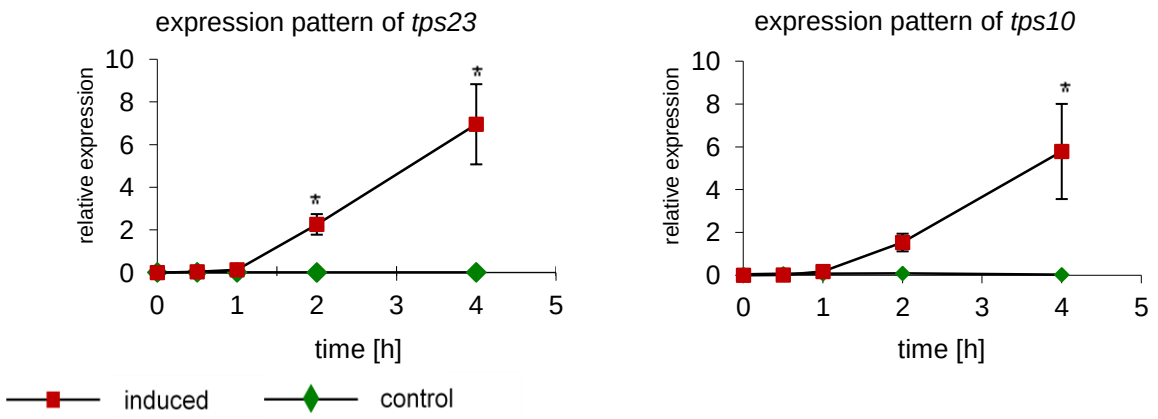



**Fig.3.7: Relative expression pattern of selected transcription factors and terpene synthases.** Plants were treated with *S. littoralis* caged for 30 min on a single leaf. Material was harvested after: 0 h, 0.5 h, 1 h, 2 h, and 4 h. Means and standard error are shown (n=4). The relative expression levels were calculated as described in 2.4.9. Two-Way ANOVA was used to calculate statistical differences with time as factor one and treatment as second variable. * indicate significant differences between treatments within time points ($p<0.05$).

### 3.2.2 Transcript accumulation is affected by the duration of caterpillar feeding

After testing the induction kinetics of transcription factors in response to an herbivore attack of 0.5 h, we investigated the effect of different durations of herbivore feeding. In the following experiments, the caterpillar larvae were caged on a single leaf and were allowed to feed until the plant material was harvested. To obtain a good feeding performance, caterpillar larvae were not able to feed the night before. Leaf material was harvested after 0 h, 0.5 h, 1 h, 2 h, and 4 h and ground in liquid nitrogen. cDNA was obtained and used to test the expression level of several transcription factors by QRT-PCR. The relative expression was calculated against the expression of the housekeeping genes.

The transcript levels of the transcription factors *tf1* and *tf35* in response to different lengths of feeding time are shown in Fig.3.8. The expression kinetics of further factors can be found in the appendix (7.2). While the expression level for *tf1* increased to its maximum at 1 h after a feeding time of 30 min, the expression pattern with the continuous feeding showed significant differences. Here, transcript accumulated within 0.5 h, but then dropped and

increased again for the remaining time points. The same pattern could be observed for the transcription factor *tf35*.

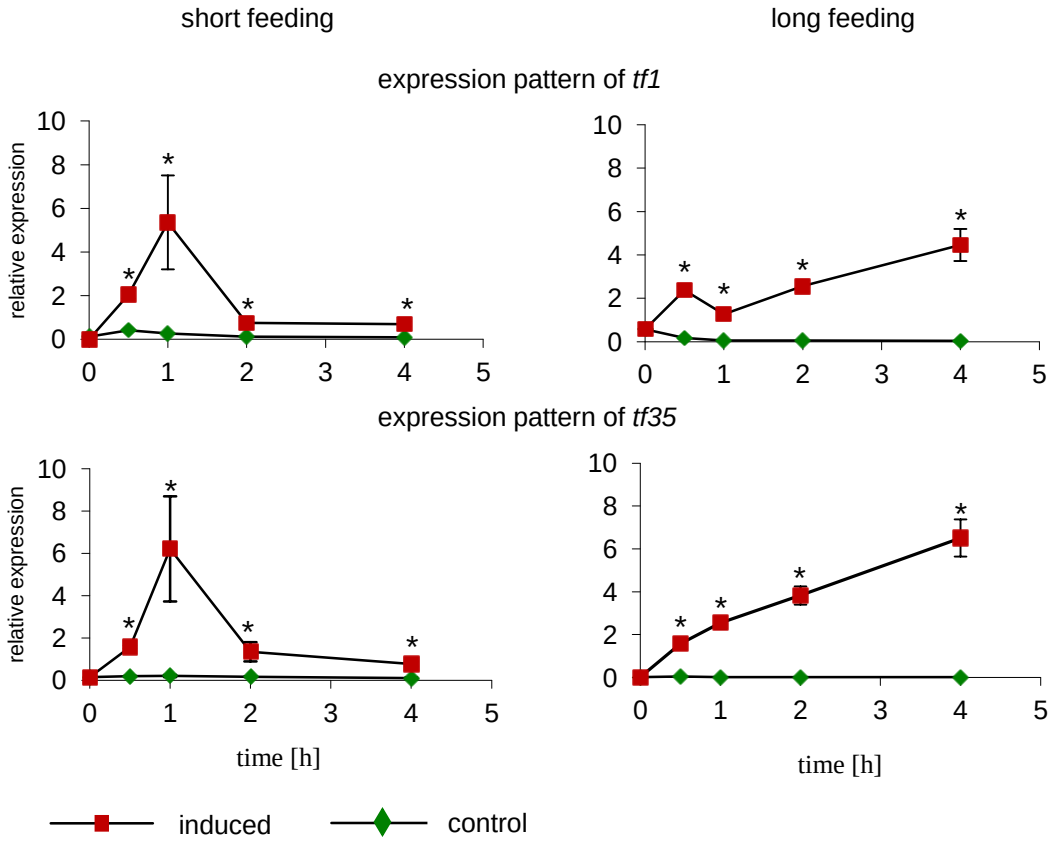



**Fig.3.8: Relative expression pattern of *tf1* and *tf35* after short and long term feeding.** Delprim maize leaves were treated either for half an hour with the caterpillar larvae *S. littoralis* (short feeding) or continuous feeding until plant material was harvested (long feeding). The expression patterns are shown over a 4 h interval. Induced expression pattern is marked with a red square, control points with a green diamond. Expression was calculated against the housekeeping genes. Standard error (n=4 for short term feeding, n=3 for long term feeding) is shown for each measurement. Two-Way ANOVA was used to test significant differences with $p<0.05$ defined as significant for the treatment within the time points (*).

### 3.2.3 The transcript patterns of transcription factors are similar in Delprim and B73 despite differences in volatile production

While most European maize lines have the ability to produce (*E*)-ß-caryophyllene after root damage, most American maize lines have lost the ability to do so (Köllner *et al.* 2008).

In our study, we used the maize variety Delprim as an example for an European, (*E*)-ß-caryophyllene-producing maize line and B73 as an American, non-producing maize line. Both maize lines are able to produce the sesquiterpenes (*E*)-ß-farnesene and (*E*)-α-bergamotene which are formed by the sesquiterpene synthase TPS10 (Bohlmann *et al.* 1998; Schnee *et al.* 2006). (*E*)-ß-caryophyllene is produced by the terpene synthase TPS23 (Köllner et al., 2008). Although the maize line B73 contains a functional *tps23* structural gene, the gene is not transcribed in B73. This suggests that some components in the signaling cascade for the expression of *tps23* are missing in B73.

To study the molecular base of *tps23* regulation, the transcript accumulation of nine of the herbivore-induced transcription factors was tested in both maize lines using QRT-PCR. The plants were induced using 3rd instar larvae. The results are shown in Fig.3.9 with the stacked columns of the control and the induced expression levels for each plant cultivar.

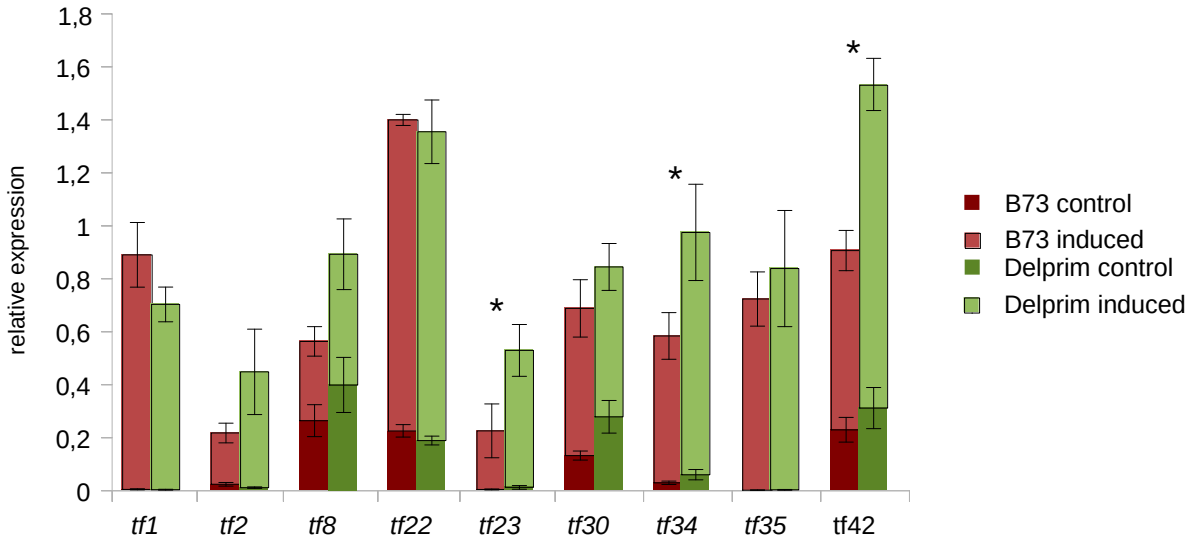



**Fig.3.9: Relative expression levels of transcription factors after herbivore damage in the maize varieties B73 and Delprim.** Four biological replicates were used for each control and induced sample. Plants were treated in the afternoon with the caterpillar larvae and harvested the next morning. The relative expression level was calculated against the two housekeeping genes as described in 2.5.9. Means and standard error bars are shown. Two-Way ANOVA was used to calculate statistical significance between B73 and Delprim. P-values <0.05 are highlighted with (*).

The transcript levels of the transcription factors were always induced after herbivory. Only transcription factors *tf23*, *tf34*, and *tf42* showed a significant difference between the two maize cultivars, but were still expressed in the B73 cultivar after herbivory. Therefore, none of the factors seems to be directly associated with the loss of the (*E*)-ß-caryophyllene signal in B73.

### 3.2.4 The application of jasmonic acid causes transcriptional changes

JA is one of the major plant hormones formed in response to many abiotic and biotic stresses (Turner *et al.* 2002). To test whether the herbivore-regulated transcription factors are located upstream or downstream of JA in the signal transduction cascade, we measured the effect of JA on those transcription factors. Plants were induced with jasmonic acid by cutting young maize plants and transferring them into glass vials containing either water or a 250 µmol jasmonic acid solution. Since cutting of maize plants also induces low levels of JA formation (Engelberth *et al.* 2004), a second control group with undamaged plants was added. In these experiments, transcript levels were only studied after 0.5 h and 1 h induction. This is the time window in which JA is known to influence the signaling cascade (Mandaokar *et al.* 2006) that leads to the production of volatile terpenes.

Plant material was harvested and QRT analysis was performed. In addition to the transcription factors, the expression profile of *tps23* was measured to determine the effect on the TPS target gene as well. The JA-induced expression profile of four transcription factors (*tf1*, *tf2*, *tf23*, and *tf30*) and *tps23* are shown in Fig.3.10. The relative expression was calculated against the housekeeping gene HG2 (Phillips *et al.* 2009). After jasmonic acid treatment, cDNA accumulation of the four transcription factors as well as *tps23* was found. Surprisingly, the transcript levels were similarly induced in mechanically treated plants where only water was added to the wounding site. This indicates that the cutting the maize plant already results in activation of JA-mediated plant defenses. The presence of jasmonic acid in the aqueous solution did not seem to have a strong impact on the expression kinetics of these transcription factors.

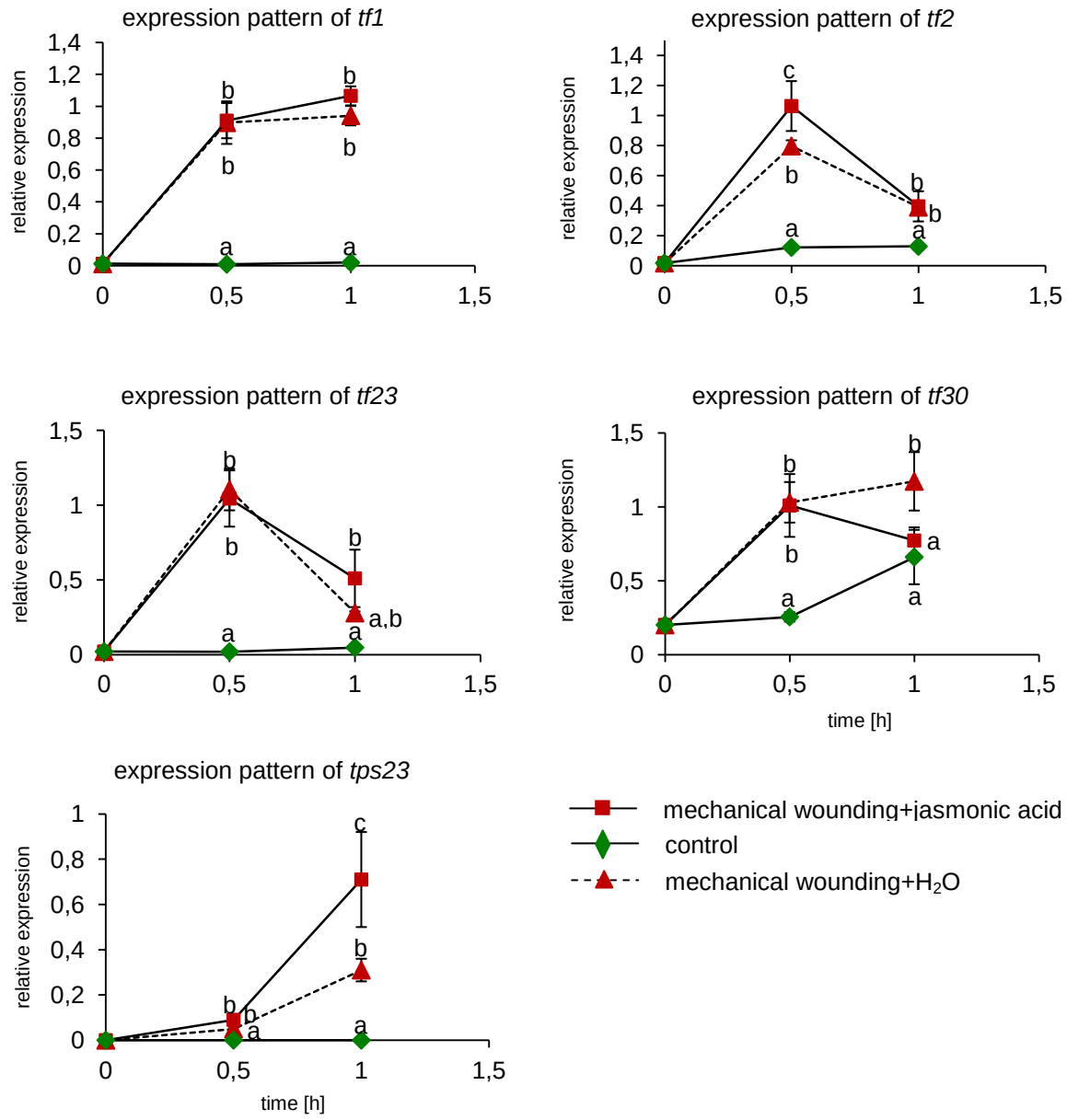



**Fig.3.10: Expression profile of transcription factors *tf1, tf2, tf23, tf30,* and *tps23* after induction with jasmonic acid.** Plants were cut and put into water or water containing jasmonic acid, to analyze early transcriptional changes of transcriptions factors during the first hour by QRT-PCR. The relative expression was calculated as the expression of the housekeeping gene HG2. Means and standard errors are shown (n=3). Two-Way ANOVA was performed with time as the first variable and treatment as second factor. Different letters indicate significant differences between treatments within time points ($p<0.05$).

In all cases, the transcript levels rose significantly after half an hour of induction. No increase was detected in the undamaged control plants. While *tf1* transcript levels did not change between 0.5 h and 1 h, transcript levels of *tf2* and *tf23* decreased somewhat after 1 h. For *tf23*, the treatment with jasmonic acid displayed a tendency to retain a higher expression level when compared to the mechanically wounded plants. In the case of *tf30* however, the cutting of the leaf alone seemed to have a higher impact on the expression level than JA treatment. After one hour, the relative expression of *tf30* decreased only when plants were treated with jasmonic acid. The behavior of all transcription factors was very specific upon mechanical wounding and only few transcription factors responded to the additional JA treatment (see appendix 7.3).The transcript levels of terpene synthase *tps23* responded much more slowly to the induction treatment than the transcription factors. Still, a significant amount of transcript was already visible after half an hour of induction and increased after one hour of induction. Only the expression level of *tps23* increased significantly in response to JA. Still, a conclusion cannot be drawn whether the identified transcription factors responded to internal or externally applied JA. To elucidate the specific function of transcription factors, further experiments have to be conducted.

## 3.3 Plant responses to mechanical damage – The Mecworm

The induction experiments with jasmonic acid (3.2.4) indicated the importance of leaf mechanical damage in the regulation of gene expression in maize. In lima bean, mechanical damage alone was shown to induce volatile production (Mithöfer *et al*. 2005). Since there is no comparable study in maize, an experiment was set up to differentiate between the effects of mechanical treatment, mechanical treatment plus application of caterpillar regurgitate, and completely unharmed plants. The time course was similar to that of the microarray hybridization experiment to obtain comparable results.

Mechanical treatment was performed with the Mecworm, an instrument which imitates caterpillar feeding by damaging the plant surface with a metallic pin. In addition to the mechanical damage, plants were also treated with 10 µl caterpillar regurgitate per leaf to imitate both induction mechanisms of herbivore feeding. Plant material was analyzed for

transcript accumulation of the transcription factors, the production of volatiles and the induction of several plant hormones.

### 3.3.1 The influence of mechanical damage on the transcript accumulation of transcription factors

The expression patterns of the transcription factors were tested after the Mecworm treatment and compared to those of undamaged controls. Relative expression was calculated as the expression of the housekeeping genes HG1 and HG2 (Tab.2.4) to exclude changes in the expression patterns due to diurnal rhythms.

Most of the transcription factors showed similar expression levels after mechanical damage with and without regurgitate (Fig.3.11). The transcript levels rose after the induction stimulus within the first hour and then decreased to the control level. The expression patterns of *tf1* and *tf2* demonstrated a very short response to the induction. Also *tf34*, *tf42* and *tf46* showed a similar expression pattern (figures in the appendix 7.4). Overall, the mechanical wounding seemed to induce the expression of the transcription factors by itself.

*Tf23* and *tf30* were the only factors that displayed a difference between mechanical damage and the treatment with caterpillar regurgitate. The transcript level of *tf23* was highly induced after application of oral secretion, while the transcript accumulation of *tf30* showed a higher induction after mechanical wounding alone. In both cases, expression levels of the two induction types converged after 2 h and showed an expression pattern similar to most of the other transcription factors. A factor in the oral secretion of caterpillars must be responsible for the differential expression of those transcription factors.

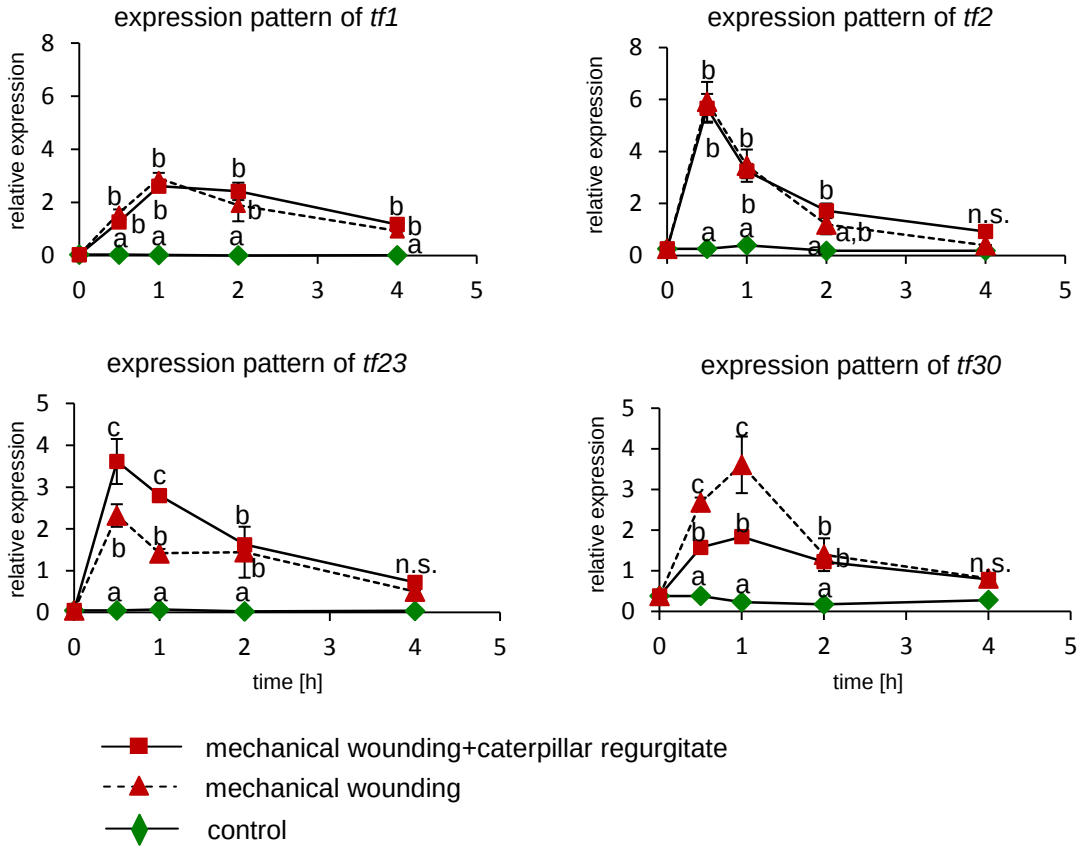



**Fig.3.11: QRT-PCR analysis of transcription factors *tf1, tf2, tf23,* and *tf30* after mechanical induction with and without caterpillar regurgitate.** Plants were treated with mechanical damage and mechanical damage plus the application of caterpillar regurgitate and harvested after 0 h, 0.5 h, 1 h, 2 h, and 4 h. Means and standard errors are shown (n=4). The relative expression was calculated as described in 2.5.9. Two-Way ANOVA was performed with time as the first variable and different induction types as second factor. Different letters indicate significant differences between treatments within time points ($p<0.05$).

## 3.3.2 The type of damage affects the amount of terpene production

Next, it was studied whether the constant mechanical damage of the caterpillar, simulated by the Mecworm, is sufficient not only for transcription factor induction but also for volatile terpene emission. To confirm the induction of plant material, the transcript level of *tps23* was measured. The expression profile showed a significant increase of cDNA for the time points 1 and 2 hours after the induction and accumulated consistently up to 4 hours after induction (Fig.3.12). Interestingly, there is no difference in the amount of *tps23* cDNA measured after

mechanical damage and mechanical damage + caterpillar regurgitate, matching the transcription profile of most transcription factors measured. Still, this result was in contrast to the transcript expression profile where plants had been treated with jasmonic acid (3.2.4). The differences could result from the different types of induction. While JA-treated plants were cut before the treatment, the Mecworm-experiment simulated a more natural herbivore attack.

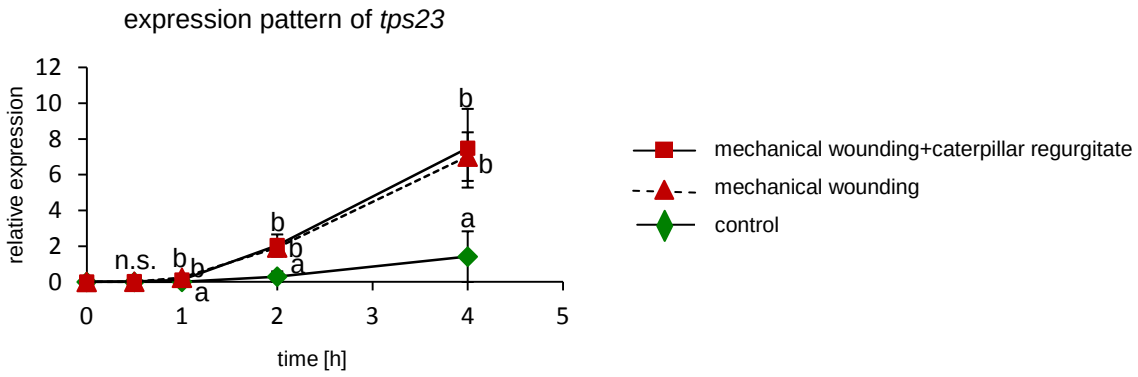



**Fig.3.12: Expression pattern of *tps23* after mechanical damage, mechanical damage plus caterpillar regurgitate and in control plants.** Leaves were treated with the Mecworm and plant material was harvested after the given time points. Means and standard errors are shown (n=4). Two-way ANOVA was performed with time as the first variable and treatment types as second factor. Different letters indicate significant differences between treatments within time points ($p<0.05$).

The same plant material was also analyzed for terpene volatiles by a GC-MS (Fig.3.13). The plant material was incubated with a SPME fiber which has the advantage of a high sensitivity compared to hexane extracts.

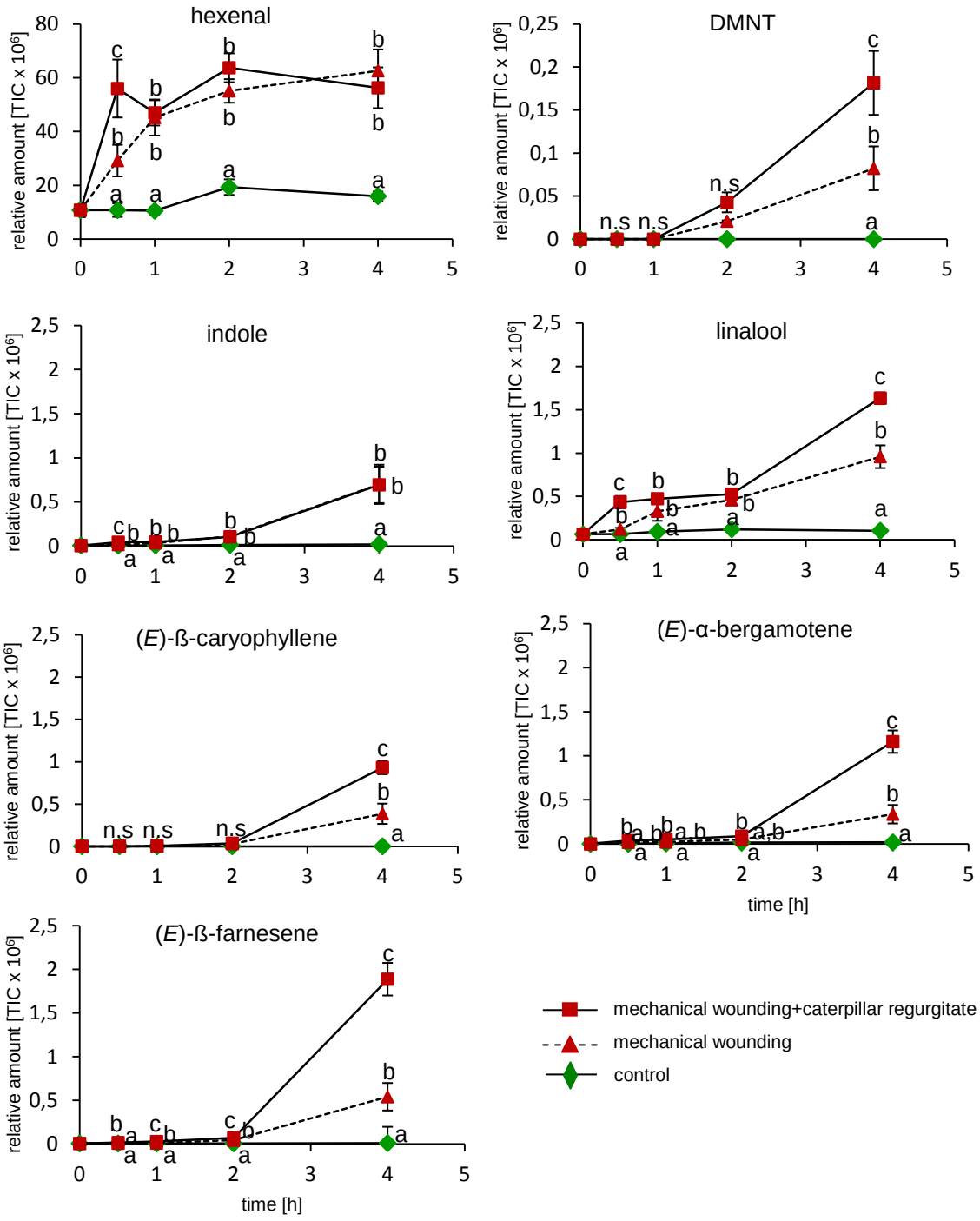



**Fig.3.13: Relative amount of volatile emission after treatment of seedlings with Mecworm and regurgitate.** Leaves of maize plants var. Delprim were treated with mechanical damage (Mecworm), mechanical damage+caterpillar regurgitate and control, respectively, and analyzed after 0 h , 0.5 h ,1 h, 2 h, and 4 h. Plant material was ground and 200 mg were measured for volatile production using SPME. Means (n=4) and standard error is shown. Two-Way ANOVA was performed with time as the first variable and treatment types as second factor. Different letters indicate significant differences between treatments within time points ($p<0.05$).

Looking at the volatile sesquiterpene (*E*)-ß-caryophyllene, the induction profile showed a picture different from the *tps23* transcript levels. While the transcript levels were detectable after 0.5 h, the corresponding volatile of *tps23*, (*E*)-ß-caryophyllene, was observed after 2 h. The amount of (*E*)-ß-caryophyllene increased between 2 h and 4 h after induction. At 4 h, plants treated with mechanical damage emitted only ~50 % (*E*)-ß-caryophyllene compared to plants treated with caterpillar regurgitate.

The sesquiterpenes (*E*)-α-bergamotene and (*E*)-ß-farnesene illustrated a similar behavior. In both cases, the terpene production was induced at 4 h but more volatiles were emitted after application of regurgitate than mechanical damage alone. The same pattern was observed for the homoterpene DMNT. The monoterpene linalool was also emitted in a significant higher amount in plants treated with caterpillar regurgitate, but could already be measured after half an hour of induction. The leaf aldehyde hexenal showed the highest production, of all VOCs measured, but with only small differences between the two treatments. This profile matched that of the heterocyclic compound indole which was released after 1 h of induction independently from the induction type. This indicated that mechanical wounding alone was sufficient to induce the production of these volatile compounds and was not elevated by the application of caterpillar regurgitate. This is in contrast to the other volatiles where extra treatment with regurgitate "boosted" the production of those volatiles.

### 3.3.3 The induction of plant hormones is dependent on the type of induction

Plant hormones play an important role in the regulation of plant growth, development, and in the response to biotic stresses (Davies 2010). In order to investigate the effect of herbivory on the induction of the plant hormones ABA, JA, JA-Ile, and SA, the hormone concentrations were measured after mechanical damage and application of caterpillar regurgitate. Previous unpublished experiments by Tobias Köllner showed that JA, JA-Ile and ABA were induced around and above the wounding site when caterpillars were able to feed on maize plants (Tobias Köllner, paper in progress). SA, on the other hand, showed increased levels towards the base of the injured leaf and was repressed in the tip of the leaf.

In the following experiments, the Mecworm was used as a method to mimic herbivore damage. The wounded area was restricted to the base of the leaves and the whole leaf was collected for analysis. The hormone analysis of the leaf is shown in Fig.3.14.

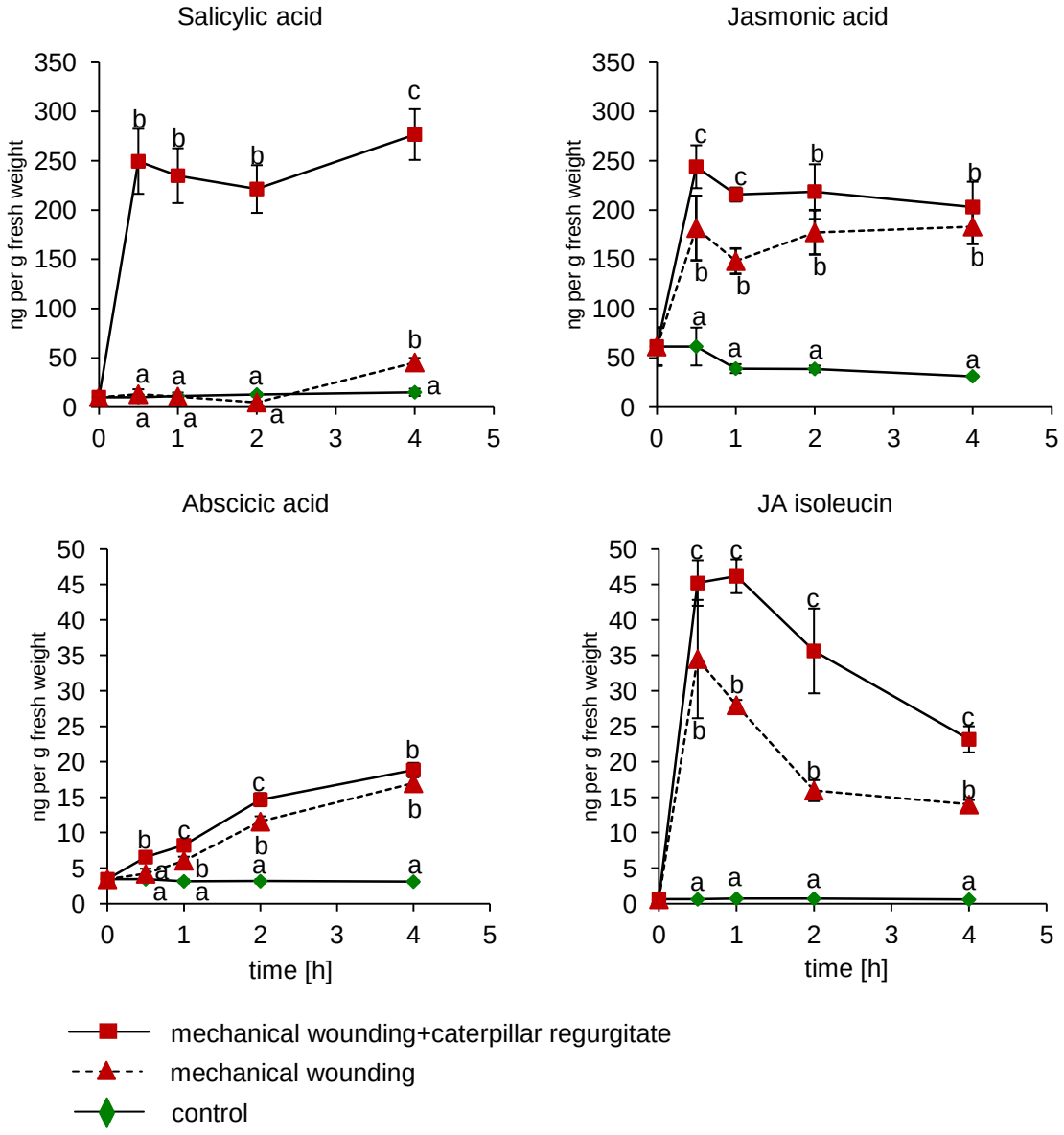



**Fig.3.14: Phytohormone concentration in damaged maize leaves.** The concentration of phytohormones were measured in ng per g fresh weight after mechanical damage, damage and caterpillar regurgitate and the controls. Leaf material was harvested at 0 h, 0.5 h, 1 h, 2 h, and 4 h after the treatment. Means and standard errors are shown (n=4). Two-way ANOVA was performed with time as the first variable and treatment as second factor. Different letters indicate significant differences between treatments within time points ($p<0.05$).

The levels of JA as well as JA-Ile increased significantly after the treatment. While the amount of JA rose to 250 ng per g fresh weight, only up to 50 ng per g fresh weight of the JA-Ile conjugate was found in leaves. Both plant hormones showed a similar pattern for the two treatments. The addition of regurgitate to the damage seemed to enhance the production of JA and JA-Ile. The increase of JA and JA-Ile after mechanical damage suggested that the damaged leaf was sufficient to induce the hormone levels.

Upon wounding, plants contained up to 20 ng per g fresh weight of ABA. The concentration of ABA is not further increased after application of regurgitate. In contrast to the hormones JA and JA-Ile, it is worth to notice that the concentration of ABA rose constitutively after wounding while the level of JA and JA-Ile already reached their maximum level after 0.5 h and then started to decline.

For JA, JA-Ile and ABA, the pattern of hormone induction was similar with the addition of regurgitate, yet the differences in the concentrations for each time point was mostly significant ($p<0.05$). In the case of SA, the hormone level after mechanical wounding was close to the hormone level of the control plants with only a slight increase at the 4 h time point. In contrast, the hormone concentration increased significantly to 300 ng per g fresh weight when the plants were wounded and regurgitate was applied. Like jasmonic acid, SA concentrations stayed elevated upon treatment with caterpillar regurgitate. SA is a signaling molecule commonly associated with pathogen attack and is often down-regulated upon herbivory in *Arabidopsis thaliana* (Lee et al. 2010). In maize, SA also seemed to play a role in the defense against herbivores and it is selectively induced by caterpillar regurgitate.

## 3.4 Promoter analysis of the terpene synthases *tps10* and *tps23*

### 3.4.1 Promoters of *tps10* and *tps23* are dissimilar among maize lines

The promoters of *tps10* and *tps23* of several maize lines were sequenced and analyzed for putative regulatory sequences. Promoter sequences were obtained by PCR or with the help of the Institute of Genomic Diversity from Cornell University. The maize lines selected for sequence analysis differed in (*E*)-ß-caryophyllene production. The lines Delprim, NC358, Du101, and F476 possess an active TPS23 enzyme and produced herbivore-induced (*E*)-ß-

caryophyllene. In the lines B73, CML247, OH7B, and MS71, on the other hand, transcript of *tps23* could not be detected (Degen *et al.* 2004; Köllner *et al.* 2008). Sequence analysis of ~800 bp revealed only minor nucleotide exchanges among the *tps23* promoter of all lines (Fig.3.15).

```
          -766                                                                -697
   Du101  CAAAGGTTGT AT-GCACAAA AGGCTGCTTC TTTGTGGTGT AGCAGCTTTG TTT-GGTCGA TTTGGCTTTG
   NC358  CAAAGGTTGT AT-GCACAAA AGGCTGCTTC TTTGTGGTGT AGCAGCTTTG TTT-GGTCGA TTTGGCTTTG
    F476  CAAAGGTTGT ATTGCACNAA AGGCTGCTTC TTTCTAGCGT TGCGGCTTTG TTTTGGTCGA TTTGGCTTTG
    OH7B  CAAAGGTTGT AT-GCACAAA NGGCTGCTTC TTTCTAGCGT TGCGGCTTTG TTTTGGTCGA TTTGGCTTTG
 Delprim  CAAAGGTTGT AT-GCACAAA AGGCTGCTTC TTTCTAGCGT TGCGGCTTTG TTTTGGTCGA TTTGGCTTTG
     B73  CAAAGGTTGT AT-GCACAAA AGGCTGCTTC TTTCTAGCGT TGCGGCTTTG TTTTGGTCGA TTTGGCTTTG
    MS71  CAAAGGTTGT AT-GCACAAA NGGCTGCTTC TTTCTAGCGT TGCGGCTTTG TTTTGGTCGA TTTGGCTTTG
  CML247  CAAAGGTTGT AT-GCACAAA AGGCTGCTTC TTTCTAGCGT TGCGGCTTTG TTTTGGTCGA TTTGGCTTTG

           -696                                                               -627
   Du101  CCGTAATGAT GTGGTCTTTA ATCATAACCA TATATCGTCA ATTATACAGG TGATCTTTAG AGATACATAT
   NC358  CCGTAATGAT GTGGTCTTTA ATCATAACCA TATATCGTCA ATTATACACG TGATCTTTAG AGATACATAT
    F476  TCGTAATGAT GTGGTGTTTA ATCATAACCA TATACCGTCA ACTATACATG TGATCTTTAG AGGTACATAT
    OH7B  TCGTAATGAT GTGGTGTTTA ATCATAACCA TATACCGTCA ACTATACATG TGATCTTTAG AGGTACATAT
 Delprim  TCGTAATGAT GTGGTGTTTA ATCATAACCA TATACCGTCA ACTATACATG TGATCTTTAG AGGTACATAT
     B73  TCGTAATGAT GTGGTGTTTA ATCATAACCA TATACCGTCA ACTATACATG TGATCTTTAG AGGTACATAT
    MS71  TCGTAATGAT GTGGTGTTTA ATCATAACCA TATACCGTCA ATTATACATG TGATCTTTAG AGGTACATAT
  CML247  TCGTAATGAT GTGGTGTTTA ATCATAACCA TATACCGTCA ACTATACATG TGATCTTTAG AGGTACATAT

           -626                                                               -557
   Du101  TGGTTCAGAT TTTGGGGACT CCTGCAGAAG GAAGAAACAT AGCAGCAAAT CCTAGTCGTG TATCATACTT
   NC358  TGGTTCAGAT TTTGGGGACT CCTGCAGAAG GAAGAAACAT AGCAGCAAAT CCTAGTCGTG TATCATACTT
    F476  TG-TTCACAT TTTAGAGACT CCTGCAGATG GAAGAAACAC AACAGCAAAT CTTAGTCGTG TATCAGACTT
    OH7B  TG-TTCACAT TTTAGAGACT CCTGCAGATG GAAGAAACAC AACAGCAAAT CTTAGTCGTG TATCAGACTT
 Delprim  TG-TTCACAT TTTAGAGACT CCTGCAGATG GAAGAAACAC AACAGCAAAT CTTAGTCGTG TATCAGACTT
     B73  TG-TTCACAT TTTAGAGACT CCTGCAGATG GAAGAAACAC AACAGCAAAT CTTAGTCGTG TATCAGACTT
    MS71  TG-TTCAGAT TTTAGAGACT CCTGCAGAAG GAAGAAACAC AACAGCAAAT CTTAGTCGTG TATCAGACTT
  CML247  TG-TTCACAT TTTAGAGACT CCTGCAGATG GAAGAAACAC AACAGCAAAT CTTAGTCGTG TATCAGACTT

           -556                                                               -487
   Du101  TGGAGGTGAT GGCCATGGAG TTCTTCGCGA GTCATGGGTG GCGGTCTAAT GCAAGGATCG ATGTGGTTTA
   NC358  TGGAGGTGAT GGCCATGGAG TTCTTCGCGA GTCACGGGTG GCGGTCTAAT GCAAGGATCG ATGTGGTTTA
    F476  TGGAGGTTAT GGCCATGGAG TTCTTCACGA GTCACGGGCG GCGGTCTAAT GCAAGGATCG ATGCCGTTTA
    OH7B  TGGAGGTTAT GGCCATGGAG TTCTTCACGA GTCACGGGTG GCGGTCTAAT GCAAGGATCG ATGCCGTTTA
 Delprim  TGGAGGTTAT GGCCATGGAG TTCTTCACGA GTCACGGGTG GCGGTCTAAT GCAAGGATCG ATGCCGTTTA
     B73  TGGAGGTTAT GGCCATGGAG TTCTTCACGA GTCACGGGTG GCGGTCTAAT GCAAGGATCG ATGCCGTTTA
    MS71  TGGAGGTTAT GGCCATGGAG TTCTTCACGA GTCACGGGTG GCGGTCTAAT GCAAGGATCG ATGACGTTTA
  CML247  TGGAGGTTAT GGCCATGGAG TTCTTCACGA GTCACGGGTG GCGGTCTAAT GCAAGGATCG ATGYCGTTTA

           -486                                                               -417
   Du101  GTGTTTATGG TCTTCTATTC CATATCATGT TTTAAGTTGA AGTTTGTTTG ATCCACAAAT TCTTGGGATG
   NC358  GTGTTTATGG TCTTCTATTC CATATCATGT TTTAAGTTGA AGTTTGTTTG ATCCACAAAT TTTTGGGATG
    F476  GTGTTTATGA TCTTTTATTC CATATCATGT TTTAAGTTGA AGTTTGTTTG ATCCATGAAT TCCTGGGATG
    OH7B  GTGTTTATGA TCTTTTATTC CATATCATGT TTTAAGTTGA AGTTTGTTTG ATCCATGAAT TCCTGGGATG
 Delprim  GTGTTTATGA TCTTTTATTC CATATCATGT TTTAAGTTGA AGTTTGTTTG ATCCATGAAT TCCTGGGATG
     B73  GTGTTTATGA TCTTTTATTC CATATCATGT TTTAAGTTGA AGTTTGTTTG ATCCATGAAT TCCTGGGATG
    MS71  GTGTTTATGA TCTTTTATTC CATATCATGT TTTAAGTTGA AGTTTGTTTG ATCCATAAAT TCCTGGGATG
  CML247  GTGTTTATGA TCTTTTATTC CATATCATGT TTTAAGTTGA AGTTTGTTTG ATCCATGAAT TCCTGGGATG

           -416                                                               -347
   Du101  ATGTAATATT TGAGGTGTAT GGTTGTATGC ATGAAAATGC AAAAGTTCGG AACGATATTT CGATTTCAAA
   NC358  ATGTAATATT TGAGGTGTAT GGTTGTATGC ATGAAAATGC AAAAGTTCGG AACGATATTT CTATTTCAAA
    F476  ATGTAACATT TGAGGTGTAT GGTTGTATGC ATGAAAATGC AAAAGTCCGG AACGATATTT CGATTTCAAA
    OH7B  ATGTAACATT TGAGGTGTAT GGTTGTATGC ATGAAAATGC AAAAGTCCGG AACGATATTT CGATTTCAAA
 Delprim  ATGTAACATT TGAGGTGTAT GGTTGTATGC ATGAAAATGC AAAAGTCCGG AACGATATTT CGATTTCAAA
     B73  ATGTAACATT TGAGGTGTAT GGTTGTATGC ATGAAAATGC AAAAGTCCGG AACGATATTT CGATTTCAAA
    MS71  ATGTGACATT TGAGGTGTAT GGTTGTATTC ATGAAAATGC AAAAGTCCGG AACGATATTT CGATTTCCAA
  CML247  ATGTAACATT TGAGGTGTAT GGTTGTATGC ATGAAAATGC AAAAGTCCGG AACGATATTT CGATTTCAAA
```

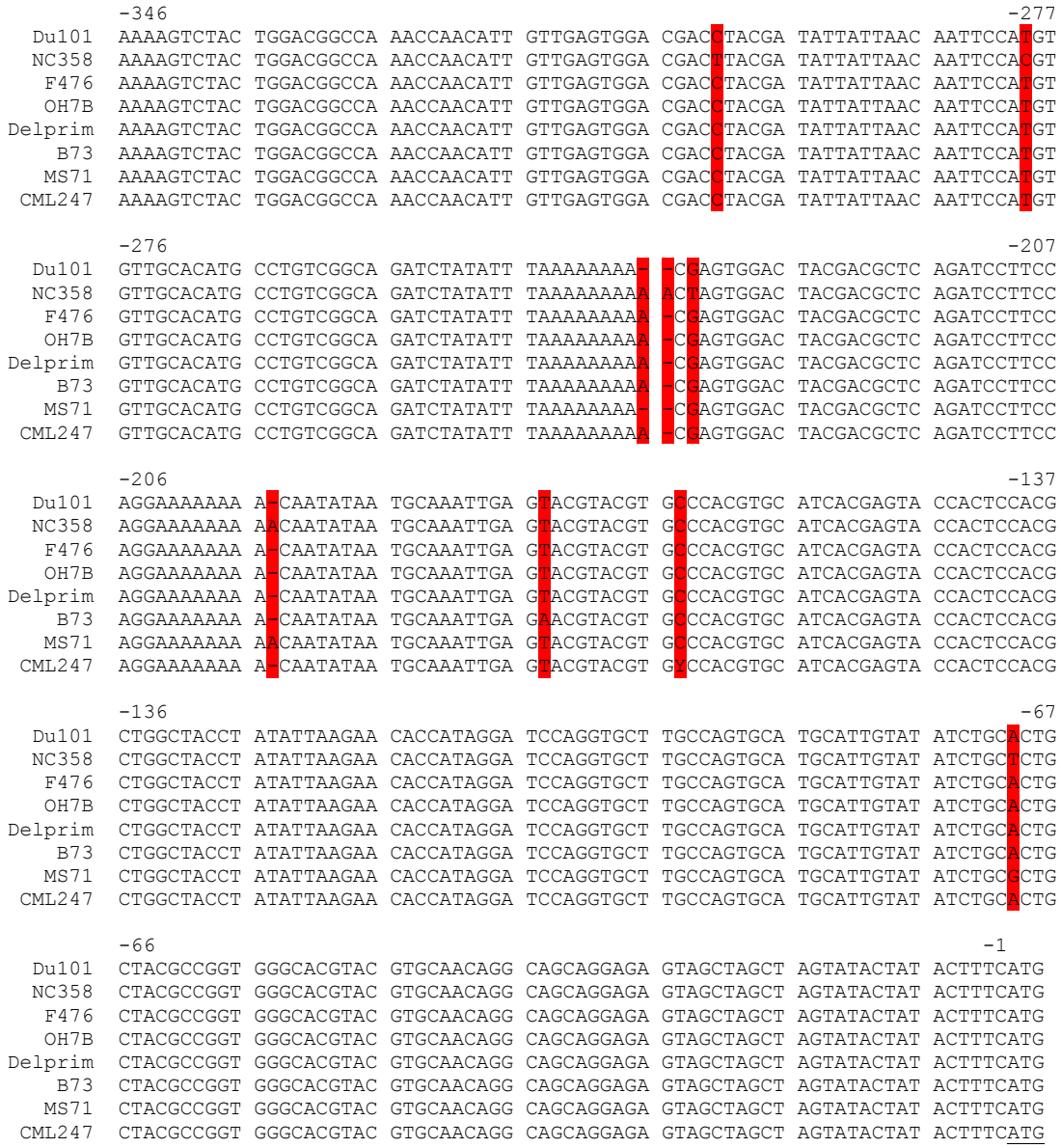
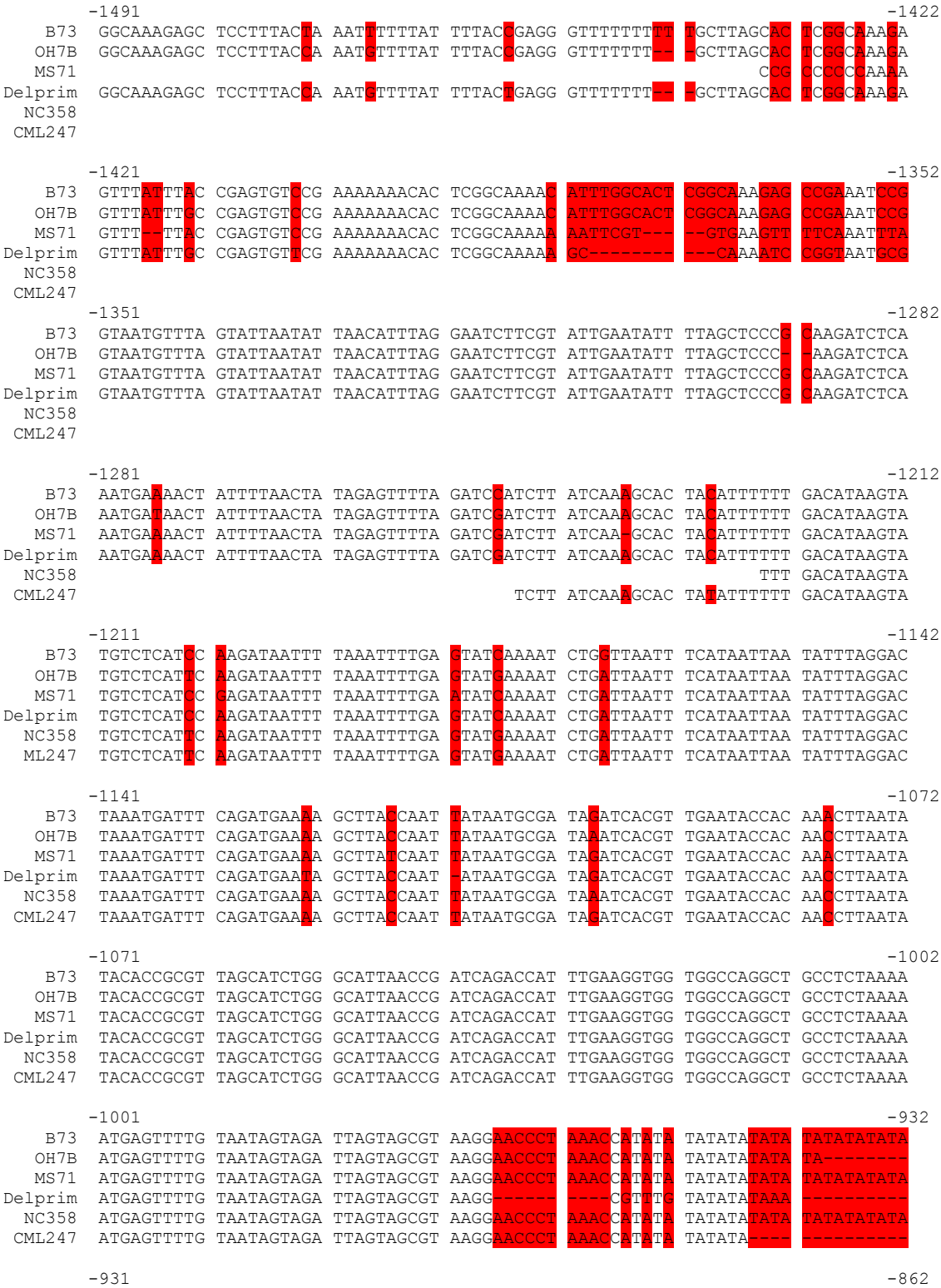


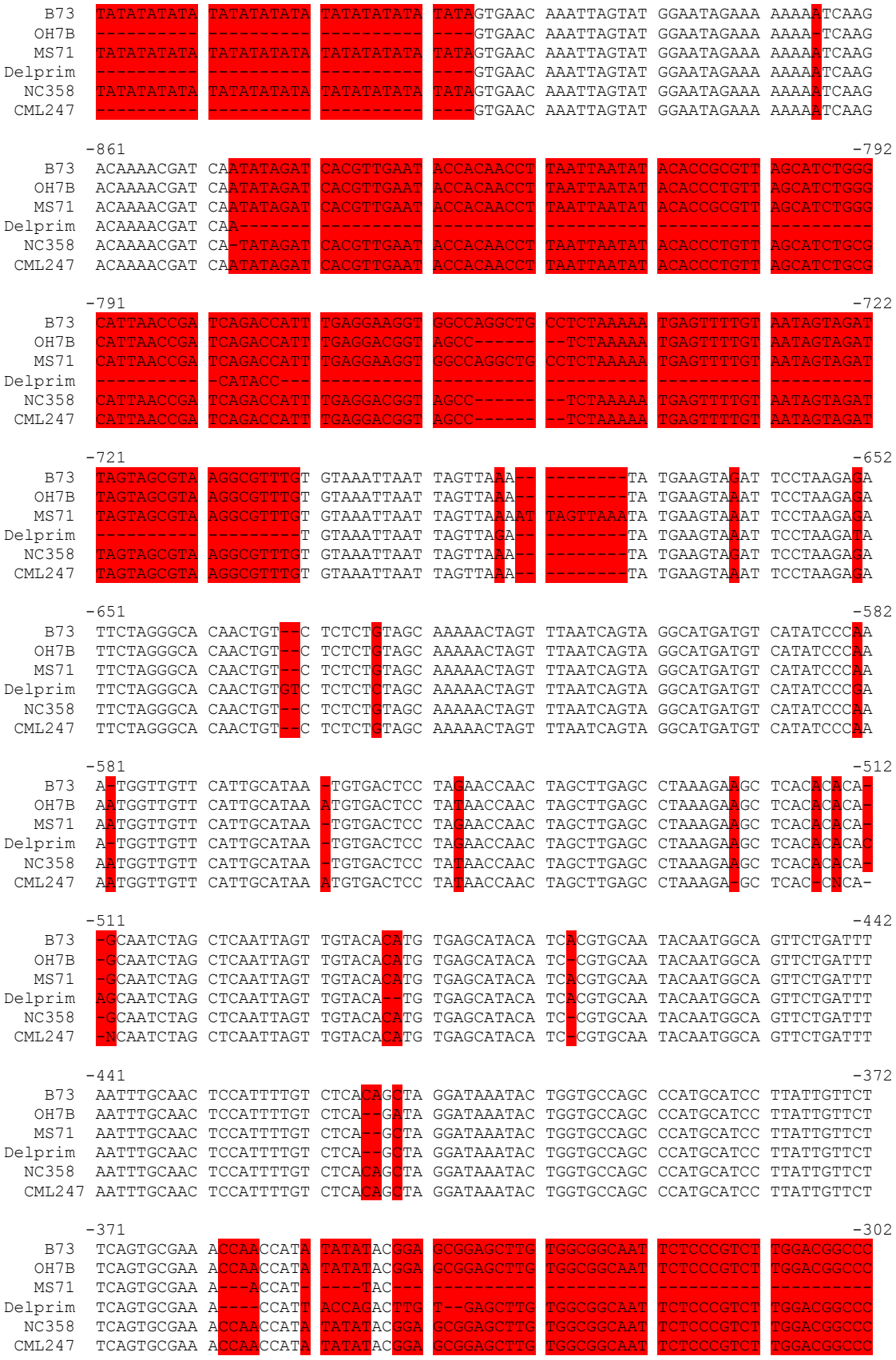

**Fig.3.15: Sequence comparison of the promoter of *tps23* from (*E*)-ß-caryophyllene producing and non-producing maize lines.** Start codon is underlined. Nucleotide differences are highlighted in red.

Nucleotide changes were present between the promoters of caryophyllene-producing and non-producing maize lines, as well as within both groups. Therefore, predictions regarding the ability to transcribe *tps23* cannot be made from the promoter nucleotide sequences.

Only the lines B73, OH7B, MS71, Delprim, NC358, and CML 247 could be used for the comparison of the *tps10* promoter. Sequences from NC358, CML247, and OH7B were obtained from the HAPMAP2 database from Cornell University because PCR on genomic

DNA was not successful (data provided by Jeff Glaubitz and Edward Buckler). Unfortunately, data from that database did not cover promoter fragments long enough for useful comparisons (Fig.3.16).




B73 TATATATATA TATATATATA TATATATATA TATAGTGAAC AAATTAGTAT GGAATAGAAA AAAAATCAAG
OH7B ---------- ---------- ---------- ----GTGAAC AAATTAGTAT GGAATAGAAA AAAA-TCAAG
MS71 TATATATATA TATATATATA TATATATATA TATAGTGAAC AAATTAGTAT GGAATAGAAA AAAAATCAAG
Delprim ---------- ---------- ---------- ----GTGAAC AAATTAGTAT GGAATAGAAA AAAAATCAAG
NC358 TATATATATA TATATATATA TATATATATA TATAGTGAAC AAATTAGTAT GGAATAGAAA AAAAATCAAG
CML247 ---------- ---------- ---------- ----GTGAAC AAATTAGTAT GGAATAGAAA AAAAATCAAG
-861 -792
B73 ACAAAACGAT CAATATAGAT CACGTTGAAT ACCACAACCT TAATTAATAT ACACCGCGTT AGCATCTGGG
OH7B ACAAAACGAT CAATATAGAT CACGTTGAAT ACCACAACCT TAATTAATAT ACACCCTGTT AGCATCTGGG
MS71 ACAAAACGAT CAATATAGAT CACGTTGAAT ACCACAACCT TAATTAATAT ACACCGCGTT AGCATCTGGG
Delprim ACAAAACGAT CAA------- ---------- ---------- ---------- ---------- ----------
NC358 ACAAAACGAT CA-TATAGAT CACGTTGAAT ACCACAACCT TAATTAATAT ACACCCTGTT AGCATCTGCG
CML247 ACAAAACGAT CAATATAGAT CACGTTGAAT ACCACAACCT TAATTAATAT ACACCCTGTT AGCATCTGCG
-791 -722
B73 CATTAACCGA TCAGACCATT TGAGGAAGGT GGCCAGGCTG CCTCTAAAAA TGAGTTTTGT AATAGTAGAT
OH7B CATTAACCGA TCAGACCATT TGAGGACGGT AGCC------ --TCTAAAAA TGAGTTTTGT AATAGTAGAT
MS71 CATTAACCGA TCAGACCATT TGAGGAAGGT GGCCAGGCTG CCTCTAAAAA TGAGTTTTGT AATAGTAGAT
Delprim ---------- -CATACC--- ---------- ---------- ---------- ---------- ----------
NC358 CATTAACCGA TCAGACCATT TGAGGACGGT AGCC------ --TCTAAAAA TGAGTTTTGT AATAGTAGAT
CML247 CATTAACCGA TCAGACCATT TGAGGACGGT AGCC------ --TCTAAAAA TGAGTTTTGT AATAGTAGAT
-721 -652
B73 TAGTAGCGTA AGGCGTTTGT GTAAATTAAT TAGTTAAA-- --------TA TGAAGTAGAT TCCTAAGAGA
OH7B TAGTAGCGTA AGGCGTTTGT GTAAATTAAT TAGTTAAA-- --------TA TGAAGTAAAT TCCTAAGAGA
MS71 TAGTAGCGTA AGGCGTTTGT GTAAATTAAT TAGTTAAAAT TAGTTAAATA TGAAGTAAAT TCCTAAGAGA
Delprim ---------- ---------T GTAAATTAAT TAGTTAGA-- --------TA TGAAGTAAAT TCCTAAGATA
NC358 TAGTAGCGTA AGGCGTTTGT GTAAATTAAT TAGTTAAA-- --------TA TGAAGTAGAT TCCTAAGAGA
CML247 TAGTAGCGTA AGGCGTTTGT GTAAATTAAT TAGTTAAA-- --------TA TGAAGTAAAT TCCTAAGAGA
-651 -582
B73 TTCTAGGGCA CAACTGT--C TCTCTGTAGC AAAAACTAGT TTAATCAGTA GGCATGATGT CATATCCCAA
OH7B TTCTAGGGCA CAACTGT--C TCTCTGTAGC AAAAACTAGT TTAATCAGTA GGCATGATGT CATATCCCAA
MS71 TTCTAGGGCA CAACTGT--C TCTCTGTAGC AAAAACTAGT TTAATCAGTA GGCATGATGT CATATCCCAA
Delprim TTCTAGGGCA CAACTGTGTC TCTCTCTAGC AAAAACTAGT TTAATCAGTA GGCATGATGT CATATCCCGA
NC358 TTCTAGGGCA CAACTGT--C TCTCTGTAGC AAAAACTAGT TTAATCAGTA GGCATGATGT CATATCCCAA
CML247 TTCTAGGGCA CAACTGT--C TCTCTGTAGC AAAAACTAGT TTAATCAGTA GGCATGATGT CATATCCCAA
-581 -512
B73 A-TGGTTGTT CATTGCATAA -TGTGACTCC TAGAACCAAC TAGCTTGAGC CTAAAGAAGC TCACACACA-
OH7B AATGGTTGTT CATTGCATAA ATGTGACTCC TAAAACCAAC TAGCTTGAGC CTAAAGAAGC TCACACACA-
MS71 AATGGTTGTT CATTGCATAA -TGTGACTCC TAGAACCAAC TAGCTTGAGC CTAAAGAAGC TCACACACA-
Delprim A-TGGTTGTT CATTGCATAA -TGTGACTCC TAGAACCAAC TAGCTTGAGC CTAAAGAAGC TCACACACAC
NC358 AATGGTTGTT CATTGCATAA -TGTGACTCC TAAAACCAAC TAGCTTGAGC CTAAAGAAGC TCACACACA-
CML247 AATGGTTGTT CATTGCATAA ATGTGACTCC TAAAACCAAC TAGCTTGAGC CTAAAGA-GC TCAC-CNCA-
-511 -442
B73 -GCAATCTAG CTCAATTAGT TGTACACATG TGAGCATACA TCACGTGCAA TACAATGGCA GTTCTGATTT
OH7B -GCAATCTAG CTCAATTAGT TGTACACATG TGAGCATACA TC-CGTGCAA TACAATGGCA GTTCTGATTT
MS71 -GCAATCTAG CTCAATTAGT TGTACACATG TGAGCATACA TCACGTGCAA TACAATGGCA GTTCTGATTT
Delprim AGCAATCTAG CTCAATTAGT TGTACA--TG TGAGCATACA TCACGTGCAA TACAATGGCA GTTCTGATTT
NC358 -GCAATCTAG CTCAATTAGT TGTACACATG TGAGCATACA TC-CGTGCAA TACAATGGCA GTTCTGATTT
CML247 -NCAATCTAG CTCAATTAGT TGTACACATG TGAGCATACA TC-CGTGCAA TACAATGGCA GTTCTGATTT
-441 -372
B73 AATTTGCAAC TCCATTTTGT CTCACAGCTA GGATAAATAC TGGTGCCAGC CCATGCATCC TTATTGTTCT
OH7B AATTTGCAAC TCCATTTTGT CTCA--GATA GGATAAATAC TGGTGCCAGC CCATGCATCC TTATTGTTCT
MS71 AATTTGCAAC TCCATTTTGT CTCA--GCTA GGATAAATAC TGGTGCCAGC CCATGCATCC TTATTGTTCT
Delprim AATTTGCAAC TCCATTTTGT CTCA--GCTA GGATAAATAC TGGTGCCAGC CCATGCATCC TTATTGTTCT
NC358 AATTTGCAAC TCCATTTTGT CTCACAGCTA GGATAAATAC TGGTGCCAGC CCATGCATCC TTATTGTTCT
CML247 AATTTGCAAC TCCATTTTGT CTCACAGCTA GGATAAATAC TGGTGCCAGC CCATGCATCC TTATTGTTCT
-371 -302
B73 TCAGTGCGAA ACCAACCATA TATATACGGA GCGGAGCTTG TGGCGGCAAT TCTCCCGTCT TGGACGGCCC
OH7B TCAGTGCGAA ACCAACCATA TATATACGGA GCGGAGCTTG TGGCGGCAAT TCTCCCGTCT TGGACGGCCC
MS71 TCAGTGCGAA A---ACCAT- ----TAC--- ---------- ---------- ---------- ----------
Delprim TCAGTGCGAA A----CCATT ACCAGACTTG T--GAGCTTG TGGCGGCAAT TCTCCCGTCT TGGACGGCCC
NC358 TCAGTGCGAA ACCAACCATA TATATACGGA GCGGAGCTTG TGGCGGCAAT TCTCCCGTCT TGGACGGCCC
CML247 TCAGTGCGAA ACCAACCATA TATATACGGA GCGGAGCTTG TGGCGGCAAT TCTCCCGTCT TGGACGGCCC

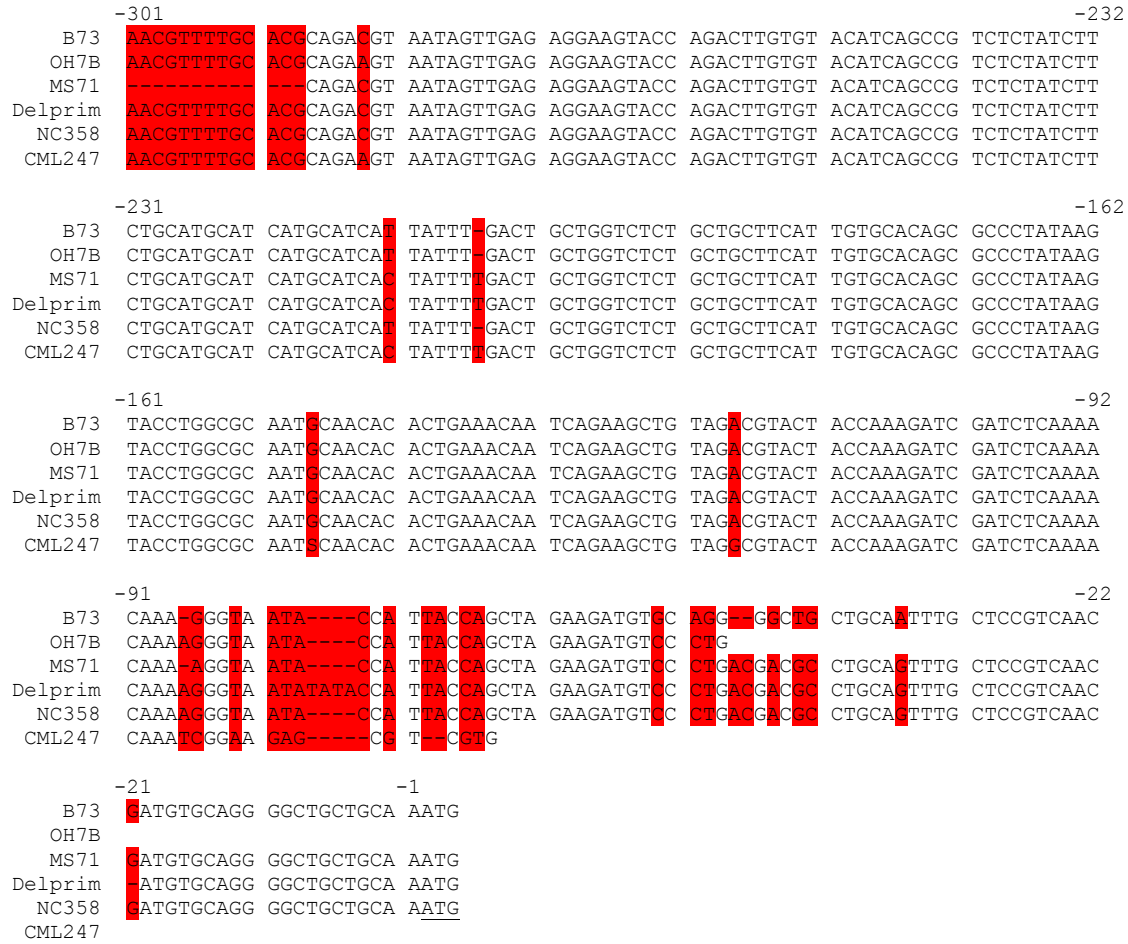



**Fig.3.16: Sequence comparison of the promoter fragment of *tps10* in different maize lines.** Start codon is underlined. Differences in the sequences are marked in red.

Interestingly, far more nucleotide changes could be observed in the *tps10* promoter than in the promoter of *tps23.* While line MS71 and CML247 are not able to produce TPS10-specific sesquiterpenes, all other lines have an active TPS10 enzyme. Looking at the raw promoter sequence, an essential difference between TPS10-producing and non-producing cannot be predicted. In a next step, both promoter fragments from line Delprim were analyzed for regulatory sequences. Database analysis was conducted using either PLACE (plant *cis*-acting regulatory DNA elements) or PlantCARE (*cis*-acting regulatory element). 530 potential boxes were revealed in the promoter of *tps23* and 379 in the promoter of *tps10.* An overview of all identified regulatory elements is attached in the appendix (7.8, 7.9). Several core promoter elements were identified in both promoters as well as stress- and defense-related

*cis*-acting elements. Truncation experiments were conducted to isolate essential regulatory elements involved in the herbivore-induced responses (3.4.3).

### 3.4.2 Analysis of the promoters of *tps10* and tps23 for binding activity to TF1, TF8, TF20 and TF22

To investigate whether the transcription factors TF1, TF8, TF20, and TF22 bind to the promoters of *tps10* and *tps23*, 1 kb sequence upstream of the start codon of both genes from the maize line Delprim was cut into ~200 bp fragments and used as targets for band shift assays. This technique serves to identify *cis*-acting promoter elements involved in the regulation of *tps10* or *tps23* after herbivore attack. Herbivore-regulated transcription factors with a transcript accumulation between 1 and 2 hours (Tab.3.1) were selected for analysis. The full length sequences for TF1, TF8, TF20, and TF22 were obtained by PCR or RACE and can be found in the appendix (7.5). The sequences were cloned into a pHIS vector containing the codons for 8 histidine residues at the N-terminal end of the inserted sequence. The constructs were transformed into the *E. coli* strain BL21 which allowed the IPTG-induced overexpression of the transcription factor genes. The expressed and partially purified transcription factors were analyzed using SDS-PAGE and Western Blot with His-tag specific antibodies.

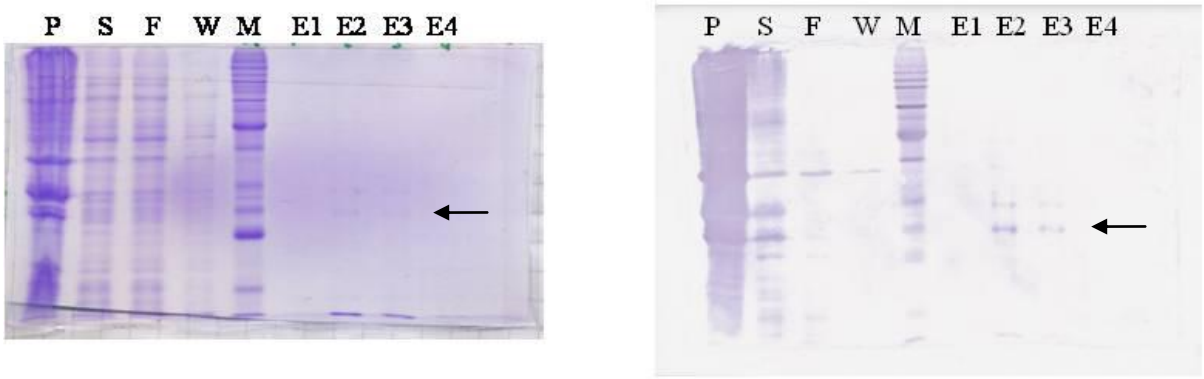



**Fig.3.17: SDS-Page and Western blot of transcription factor TF1.** Protein was overexpressed in BL21 cells and purified using a Ni-NTA-column. 4 elution fractions were collected for analysis. The left picture displays the SDS-gel, the right picture shows the western blot. M = Bench Mark from Invitrogen, P = pellet, S = supernatant, F = flow through, W = washing step, E1-E4 = elution fraction 1-4.

In Fig.3.17, the Western blot and SDS-PAGE of transcription factor TF1 are shown. A distinct band in elution fraction 3 and 4 with the approximate size of the protein (28 kDa with 239 aa) was observed. TF22 consisted of 162 amino acids and was calculated to a protein size of 17.4 kDa including the HIS-tag. TF20 has a molecular weight of 28.7 kDa with HIS-tag (266 aa), and TF8 runs at 13.9 kDa including the HIS-tag and 129 aa (data not shown). After expression and purification of the protein, 250 ng of the purified transcription factors were added to isotope-labeled promoter fragments. Binding results were evaluated on a non-denaturating polyacrylamide gel and visualized with a phosphor imager. Theoretically, DNA fragments bound to a specific protein would travel at a lower speed through the acrylamide gel while unbound DNA would move faster through the matrix. The transcription factor TF1 was analyzed for the binding ability to the promoter fragments of *tps23* (Fig.3.18). The promoter fragments were designed with overlapping ends to each other, so that the chance of cutting an important region site of recognition would be limited.

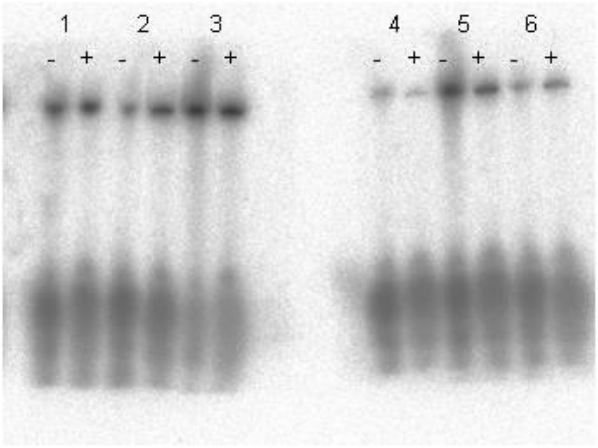



**Fig.3.18: Band shift assay of transcription factor TF1 with the promoter fragments of *tps23*.** Binding reaction was analyzed on a nondenaturating acrylamide gel and a phosphor imager. For each promoter fragment, a positive and a negative (no labeled fragment was added) probe was run. Fragments represent the complete *tps23* promoter from nucleotide 1:-762- (-607), 2: -675- (-491), 3: -528- (-374), 4: -410- (-250), 5: -277- (-115), 6: -137- (+13).

The unbound promoter fragments appeared at the bottom of the gel as a smeared band. A shifted band could be observed in each lane. Because this particular band appeared in each

lane, it was probably not a specific shift of bound promoter-protein complex. It is possible that the band consisted of probe artefacts of the rather long oligonucleotides.

The results for the promoter fragments of *tps10* with the transcription factor TF1 showed a similar picture (Fig.3.19). Each promoter of both alleles of *tps10* was cut into several fragments. Promoter A was divided into 8 fragments while only 2 fragments represent promoter B due to the high similarity between the two alleles. The unbound, labeled fragments could be seen at the base of the gel, while the previously observed unspecific band ran at the top of the gel. All tested transcription factors showed similar results (data not shown), so that a specific binding between the transcription factors and promoters could not be shown.

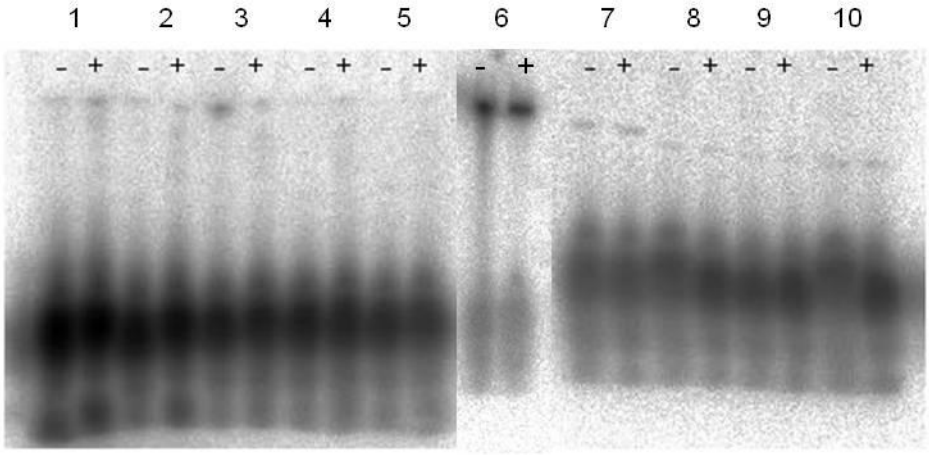



**Fig.3.19: Band shift assay of promoter fragments of *tps10* with the transcription factor TF1.** Labeled fragments were added to 250 ng of purified protein. Binding reaction was analyzed on a $^{32}P$ sensitive screen and a phosphor imager. For each fragment, a positive (with protein) and a negative (without protein) sample was run. Overlapping fragments run from nucleotide 1: -976- (-822), 2:-869- (-692), 3: -713- (-592), 4: -589- (-417), 5: -362- (-127), 6:-424- (-264), 7: -289- (-127), 8: -142- (+22) of promoter A and 9: -817- (-643), 10: -360- (-127) of promoter B.

### 3.4.3 Analysis of *tps10* and *tps23* promoter constructs in Arabidopsis

To gather information as to how the promoters of *tps10* and *tps23* are regulated and to narrow down important regulatory elements, promoter deletion analysis was performed. In this set of experiments, Arabidopsis was chosen as a heterologous system because it is an

easy transformable plant with a shorter reproduction time compared to maize. Several plasmid constructs were produced containing different promoter fragments fused to the reporter gene ß-glucuronidase (GUS). This reporter gene enabled us to observe whether the promoter fragments are active after different types of treatment in the Arabidopsis-system. The resulting plasmids were cloned using the Gateway cloning system into the destination vector pBGWFS7.0. These constructs were then transferred into *Arabidopsis thaliana* using *A. tumefaciens* as a vector system. Transformed plants were cultivated to the T2 generation. For induction experiments, the leaves of the plants were induced by scratching with a razor blade with or without addition of jasmonic acid to the wounded area. This type of induction was used to mimic mechanical damage as well as local herbivore damage. Promoter activity was tested using GUS-staining and GUS-assay. As a negative control, wild-type plants (var. Columbia) were used and induced analogous to the transformed plants.

The longest promoter fragment of both terpene synthases *tps10* and *tps23* was inactive in undamaged plants, but displayed activity when plants were treated with mechanical damage and jasmonic acid. This indicated that the herbivore-induced signal transduction pathway between the evolutionary distinct plants maize and Arabidopsis are somewhat conserved. Consequently, we investigated the promoters of *tps10* and *tps23* using promoter::reporter gene constructs in the Arabidopsis-system.

In the first set of experiments, the transformed plants were treated with mechanical damage alone. Deletion analysis revealed an active, damage-regulated *tps23* promoter in the longer promoter fragments 1.8 kb, 1.2 kb and 600 bp (Fig.3.20). Here, GUS-staining was distributed throughout the whole leaf. Unwounded leaves of damaged plants (systemic leaves) and control leaves showed a weak staining in the midvein of the leaf. The promoter constructs *tps23* 400 bp::GUS and *tps23* 200 bp::GUS showed no visible promoter activity in the undamaged and control leaves. Systemic leaves and the controls displayed a slight GUS-staining along the midvein only with the 1.8 kb, 1.2 kb, and 600 bp promoter constructs. This could be a response to the wounding that resulted from the cutting of the leaf. Plant material incubated with GUS-staining solution was not frozen in liquid nitrogen and therefore was still able to respond to environmental cues while it was stained.

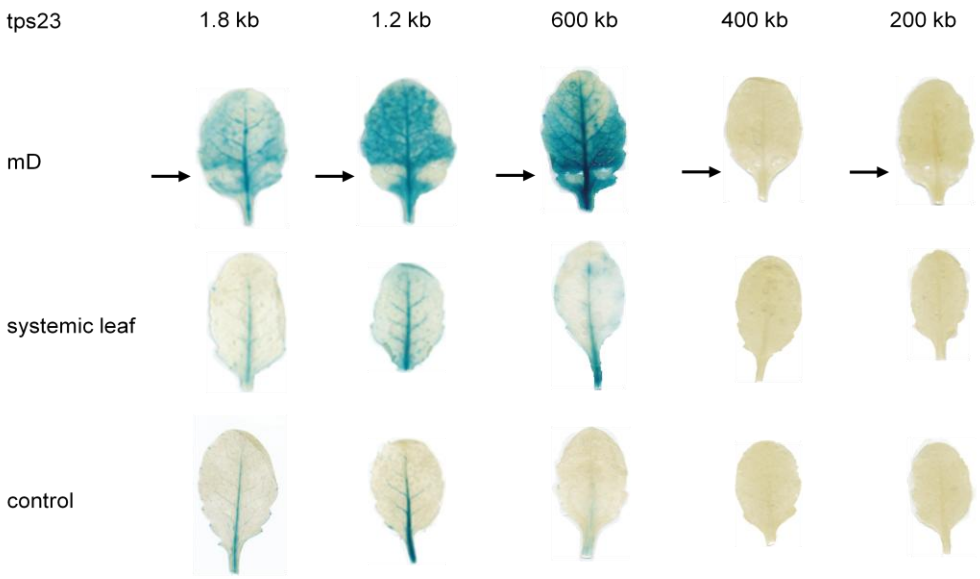



**Fig.3.20: Gus-staining of *tps23* promoter constructs after mechanical damage.** Arabidopsis plants containing a *tps23* promoter fragment fused to the ß-glucuronidase were induced by scratching the leaf with a razor blade (mD). A leaf of an induced plant was taken as reference (systemic) as well as a transformed plant without treatment as control. Arrows indicate the wounding site.

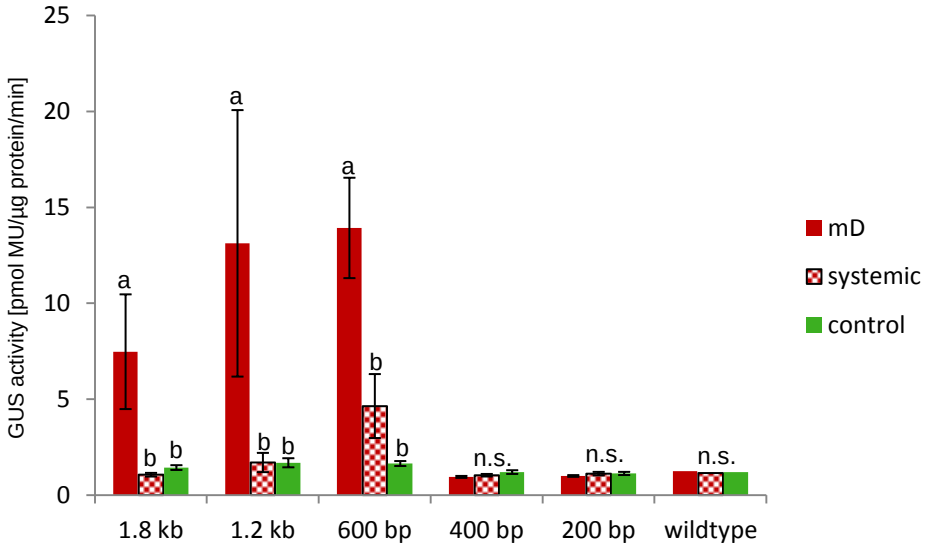



**Fig.3.21: Promoter activity of the *tps23* constructs 1.8 kb, 1.2 kb, 600 bp, 400 bp, 200 bp, and Columbia wild-type, respectively, after mechanical treatment.** Arabidopsis plants (n=4) were treated with mechanical damage (mD) by scratching the leaves with a razor blade. Undamaged leaves were taken as well as not treated plants as control. Means and standard error are shown. Statistical analysis was performed using t-test for the treatment mD and control and a paired t-test for mD and undamaged treatment. Undamaged and control were tested using a t-test. Different letters indicate significant activity ($p<0.05$) between the treatments.

There was a significant difference in the activity of the promoter constructs after mechanical damage (Fig.3.21). The three longest promoter fragments, 1.8 kb, 1.2 kb, and 600 bp, were able to induce the reporter gene ß-glucuronidase, while the shorter fragments of the *tps23* promoter and control plants didn't show reporter gene activity. In systemic leaves and control plants, the promoters were not active.

After testing the effect of mechanical damage, the role of jasmonic acid on the promoter activity was investigated. Plants were damaged according to the previous experiment but jasmonic acid was added. The *tps23* promoter was active in the constructs with 1.8 kb, 1.2 kb and 600 bp in the wounded leaves of transformed Arabidopsis plants (Fig.3.22). The shorter constructs with only 400 bp or 200 bp of the *tps23* promoter displayed no GUS staining and were therefore considered to be too short to induce expression. In treated plants, the longer fragments showed promoter activity along the veins of the leaves as well as in the surrounding cells. The activity decreased towards the top of the leaf. Interestingly, the promoter was active not only around and above the wounding site but below as well. Here, the promoter activity of *tps23* might correspond to the distribution of the jasmonic acid in the leaf. Jasmonic acid is transported via the phloem (Li *et al.* 2002) and could therefore act as an activator on the *tps23* promoter.

The promoter activity of *tps23* was confirmed with the GUS-assay. A significant difference in activity was found between treated and control plants in the constructs *tps23* 1.8 kb::GUS, 1.2 kb::GUS, and 600 bp::GUS (Fig.3.23). Systemic leaves of plants treated with damage and JA showed no significant induction of promoter activity, similar to those treated with mechanical damage only.

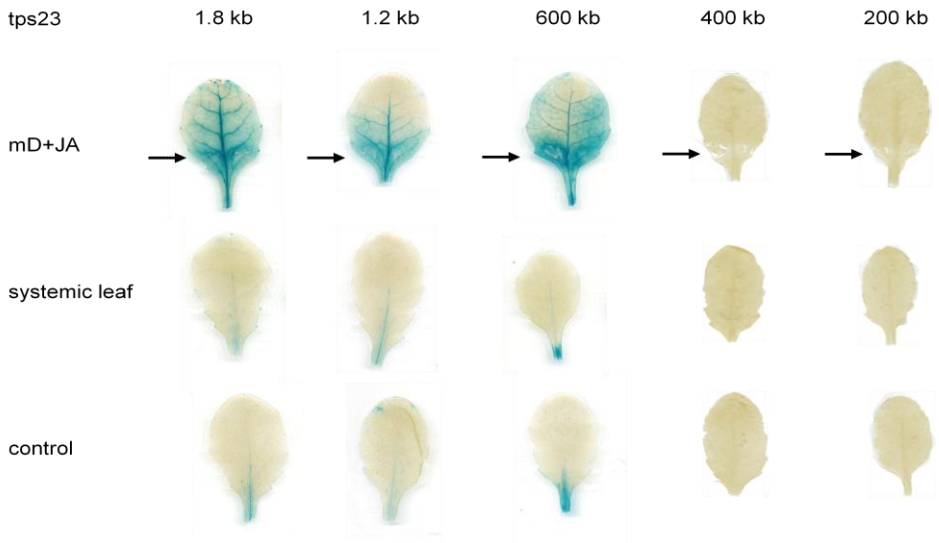



**Fig.3.22: Gus-staining of *tps23* promoter constructs after mechanical damage and application of jasmonic acid.** Arabidopsis plants containing a *tps23* promoter fragment fused to the ß-glucuronidase were induced by scratching the leaf with a razor blade and adding 250 µM jasmonic acid (mD+JA). A leaf of an induced plant was taken as reference (systemic) as well as a transformed plant without treatment as control. Arrows indicate the wounding site.

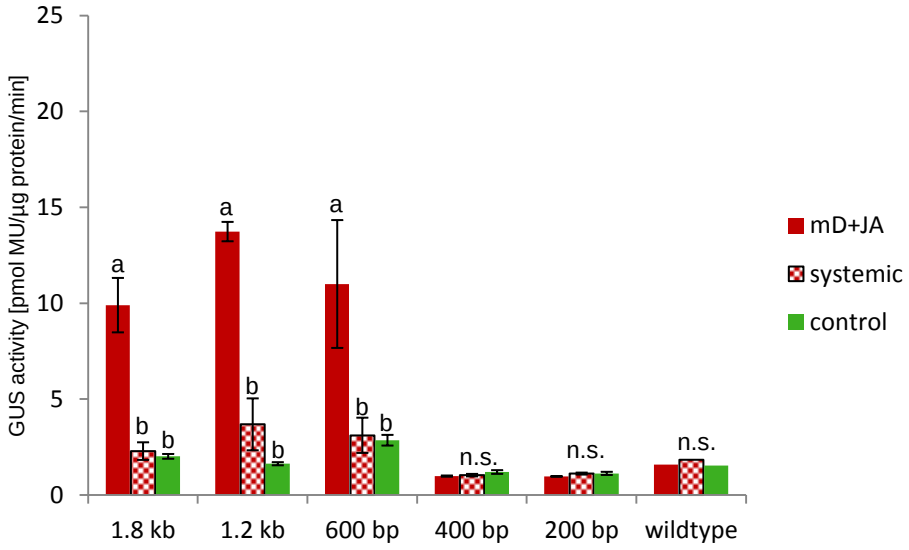



**Fig.3.23: Quantitative GUS-activity in leaves of Arabidopsis transformed with *tps23* promoter constructs and Columbia wild-type.** Arabidopsis plants were induced by mechanical damage plus the application of jasmonic acid (mD+JA). Undamaged leaves were taken from damaged plants to reflect systemical damage. Standard error and means are shown (n=4). Statistical analysis was performed using t-test for the treatment mD+JA and control and a paired t-test for mD+JA and undamaged treatment. Undamaged and control were tested using a t-test. Different letters indicate significant activity ($p<0.05$) between the treatments.

To analyze the effect of JA to the promoter activity, plants were induced without mechanical damage. Because the induction methods of plants without harming the leaves were not successful, plants were watered with a jasmonic acid-containing solution. After 3 days of watering with a JA-solution, the leaves were harvested and treated as described above. Here, the promoter activity (Fig.3.24) was limited to the veins of the leaf, corresponding to the transport of jasmonic acid. Unlike the damaged leaves, treatment with jasmonic acid induced the 1.8 kb and 1.2 kb promoter fragments. The 600 bp promoter constructs displayed some minor staining along the mid vein while the 400 bp and 200 bp promoter fragments were completely inactive.

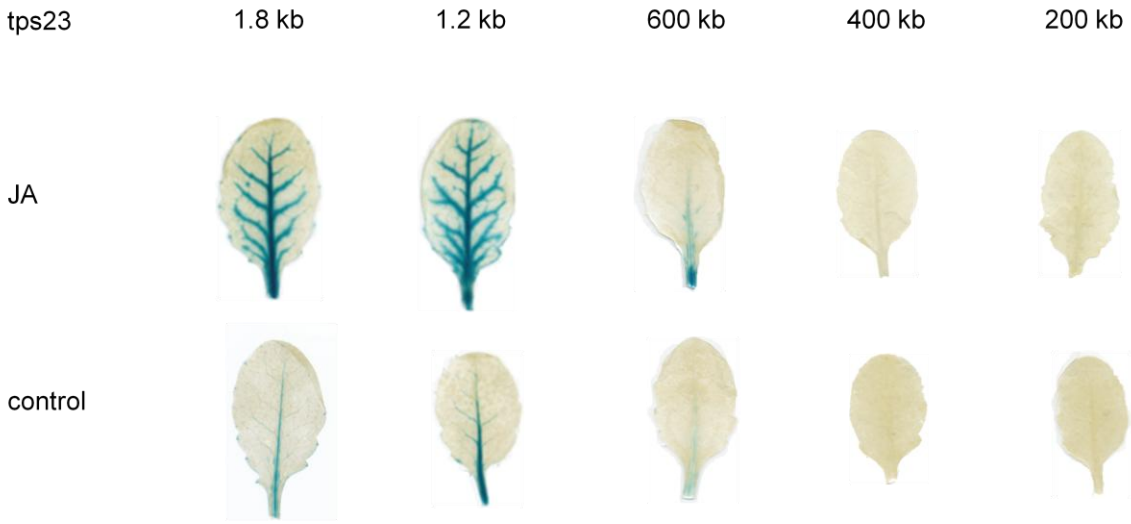



**Fig.3.24: GUS-staining of transformed Arabidopsis leaves treated with jasmonic acid over 3 days (JA).** Transformed Arabidopsis plants containing the *tps23* promoter constructs were induced by watering with a jasmonic acid containing solution over 3 days.

Additionally, the activity of the *tps23* promoter was tested using a quantitative GUS-assay (Fig.3.25). The behavior of the promoter activity was similar in both analysis methods.

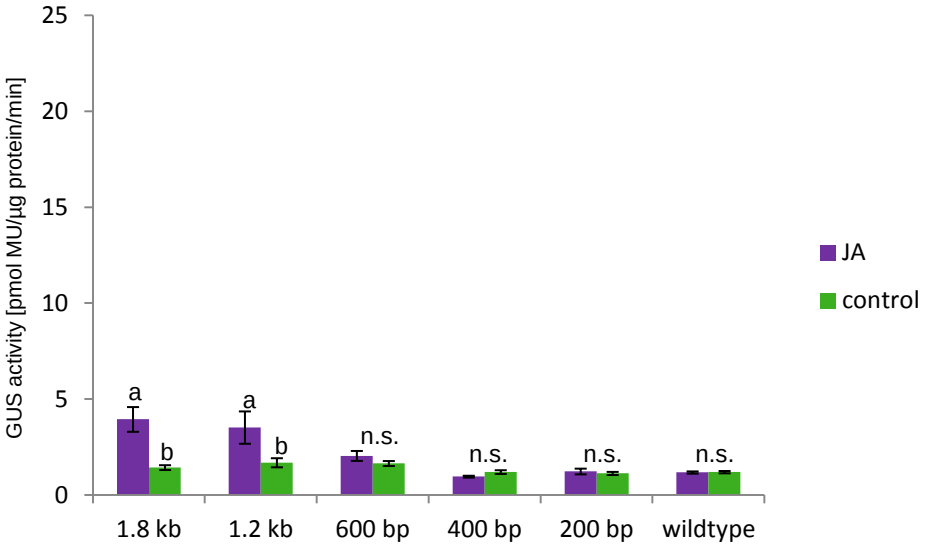



**Fig.3.25: Quantitative GUS-assay in Arabidopsis plants transformed with different *tps23* promoter::GUS constructs after induction with jasmonic acid.** Plants (n=4) were watered with jasmonic acid for 3 days. Means and standard errors are shown. To calculate the statistical relevance, One-Way ANOVA was performed for the different treatment within the constructs. Undamaged leaves were left out in this analysis because material is not independently from the mechanical damage treatment. Different letters indicate significant activity ($p<0.05$) between the treatments.

In a next step, the promoter constructs of *tps10*::GUS were tested. Analog to the experiments with *tps23*, promoter fragment lengths of 1.5 kb, 800 bp, 500 bp and 200 bp were fused to the ß-glucuronidase gene and treated with mechanical damage with or without addition of jasmonic acid. In the first round of experiments, transformed Arabidopsis plants were mechanical damaged with a razor blade. The longest *tps10* promoter fragment of 1.5 kb::GUS showed minor GUS staining around the wounded area (Fig.3.26). Promoter activity was not found in systemic leaves and only slightly present at the cutting site in control plants. The more reliable, quantitative GUS assay revealed no promoter activity in the 1.5 kb construct, indicating that the longest promoter construct cannot be induced after mechanical damage (Fig.3.27). Therefore, smaller fragments were not included in this experiment.

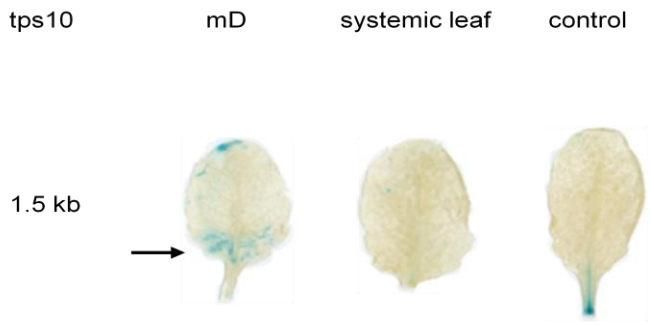



**Fig.3.26: GUS-staining of Arabidopsis plants transformed with the construct *tps10* 1.5 kb::GUS.** Plants were induced by scratching the leaf with a razor blade (mD). Systemic leaves of induced plants and uninduced plants were taken as controls. Arrows indicate the wounding site.

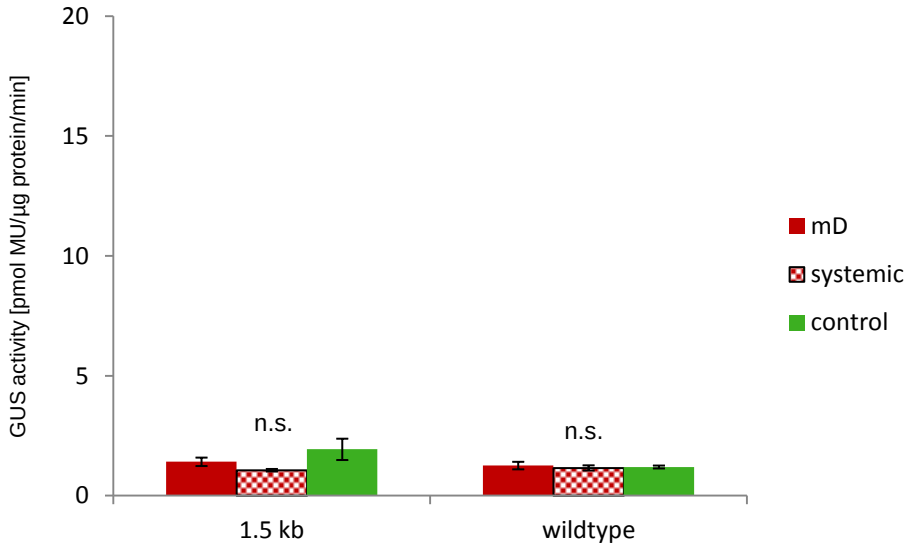



**Fig.3.27: Promoter activity *tps10* 1.5kb::GUS after mechanical damage.** Wounding of the leaves resulted from scratching the leaves with a razor blade (mD). Systemical induced leaves from the mechanical wounded plants and untreated plants were taken as controls (control). Means (n=4) and standard errors are shown. One-Way ANOVA was performed for statistical analysis.

Different results were obtained when transformed Arabidopsis plants were treated with mechanical damage and jasmonic acid. In these experiments, all *tps10* promoter constructs were included. However, the 1.5 kb promoter construct was the only one exhibiting a promoter activity above and around the wounding site in the cells next to the harmed area (Fig.3.28). GUS staining was slightly distributed along the veins, without spreading to the top of the leaf. The 800 bp and 500 bp fragments showed no promoter activity, while the 200 bp fragment of the *tps10* promoter displayed a very weak promoter activity next to the wounding site. The systemic leaves as well as the control plants showed no promoter activity.

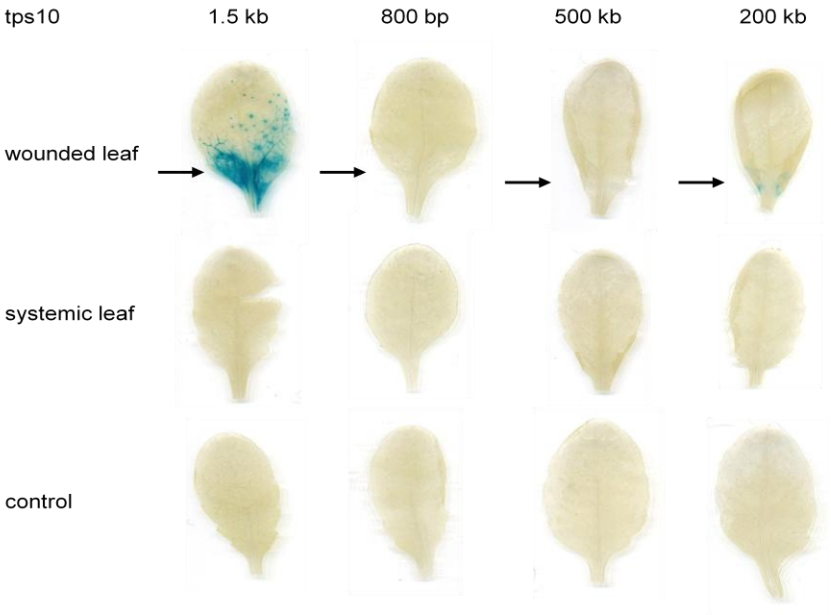



**Fig.3.28: Gus-staining of *tps10* promoter constructs after mechanical damage and application of jasmonic acid.** Arabidopsis plants containing a *tps23* promoter fragment fused to the ß-glucuronidase were induced by scratching the leaf with a razor blade and adding 250 µM jasmonic acid (mD+JA). A leaf of an induced plant was taken as reference (systemic) as well as a transformed plant without treatment as control. Arrows indicate the wounding site.

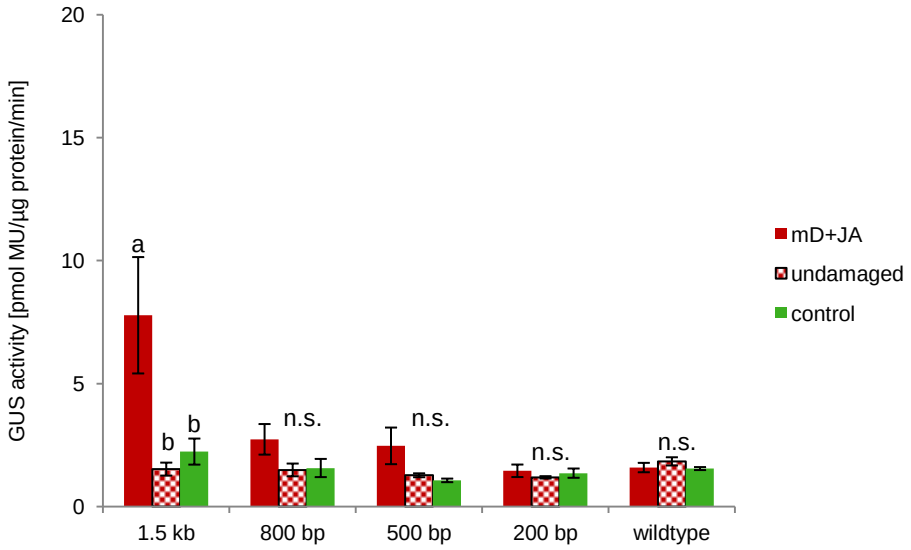



**Fig.3.29: Quantitative analysis of GUS-activity in the different *tps10*::GUS constructs.** Arabidopsis plants were induced with mechanical damage by scratching the leaf and adding jasmonic acid. Systemic leaves were taken from induced plants. The control plants were left unharmed. Means (n=4) and standard errors are shown with the statistical differences indicated by different letters between the treatments for each construct ($p<0.05$). Analysis was performed using a regular t-test for the damaged plants versus the control plants. The significance between damaged and undamaged leaves was calculated using a paired t-test.

Analog to the GUS-staining, the quantitative analysis (Fig.3.29) showed a significant promoter activity with the induced *tps10* 1.5 kb::GUS construct after treating the plants with mechanical damage plus application of JA. Shorter promoter fragments were not active. Systemic leaves and control plants didn't show a significant promoter activity between the treatments.

Arabidopsis plants transformed with the construct *tps10* 1.5 kb::GUS were induced with jasmonic acid by watering over 3 days analog to the former experiment. Similar to the results of the GUS-staining method (data not shown), this promoter construct showed no significant induction of reporter gene activity after the treatment with jasmonic acid (Fig.3.30). These results indicate that the *tps10* promoter cannot be induced by mechanical damage or jasmonic acid alone, but needs the combination of both stimuli.

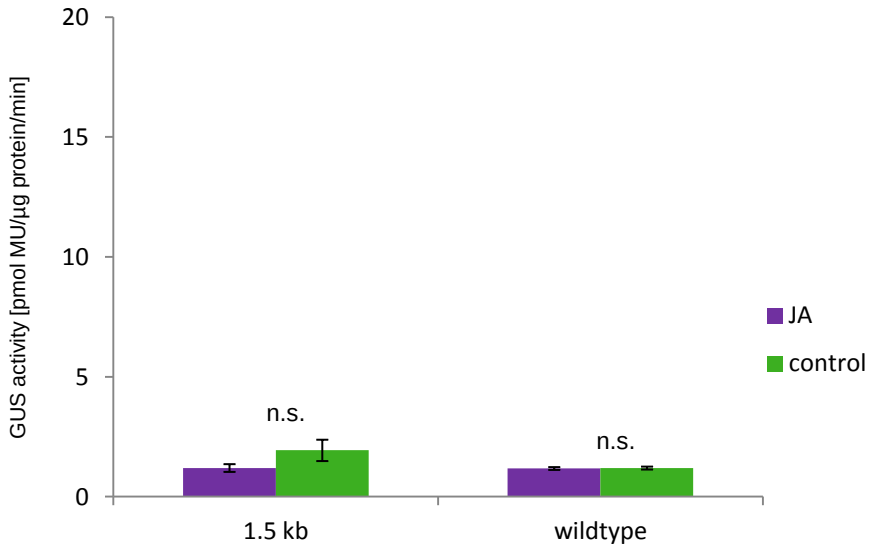



**Fig.3.30: GUS-analysis of *tps10* 1.5 kb::GUS and wild-type plants after jasmonic acid treatment.** Plants were watered with jasmonic acid over 3 days. Control plants were left untreated. Means and standard error are shown (n=4). One-Way ANOVA was performed for statistical analysis.

## 3.5. Identification of transcription factors induced by local, systemical and mechanical wounding in roots and leaves

In order to respond to an herbivore threat, plants react to herbivore damage in their non-damaged parts (Erb *et al.* 2009). Therefore, we wanted to investigate the cross talk between plant organs after herbivory and mechanical damage. Using the Long Oligo Microarray, the interaction between roots and shoots were analyzed. In particular, the influence of *D. virgifera* infested roots upon uninfested leaves (systemic induction) and the influence of *S. littoralis* infested leaves upon uninfested roots was tested. To investigate whether the transcriptional changes caused by *D. virgifera* attack are a general wound response or a specific reaction of the plant, roots were also damaged mechanically. Plant material was harvested 18 h after the treatment. Infested or mechanically damaged roots and herbivore-induced leaves as well as the systemically induced material were provided by Matthias Erb and analyzed with the Long Oligo Microarray for differences in gene expression. Since the main focus of this work were herbivore-regulated transcription factors, only the differentially expressed transcription factors will be presented here. The analysis comprised all proteins annotated as transcription factors although some might not be functional. The total number of differentially regulated transcription factors is displayed in Fig.3.31.

After treatment with the *D. virgifera* larvae, 29 putative transcription factors showed a higher expression in roots while only 3 genes were suppressed. Systemic induction by *S. littoralis* larvae resulted in an induced expression of 10 transcription factors while 9 showed a decreased expression. After roots were treated with mechanical damage, 20 transcription factors were up-regulated while 4 transcription factors were down-regulated. Overall, the roots of *Zea mays* react to local herbivory by altering the expression of more transcription factors than upon systemic induced leaves. Leaves on the other hand, showed far less differentially expressed transcription factors. Eight putative transcription factors were repressed in the leaves when roots were infested with *D. virgifera* while only one factor was induced. Even after wounding by *S. littoralis* larvae for 18 h, only 6 transcription factors in the damaged leaf showed a transcript accumulation while one gene was negatively regulated. After mechanical damage in roots, only 2 induced and 1 suppressed transcription factors were found in leaves.

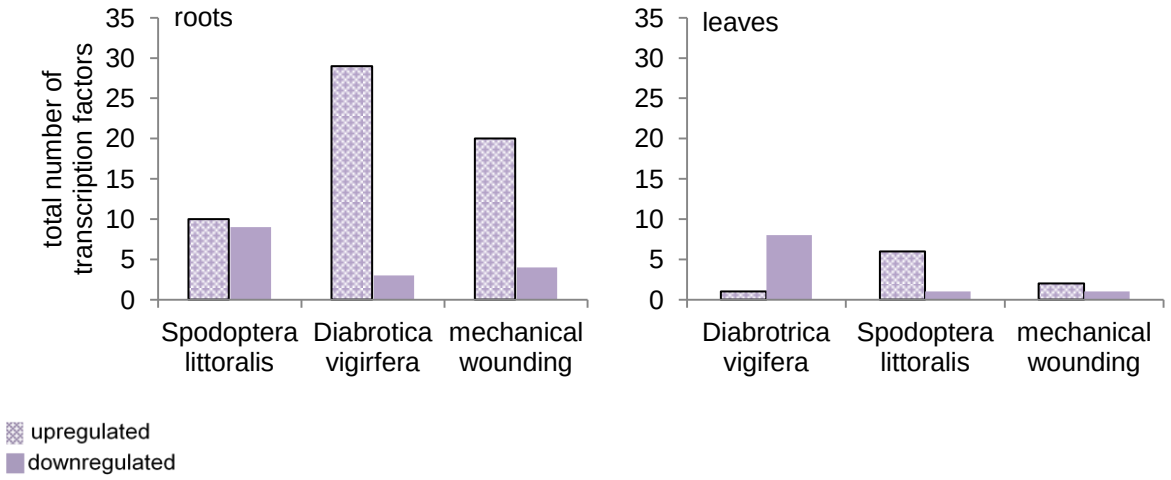



**Fig.3.31: Overview of transcriptional changes of transcription factors in herbivore-infested plants.** *S. littoralis* feeding upon the leaves resembles the systemical wounding to the roots, while *D. virgifera* feeding upon the roots displays the local wounding on the roots and vice versa. Mechanical wounding was performed by stabbing the roots several times with a scalpel.

A closer analysis of differentially regulated transcription factors in roots revealed some similarities between the treatments (Fig.3.32). A total number of 32 transcription factors showed changes in gene expression. Nine of them were also affected after mechanical damage to the roots while 2 transcription factors showed different transcript levels after *S. littoralis* attack. Only 2 transcription factors displayed a difference in gene expression after all three treatments. Eleven and 13 transcription factors were regulated in response to mechanical wounding or feeding of *S. littoralis*, respectively. Their corresponding MZ-numbers are listed in Tab.3.2. Annotation of these accession numbers can be found in the appendix (7.7).

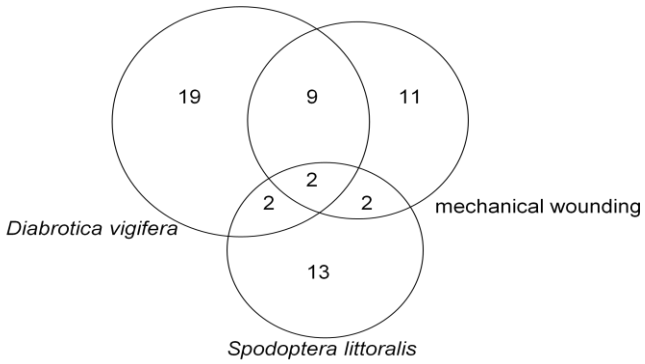



**Fig.3.32: Venn-diagram of transcription factors with herbivore-regulated expression in root material after local damage by *D. virgifera*, damage in the leaves by *S. littoralis* larvae, and mechanical damage.** Numbers in the circles represent the numbers of equal MZ-numbers between the treatments. Diagram was constructed using http://bioinforx.com.

**Tab.3.2: List of shared MZ-numbers from the roots after different treatments.**

| ***S. littoralis*-*D. virgifera*** | ***S. littoralis*-*D. virgifera* -mechanical damage** | ***S. littoralis*-mechanical damage** | ***D. virgifera*-mechanical damage** |
|---|---|---|---|
| MZ00004381 | MZ00004381 | MZ00004381 | MZ00004381 |
| MZ00017495 | | | MZ00020499 |
| MZ00026127 | MZ00026127 | MZ00026127 | MZ00026127 |
| MZ00036067 | | MZ00028351 | MZ00026538 |
| | | MZ00054846 | MZ00026661 |
| | | | MZ00028044 |
| | | | MZ00035959 |
| | | | MZ00036019 |
| | | | MZ00041768 |
| | | | MZ00042353 |
| | | | MZ00046918 |

Two transcription factors, MZ00004381 and MZ00026127 were expressed after local, systemical and mechanical wounding. MZ0004381 is a putative bZIP transcription factor and MZ00026127 is only annotated as development regulation gene. Interestingly, there were no overlapping transcription factors within the leaf material, while there were several shared transcription factors between root and leaf material. The graphical outline can be viewed in

Fig.3.33 and annotation is presented in Tab.3.3. After local damage in leaves and local damage in roots, five transcription factors showed the same transcriptional changes. Local herbivory in shoots and systemic herbivory in roots had only one transcription factor in common. Also one transcription factor with the same transcriptional change was found in leaves and roots after mechanical root-damage.

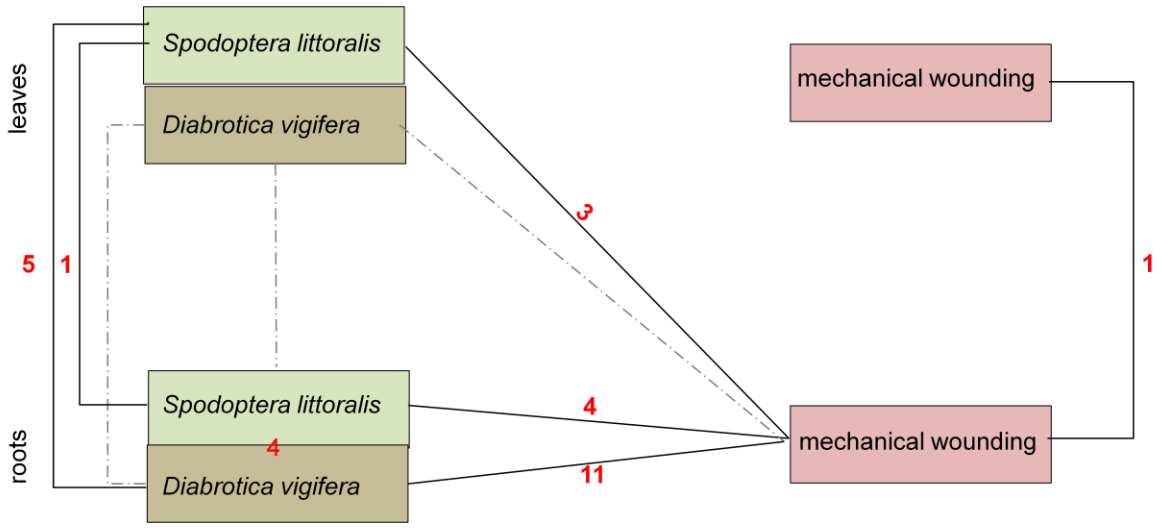



**Fig.3.33: Similarities in gene expression patterns of transcription factors between leaves and roots after different types of induction.** Leaves were investigated after attack of *S. littoralis*, infestation of roots by *D. virgifera* or mechanical damage. Root material was harvested after local damage by *D. virgifera*, mechanical damage and after *S. littoralis* herbivory upon the leaves (systemical damage). Bold lines indicate equal MZ-number between two treatments with the total number in red. Dashed lines indicate no similarity.

**Tab.3.3: List of shared transcription factors between leaves and roots after different induction treatment.**

| ***S. littoralis*: leaf-root** | ***S. littoralis*: leaf-*D. virgifera*: root** | **leaf- mechanical damage: root** | ***S. littoralis*: leaf-mechanical wounding:root** |
|---|---|---|---|
| | MZ00012674 | MZ00028419 | |
| MZ00017495 | MZ00017495 | | |
| | MZ00026538 | | MZ00026538 |
| | MZ00036019 | | MZ00036019 |
| | MZ00041768 | | MZ00041768 |

While MZ00017495 was induced in both roots and leaves after different induction stimuli, the ZIM-motif family protein MZ00026538 was also found in roots and leaves after mechanical damage in roots, as well as in earlier time course experiments. The putative zinc finger protein MZ00041768 was highly induced after local wounding and mechanical damage of the roots and was also found after 2 h after herbivore induction by *S. littoralis* in the leaves. The data f this microarray experiment were only evaluated using the program R. Validation of these results by QRT-PCR is necessary to verify the complex regulatory patterns of these transcription factors.

An overview of all other differentially regulated genes of this experiments can be found in Erb *et al.* (Erb *et al.* 2009).

# 4. Discussion

## 4.1 Microarray analysis as a tool to find genes in the plant responses against herbivore damage

Plants and insects have been coexisting for over 350 million years and therefore evolved a diversity of complex interactions (Gatehouse 2002). When plants recognize herbivore-associated molecular patterns (HAMPs; (Mithöfer and Boland 2008)), several reactions take place in plant cells, including changes in the ion flux, protein phosphorylation, formation of ROS and oxylipins, and initiation of various defense reactions (Kessler and Baldwin 2002; Maffei *et al.* 2007). The defense reactions include the generation of the phytohormones JA, SA, and ET (Pieterse and van Loon 1999; Glazebrook 2001; Dicke and Van Poecke 2002), as well as the synthesis of secondary compounds (Baldwin and Callahan 1993; De Moraes *et al.* 1998), among them volatile terpenes (Turlings *et al.* 1990; Kessler and Baldwin 2001).

Microarray hybridization has been used to study the transcriptome in several plant species. The transcript profiles responding to insect feeding, mechanical wounding, JA, $H_2O_2$, and herbivore-induced volatiles were investigated using microarray technology in lima beans, *Arabidopsis thaliana*, and *Nicotiana attenuata*, (Arimura *et al.* 2000; Reymond *et al.* 2000; Halitschke *et al.* 2003; Reymond *et al.* 2004). In Rice, more than half of the genes identified in insect-induced indirect defense belonged to the category "involved in secondary metabolism". The genes included terpene synthases, P450 enzymes, methyltransferases, and BAHD acyltransferases (Yuan *et al.* 2008). Transcription factors were the second largest group of genes influenced by herbivory. Temporal changes in expression patterns were only conducted in tobacco and Arabidopsis (Durrant *et al.* 2000; Reymond *et al.* 2000).

One aim of this work was the identification of early transcriptional changes in maize after herbivore induction. With a large fraction of the transcriptome of the maize line B73, the microarray chip from the University of Arizona enabled us to investigate gene expression after herbivory. The results of the microarray experiment were verified by QRT-PCR which confirmed the microarray data in most cases. Limitations to this method are present because only genes showing a differential regulation after herbivore attack could be identified. Constitutively expressed proteins were not detectable. The genome-wide mapping of a maize

population would be the method of choice to detect genes that do not undergo changes in gene expression. Although, the microarray was generated from sequences of the maize line B73, Delprim was chosen as target maize line because of its ability to produce high levels of volatiles including (*E*)-ß-caryophyllene. Still, only slight limitation should result from this due to the high genetic similarity between Delprim and B73. B73 is a homozygous inbred line while Delprim is a heterozygous hybrid line. Considering an allelic polymorphism of about 3 % between maize lines in general, there is a high probability that at least one of the alleles from Delprim can hybridize with the allele of B73. The herbivore-induced genes of Delprim belonged to many classes including transcription factors, kinases and phosphates, metabolic enzymes, developments genes, and several more. Several genes, including FPP synthases, terpene synthases, and methyl transferases, have also been found in other plant species after herbivory (Yuan *et al.* 2008). Thus, this method was appropriate to identify temporal changes in herbivore-induced maize.

## 4.2 The regulation of herbivore-induced transcription factors

### 4.2.1 Herbivore feeding influences the expression of transcription factors

Transcription factors act as switches of regulatory cascades (Scott 2000) and a combination of *cis*-acting elements are needed for the appropriate responses to stimuli (El-Shehawi *et al.* 2011). In Arabidopsis, up-regulation of transcriptions factors was demonstrated to cause a general shift in transcriptional regulation in response to insect damage (Reymond *et al.* 2004). In maize, we found a total number of 90 differentially regulated transcription factors in the leaves of herbivore-induced maize within 0.5 h and 4 h after damage. Out of that number, 12 genes had multiple hits. The majority of herbivore-regulated transcription factors were found at 0.5 h and 1 h while the number of differentially regulated metabolic enzymes started to increase after 1 h.

After an 18 h treatment with *S. littoralis*, only 7 transcription factors were identified in the leaves. The discrepancies in these observations are due to the sustained time of damage by the herbivore. Some of the early induced transcription factors were already down-regulated after 18 h. A distinct picture was observed in roots of maize. Many transcription factors

displayed a differential regulation pattern independently of the induction type (*D. virgifera* herbivory, mechanical damage, and systemic induction). A difference in the total number of transcription factors could be observed between *D. virgifera* feeding and mechanical damage in roots, indicating that some transcription factors function in an herbivore-specific pathway. Transcription factors induced by herbivory and mechanical damage might mediate a general wound-response of the roots. Roots of maize react strongly in response to above-ground herbivory. Still, the function and relevance of this type of response remains to be resolved. The results from these data implicate that there are similarities as well as differences in the signal transduction pathways between a systemic and a local damage reaction to herbivore attack (Erb *et al.* 2009).

The transcription factors identified in this study belong to several classes that are linked to plant stress responses. These include AP2/EREBP transcription factors, WRKY transcription factors, MYB transcription factors, and bZIP factors (Stracke *et al.* 2001; Singh *et al.* 2002). AP2/EREBPs, for example, were found in insect-induced defense in poplar (Ralph *et al.* 2006). In *Catharanthus roseus,* members of the AP2/EREBP family responded to jasmonic acid (Menke *et al.* 1999). A homolog of the maize transcription factor, *tf1*, was first identified in Arabidopsis (ATAF1/2). It shares a 74 % homology (amino acid level) to the ARAF1/2 in Arabidopsis and 94 % homology to rice. Both proteins were found to be expressed after herbivore attack (Delessert *et al.* 2005; Yuan *et al.* 2008). A similar expression pattern for *tf1* and its homologs was found in herbivore-challenged species like Arabidopsis (Reymond *et al.* 2004) and poplar (Ralph *et al.* 2006). Binding to a drought-responsive element, the DRE transcription factors were first related to the response to cold stress and salt stress (Zhao *et al.* 2006). Newer studies placed the DRE transcription factors into the group of AP2/EREB proteins, connecting them to the ethylene-dependent signaling pathway (Sun *et al.* 2008). One DRE transcription factor found in this study is *tf40* which showed a strong early induction after continuous herbivore feeding. A 53 % homolog from *Aloe vera* was found to be induced 12 h after cold stress (Wang and He 2007). It is therefore unlikely that the Aloe DREB1 and maize *tf40* have similar functions.

Also, maize CAF1-like protein *tf2*, is involved in defense responses in Arabidopsis and rice (Walley *et al.* 2007; Yuan *et al.* 2008). The AtCAF1a/b factor responds to wounding and biotic stresses within 5 min after induction stimuli and is under a circadian control (Walley *et*

*al.* 2007; Walley *et al.* 2010). The homology to *tf2* is 51 % based on amino acid level. The family of CCR4 associated factors (CAF) are factors involved in the post transcriptional regulation of genes. In yeast, they are part of the major cytoplasmic deadenylase, initiating mRNA turnover by removing the poly(A)-tail (Tucker *et al.* 2001). Recent studies indicate that CAF1 proteins might degrade repressors of the pathogen-related genes PR1 and PR2, assuming that this factor plays a role in the plant defense response (Liang *et al.* 2009). In this work, *tf2* showed an early induction in response to herbivore feeding and mechanical damage, suggesting a general role in maize defense responses.

MYB-transcription factors are involved in several developmental steps of the plant. It has been demonstrated that the transcription factor ODORANT1, a R2R3 MYB-transcription factor, controls the synthesis of volatile benzenoids present in the floral scent of petunia (Verdonk *et al.* 2005). We also identified two MYB-(like) factors in maize, *tf12* and *tf28*. While *tf12* was suppressed after herbivore feeding, *tf28* showed an induced expression. A 48 % amino acid identity was found between *tf12* and the R2R3 MYB-transcription factors that play a role in abiotic stress responses in *Triticum aestivum* (Zhang *et al.* 2011). But the low amino acid identity to bread wheat raises the question about the specific function of *tf12* in maize. Only 17 % sequence similarity of the maize *tf28* and TaMYB13 of *Triticum aestivum* was predicted by NCBI. TaMYB13 functions as an activator of fructosyltransferase genes (Xue *et al.* 2011), but due to the low similarity a functional consensus can not be assumed.

An I-box binding factor has first been described in tomato and was associated to the class of MYB-like proteins (Rose *et al.* 1999). The transcription factor *tf35* from maize was annotated as putative I-box binding factor and can therefore be grouped to the class of MYB transcription factors. *Tf35* was highly induced by herbivory and its homolog in bread wheat is implicated in abiotic stress responses (Zhang *et al.* 2011). Due to the low amino acid sequence similarity of 24 %, a prediction about the specific role of *tf35* in maize cannot be made.

One zinc-finger transcription factor of maize, *tf29,* showed a negative regulation of gene expression after herbivore attack. This factor shares a 95% amino acid sequence identity to OsLDS1 from *Oryza sativa*. Here, it has been described as a negative regulator of programmed cell death in plants (Wang *et al.* 2005). Programmed cell death is often associated with a hypersensitive response of plants to pathogen attack (Greenberg *et al.*

1994). The down-regulation of *tf29* after herbivory could be a precautious step to increase resistance towards a subsequent pathogen attack.

The class of bHLH proteins is represented by *tf8* in maize. This transcription factor is strongly induced after herbivore attack, but no homolog of *tf8* has been described in other plant species yet.

An example of WRKY transcription factors induced by herbivory is the maize transcription factor *tf34.* WRKY transcription factors are unique to the plant kingdom (Eulgem *et al.* 1999) and have been identified to bind to W-boxes (Chen *et al.* 2002) which are found in the promoters of many plant defense genes (Kalde *et al.* 2003). A homolog of maize *tf34,* OsWRKY71 (90 % amino acid identity), encodes a transcriptional repressor of the gibberellin signaling pathway in rice (Zhang *et al.* 2004).

Further factors include an ETTIN-like auxin response factor (maize *tf20*) and putative phi-1-proteins (maize *tf42*) which respond both with an induced expression after herbivore attack. Characterization of *tf20* or putative homologs has not been conducted so far. As a homolog to the transcription factor *tf42,* phi-1 has only be implemented in the process of phosphorylation (Sano *et al.* 1999).

Although the maize transcription factors found in this study are regulated by herbivory on the level of expression, they might not necessarily be directly involved in terpene production or plant defenses. Generally, specific functions or putative targets cannot be predicted based on the low sequence similarities to other species. To unravel the functionality of these factors, further studies have to be conducted.

### 4.2.2 Specific induction stimuli lead to explicit expression patterns

Production of defense compounds like volatiles is cost-intensive and therefore often activated when needed (Wright *et al.* 1979). To orchestrate these specific responses, multiple signaling pathways regulate the stress response of plants (Glazebrook 2001; Knight and Knight 2001). However, gene expression patterns share significant similarities after different abiotic or biotic stresses (Durrant *et al.* 2000; Schenk *et al.* 2000; Seki *et al.* 2001; Chen *et al.* 2002; Erb *et al.* 2009).

The results in this work showed that maize discriminates between a short herbivore attack, long damage by herbivore feeding, and mechanical wounding by itself. *Tf1* and *tf35* are

maize transcription factors which are specifically induced in response to these different cues (Fig.4.1).

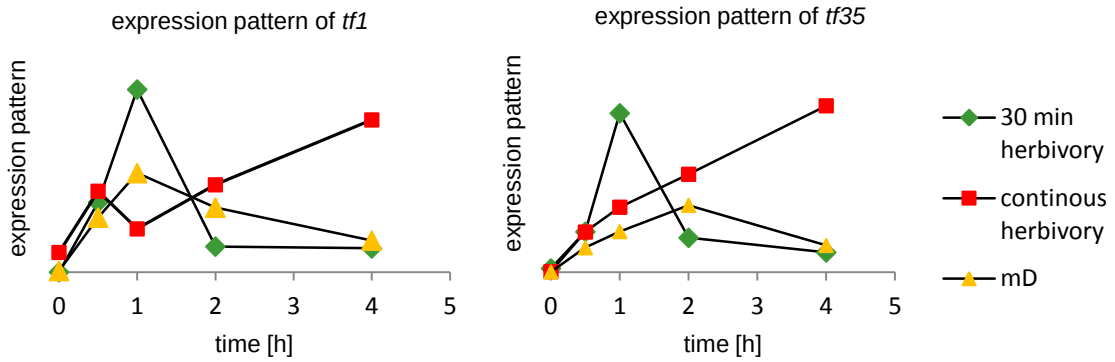



**Fig.4.1: *Tf1* and *tf35* have a different expression pattern after diverse induction types.** Maize plants were either treated with 30 min herbivore feeding, continuous feeding until harvesting, and continuous mechanical damage until harvesting (mD). Induction patterns are combined from independent experiments which were all standardized by the housekeeping genes. Therefore only the expression patterns are displayed without a relative expression fold.

The NAC-like transcription factor *tf1* reached maximum expression within an hour in mechanically damaged plants and in plants treated with 30 min of herbivory. The continuous herbivory of *S. littoralis* resulted in a steady increase of expression after 1 h of treatment. This indicated that maize plants recognize the different types of wounding. The same induction pattern could be observed for transcription factor *tf35*, a putative I-box binding factor.

In order to elucidate the function of transcription factors, maize plants with transposon knockouts were investigated. There was only one transposon-insertion line available for all of the identified transcription factors, with the transposon inserted in the 3' region of *tf1*. Unfortunately, this line could not be used to investigate the role of *tf1* since the background line, W22, is unable to produce herbivore-induced VOCs.

To be a reliable cue for herbivore enemies, the volatile signals emitted by the plant need to start quickly after the onset of feeding and stop when the herbivore moves on. Specific volatile profiles and kinetics were found for *tps23*. Gene expression was significantly up-regulated at 2 h and 4 h after mechanical damage with and without addition of caterpillar

regurgitate. Both kinds of treatments induced the transcript level of *tps23* to an equal amount. This suggests that wounding already fully induces *tps23* expression and regurgitate application does not provide a further increase. The emission of (*E*)-ß-caryophyllene, formed by TPS23, was detected at 4 h after induction but a significant difference was found between the treatments. The volatile sesquiterpene was emitted after plants were treated with mechanical damage. However, addition of caterpillar regurgitate enhanced the level of this volatile compound significantly.

The difference in time lag between induction of transcript accumulation and volatile production can be explained by the period it takes to translate *tps23* mRNA into a sufficient amount of TPS23 enzyme. An adequate amount of TPS23 must be present to produce enough volatiles that can be measured by SPME. Still, this does not explain the discrepancy in the concentration of (*E*)-ß-caryophyllene measured after mechanical damage and damage with regurgitate. The results indicate a posttranslational control point for TPS23 expression or product formation. Another regulatory step responsible for the increase of terpene production after regurgitate application could be the expression of FPP-synthases which synthesize the substrate for terpene synthases (Köllner *et al.* 2008). Putative FPP-synthases were identified with the microarray and showed an increased expression level at 2 h and 4 h after herbivore attack. Unfortunately, the influence of mechanical damage on the expression pattern of FPP-synthases has not been investigated yet. A similar mechanism of regurgitate-specific regulation might also control the emission of the volatile compounds (*E*)-ß-farnesene, (*E*)-α-bergamotene, linalool, and DMNT. The responsible terpene synthases have not been investigated in this study, but the same explanation could apply.

On the other hand, the aromatic heterocyclic compound indole and the green leaf volatile hexenal were emitted in similar amounts after mechanical damage with and without caterpillar regurgitate. Putative indole synthases were found induced in the microarray data at 2 h after herbivore induction and have also been described to be induced after volicitin treatment (Frey *et al.* 2000). However, the data in this study indicate that mechanical damage is sufficient for the induced emission of indole and hexenal and does not require an additional elicitor.

Differential expression patterns of transcription factors can not only be found after different induction stimuli, but they also vary between maize lines. The variety Delprim is able to

produce (*E*)-ß-caryophyllene above- and belowground after herbivore attack (Rasmann *et al.* 2005). The American inbred line B73 lost this ability and lacks a potential resistance mechanism against herbivore attackers (Köllner *et al.* 2008). Both maize lines express TPS10 after leaf attack by *S. littoralis*, which forms the major sesquiterpenes (*E*)-ß-farnesene and (*E*)-α-bergamotene (Schnee *et al.* 2006). The *tps23* structural gene is intact in several American maize lines, but it is not transcribed after herbivore treatment (Köllner *et al.* 2008). The loss of *tps23* transcript accumulation might be the result of a disruption in the signaling cascade. To test the involvement of nine transcription factors into the regulation of TPS23, we tested their expression in B73 and Delprim. All factors were induced after herbivory in B73 and Delprim. Only three factors, *tf23*, *tf34*, and *tf42*, displayed a significantly higher transcript level in Delprim than in B73. Most likely, the difference in TPS23 volatile production cannot be explained by those factors.

### 4.2.3 Herbivore-induced transcription factors are localized throughout the genome

Transcription factors with altered expression level after herbivore feeding were mapped against the genome of *Zea mays* variety B73 in order to investigate their spatial distribution. The sesquiterpene synthases *tps10* and *tps23* were also added to this map (Fig.4.2). The differentially expressed transcription factors were evenly distributed among the chromosomes in maize and no clear pattern could be observed. Also, the transcription factors did not seem to cluster specifically to one region.

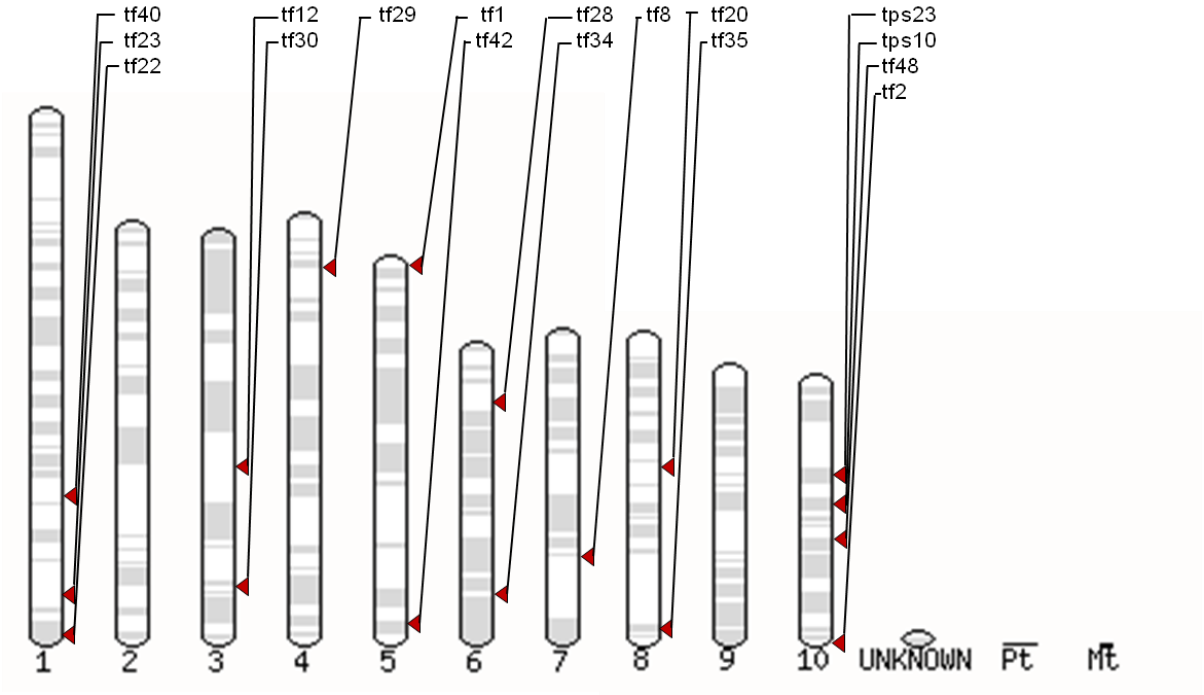



**Fig.4.2: Approximate localization of the differentially expressed transcription factors among the maize genome.** Sequences of transcription factors were blasted using maizesequence.org. In addition *tps10* and *tps23* are displayed. (maizesequence.org)

An operon-like gene cluster required for the triterpene synthesis (thalianol pathway) was reported for *Arabidopsis thaliana* (Field and Osbourn 2008). Also a cluster for the synthesis of antimicrobial terpenes (avenacins) was identified in oat (*Avena strigosa*). Avenacins accumulate in roots after the attack of pathogens (Wegel *et al.* 2009). However, results from this work indicate that herbivore-induced genes and their regulators are not organized in such a way.

## 4.3 The plant hormonal response is specific for the induction stimuli

The phytohormones JA, SA, and ET play an essential role in the regulation of induced defenses which are specific for the attacker (Reymond and Farmer 1998; Pieterse and van Loon 1999; Glazebrook 2001). Biotrophic pathogens are sensitive to SA-dependent responses, whereas JA/ET-dependent mechanisms are more effective against herbivore insects and necrotrophic pathogens (Thomma *et al.* 2001; Glazebrook 2005). De Vos and coworkers showed that herbivore feeding can induce cross-resistance against several

microbial pathogens. Also, ET can act synergistically on SA-inducible defenses and might therefore be responsible for an enhanced resistance against the biotrophic pathogen *Turnip crinkle virus* (De Vos *et al.* 2006).

In this work, the hormone level after mechanical wounding with or without the application of caterpillar regurgitate was investigated. Addition of caterpillar regurgitate to the mechanically damaged area imitated herbivore feeding. The results demonstrated that all measured phytohormones, JA, SA, JA-Ile, and ABA take part in the formation of the anti-herbivore responses. While jasmonic acid is highly induced when plants experience mechanical damage in connection with caterpillar regurgitate, the jasmonic acid-isoleucin derivate was increased only after half an hour to one hour after regurgitate treatment and declined afterwards. The level of both hormones was also significantly increased after mechanical damage only, but not as high.

Abscic acid, an indicator for plant stress (Davies and Zhang 1991), was present at all times during the experiments. The levels of this hormone were significantly higher after induction with regurgitate compared to mechanical damage only. Since ABA is also involved in the regulation of stomata closure and water stress (Tardieu and Davies 1992), it is likely that this hormone is produced when the plants suffer from leaf damage connected with water loss (Erb *et al.* 2011).

The most intriguing observation was made for the plant hormone salicylic acid. SA is known to be induced after pathogen attack (Glazebrook 2005) and recent studies showed that there is synergistic cross talk between SA and JA, depending on the dose of SA (Mur *et al.* 2006). This is in contrast to observations where SA and JA acted antagonistically (Kazan and Manners 2008). To make the situation even more complex, SA was also found to be involved in plant defenses against herbivore attack (Zarate *et al.* 2007).

We observed that the level of SA increased similar to the level of JA after mechanical damage and caterpillar regurgitate. Mechanically damaged plants did not show an induction of SA level, except for the 4 h time point measurement. This indicates that the induction stimulus for SA is not mechanical damage by itself but rather the combination of damage and regurgitate. It was not possible to test whether this effect was due to regurgitate alone, since the development of induction methods of plants without harming the leaf surface were not successful. It is possible that maize reacts to herbivory with the production of SA to be

prepared for a subsequent pathogen attack at the site of herbivore damage. Herbivory does not alter SA level in infested maize roots (Erb *et al.* 2010), indicating that roots and leaves act differently upon attack. Caution has to be taken with this assumption, since the data from this work resemble time points within four hours after treatment. This differs from the *D. virgifera* infested roots used by Erb *et al* (Erb *et al.* 2009) which were induced for 18 h. Also, the concentration of JA and JA-Ile in herbivore-induced roots differ from those of induced leaf material (Erb *et al.* 2009), indicating that hormone production is regulated differently in roots and leaves.

## 4.4 The transcription factors TF23 and TF30 are differentially regulated

Only two transcription factors, *tf23* and *tf30*, displayed an expression pattern specific for mechanical damage and caterpillar regurgitate, respectively. *Tf30,* annotated as ethylene responsive element, belongs to the class of AP2/EREBP transcription factors. This class of transcription factors is unique to plants (Riechmann *et al.* 2000) and binds two similar regulatory elements: the GCC-box and dehydration-responsive element (Singh *et al.* 2002). The large group of ethylene responsive factors has been implicated in regulating gene expression after several stresses like cold, drought, and pathogen attack, as well as responses to the hormones ET, SA, and JA (Onate-Sánchez and Singh 2002; Singh *et al.* 2002). Ethylene-responsive transcription factors that interact with the GCC-box were characterized in tobacco and Arabidopsis (Ohme-Takagi and Shinshi 1995; Solano *et al.* 1998; Fujimoto *et al.* 2000). Other studies showed that ERF are able to bind to the APETALA2 domain in the ORCA proteins (octadecanoid-responsive Catheranthus APETALA2) and therefore provide a link between jasmonic acid and the accumulation of terponoid indole alkaloids (van der Fits and Memelink 2000; Memelink *et al.* 2001). An 84 % amino acid similarity was found between TF30 and the AP2/ERF9 protein in Arabidopsis. This gene was found induced after root colonization with the endophytic fungus *Piriformospora indica* (Camehl and Oelmüller 2010). Interestingly, homologes of *tf30* in tobacco and rice are known to induce hypersensitive response-like cell death after induction with *Tobacco mosaic virus* (Ogata *et al.* 2012) and are therefore implicated in defenses against pathogens.

*Tf23* is a member of the bHLH transcription factor family. Only a weak similarity was found to a basic helix-loop-helix protein in *Arabidopsis lyrata* which has not been characterized yet. In tobacco, the homolog NtWIN4 is implicated in the hypersensitive defense and induced after wounding and pathogen attack (Kodama and Sano 2006). In maize, *tf23* seems to be involved in other plant responses. While *tf23* is expressed at a higher level after mechanical wounding and caterpillar regurgitate after half an hour and one hour, *tf30* showed an inverted expression pattern. This transcription factor reacted more strongly upon mechanical damage alone, indicating that there might be two different signaling pathways present (Fig.4.3).

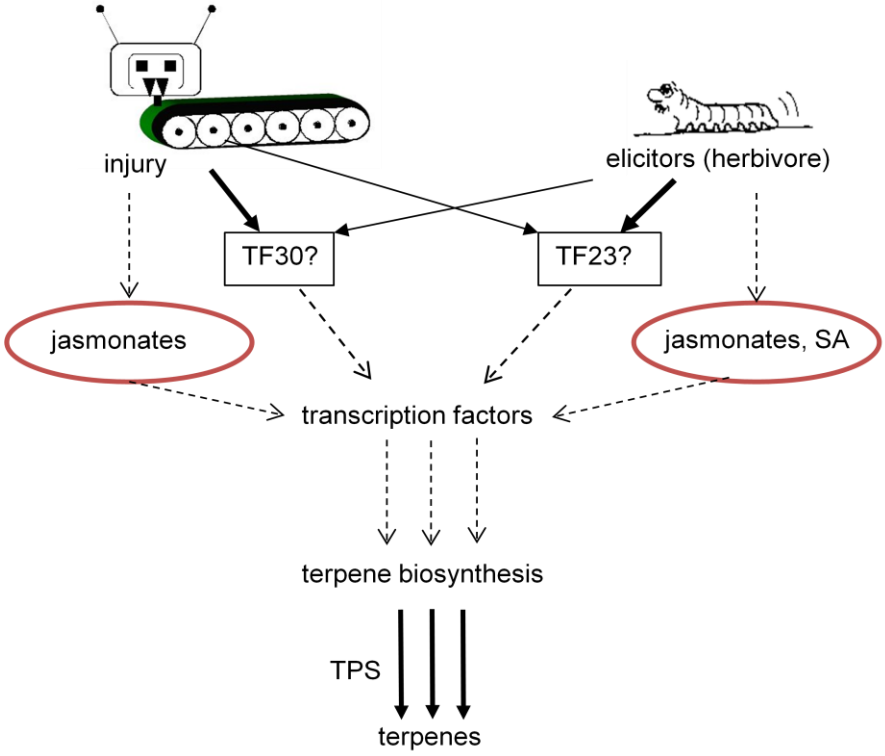



**Fig.4.3: Schematical overview of the two hypothetical induction pathways in maize.** Maize responds to mechanical damage and elicitors. The transcription factor TF30 is highly induced after mechanical damage, but only slightly after application of elicitors (caterpillar regurgitate). TF23, on the other hand, shows a higher expression level after induction with elicitors. The plant hormones react differently upon the two induction modes. While salicylate is only induced after elicitor treatment, jasmonates (JA and JA-Ile) are induced after both induction types. These hormones might act upon the regulation of transcription factors which in turn are responsible for the activation of terpene synthases (TPS). Dashed arrows represent multiple steps, bold arrows indicate a strong induction, and thin arrows indicate a weak induction.

In maize, it might be possible that transcription factor TF30 activates target genes after mechanical damage while TF23 is responsible for induction of target genes after herbivore attack. Still, it is possible that *tf23* might also reduce responses to herbivory, working in favor of the herbivore. This has been shown for *Nicotiana tabacum* and the herbivore *Helicoverpa zea*. In this example, the glucose oxidase in the caterpillar salvia suppresses the production of nicotine induced by caterpillar feeding (Musser *et al.* 2002).
Another indication for two different signaling cascades is the induction of SA after elicitor treatment only. The plant hormone jasmonic acid appears in both pathways.

## 4.5 Identification of regulatory sequences in the promoters of *tps10* and *tps23*

### 4.5.1 The binding ability of TF1, TF8, TF20, and TF22 to the promoters of *tps10* and *tps23*

In order to find transcription factors that bind to the promoter of *tps10* or *tps23*, four transcription factors were chosen for analysis. The transcription factors (TF1, TF8, TF20, and TF22) were selected because of their early induction after herbivore attack which was in contrast to the slower induction of *tps10* and *tps23*. The transcription factors *tf1* and *tf8* showed an increased expression level within half an hour after herbivore treatment. The remaining factors *tf20* and *tf22* displayed a negative regulation within the first half an hour. Both induction types were included in the band shift assays because it is not known whether *tps10* and *tps23* are subject to activation or de-repression.
Transcription factors TF1 and TF22 are annotated as NAC transcription factor (NO APICAL MERISTEM (NAM), ATAF1, 2 and CUP-SHAPED COTYLEDON (CUC2)) and have been described first by Aida *et al* (Aida *et al.* 1997). More than 90 putative NAC-domain proteins in Arabidopsis and rice are implicated in plant development (Delessert *et al.* 2005) and some are induced by pathogen infection and/or mechanical wounding (Hegedus *et al.* 2003). With a domain similar to MYB-like transcription factors (Tran et al. 2004) and a binding overlapping the site of bZIP transcription factors (Duval et al. 2002), those factors seem to be a good candidate for binding studies. Nevertheless, the NAC transcription factors bind to the

CATGTG motif (Tran *et al.* 2004) that is present in the *tps10* and *tps23* promoters. In both promoters, this motif is found twice in the maize line Delprim. In the *tps10* promoter the binding motif is found at -22 bp and -488 bp upstream of the start codon, in the *tps23* promoter at -281 bp and -649 bp.

As member of the bHLH transcription factors, TF8 was chosen for analysis. This class of transcription factors recognizes G-box motifs in the promoter of target genes (Atchley and Fitch 1997). Analysis of the promoter sequences of *tps10* and *tps23* revealed several putative G-boxes over the whole promoter region.

Transcription factor TF20 was annotated as ETTIN-like auxin response factor. Auxin response factors were found to be induced in poplar after herbivore attack (Ralph *et al.* 2006). Those auxin response factors bind to a TGTCTC motif (Tiwari *et al.* 2003). This sequence motif was only found in the promoter of *tps10* at the locations -424 bp, -634 bp, and -1211 bp upstream of the start codon. Auxin levels were not investigated in this study, but this factor was included in the analysis because of three putative binding sites.

Unfortunately, no binding could be observed between the promoter fragments and the expressed transcription factors in EMSA experiments (3.3.1). Besides the absence of the proper binding site, lack of interaction could be due to improper assembly of the ORF of the factors or secondary structures of the promoter fragments used in the EMSA.

### 4.5.2 The promoters of *tps10* and *tps23* possess similar regulatory *cis*-acting elements

Each promoter has an exclusive organization of *cis*-acting sequences and therefore a unique platform for the binding of *trans*-acting factors. This arrangement is determined by the number of *cis*-acting elements, their distance to each other, their orientation, and their super-hierarchical order (Arguello-Astorga and Herrera-Estrella 1996; Acevedo-Hernéndez *et al.* 2005; Cazzonelli and Velten 2008).

Only small nucleotide differences were observed in the *tps23* promoter sequences of several maize lines and no clear pattern of differences was observed between a functional and a non-functional promoter. This suggests that the differences between the lines are due to *trans*-acting components in the signaling cascade (transcription factors, kinases, etc.). Still, the crucial regulatory elements could be located upstream of the assayed promoter sequences.

The promoter sequences of *tps10* differed more among (*E*)-ß-farnesene-producing lines than those of *tps23*.

TPS10 and TPS23 are expressed in different organs (Köllner *et al.* 2004) and displayed varied terpene emission after herbivore feeding. Therefore, both promoter sequences were investigated to find specific elements that are responsible for the distinctive expression patterns. Truncation experiments with GUS-fusion constructs revealed an active 1.5 kb *tps10* promoter. The activity was lost in the 800 bp promoter fragment. In between those two fragments, only few *cis*-acting regulatory elements were identified: a WUN motif, 10 TATA-boxes, and four CAAT-boxes. TATA-boxes are common core promoter elements (Timko *et al.* 1985) while CAAT-boxes are common *cis*-acting elements and enhancer regions (Dorn *et al.* 1987). They respond to light, cytokinin and the functional development of plastids (Kusnetsov *et al.* 1999). Both types of regulatory sequences could be essential for *tps10* promoter activity, but are present throughout the whole promoter. The same was observed for G-boxes which are implicated in JA responsiveness and wounding (Menke et al. 1999; Delessert et al. 2004) and are distributed evenly in the promoter of *tps10*. An overview of the *cis*-acting elements that might be involved in the transcriptional regulation of *tps10* is shown in Fig.4.4.

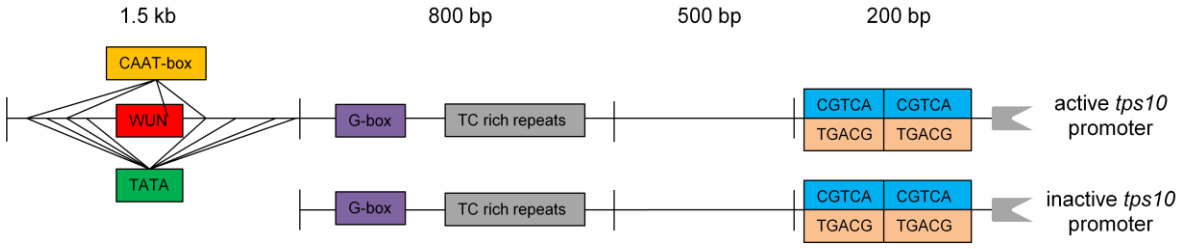



**Fig.4.4: Schematical view of the *tps10* promoter.** Truncation experiments were conducted using a 1.5 kb, 800 bp, 500 bp, and 200 bp fragment, respectively. Some elements with potential importance for regulation are displayed. Removal of the first fragment results in the loss of *tps10* promoter activity.

The results of the induction experiments revealed that *tps10* can only be activated when two induction stimuli are combined. Activity was only detected when Arabidopsis plants were induced by scratching the leaf and addition of jasmonic acid to the wounded site. Wounding

or jasmonic acid by itself were not able to induce *tps10* promoter activity. In order to get a more detailed view of the regulatory sequences of *tps10*, a promoter fragment 5' upstream of the 1.5 kb fragment should be investigated for additional elements.

For *tps23*, the mode of induction is different. While the 1.8 kb and 1.2 kb fragments were active upon JA treatment, the 600 bp fragment was active by mechanical wounding alone. The 400 bp fragment showed no promoter activity. Hence, the essential regulatory elements for *tps23* are between the 600 bp and the 400 bp fragment. Sequence analysis using PLACE and PlantCare showed several hypothetical regulatory elements (Fig.4.5).

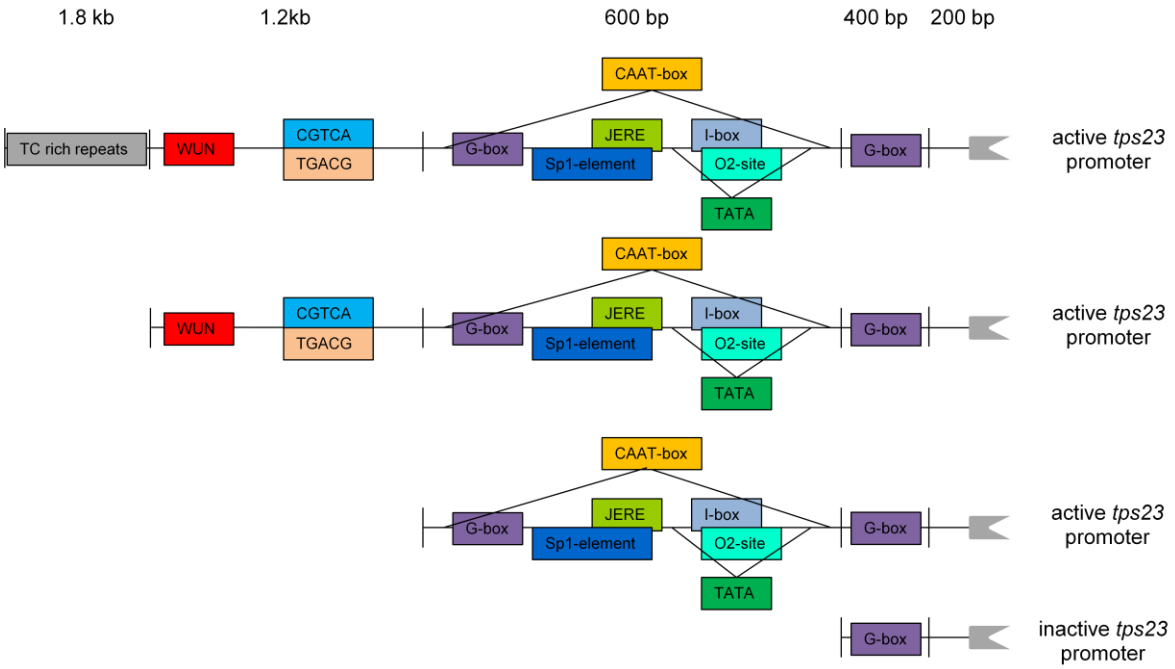



**Fig.4.5: Analysis of hypothetical regulatory sequences in fragments of the *tps23* promoter.** Deletion analysis was performed using promoter::ß-glucuronidase reporter gene constructs with promoter sizes 1.8 kb, 1.2 kb, 600 bp, 400 bp, and 200 bp. Potential regulatory elements are displayed. The 400 bp and 200 bp long promoter fragments were found to be inactive.

CAAT-boxes were also found throughout the *tps23* promoter. The Sp1 element resembles a GC box bound by the SP1 transcription factor (Letovsky and Dynan 1989). Also regulated by light and the circadian clock is the I-box element. This element was found in several promoters of cab-genes, encoding light-harvesting chlorophyll a/b binding proteins (Borello *et al.* 1993). Another potential regulatory element, the O2-site, plays a role in the zein

metabolism (Kemper *et al.* 1999) and therefore is unlikely to be involved in the regulation of *tps23*. TATA-boxes are also found in 600 bp fragment of the promoter. It has been reported that TATA-boxes are essential for transcription at positions up to -1598 bp from the start codon (Keddie *et al.* 1992) to -30 bp of the transcription start in tomato (*Lycopersicon esculentum*, (Cordes *et al.* 1989)). It is therefore not possible to say which TATA-box plays a crucial role for the regulation of *tps23*. The JERE motif responds to JA and MeJA (Menke *et al.* 1999; Chini *et al.* 2007) but cannot be an essential element regulating JA responses because the 600 bp promoter fragment containing the JERE is not active after JA treatment, but only inducible through mechanical damage. The other interesting *cis*-acting element is the G-box. Mainly involved in JA responses (Menke *et al.* 1999), it has also been found in large proportions of wound-inducible promoters (Delessert *et al.* 2004). This could be an indication for the essential role of the G-box in the *tps23* 600 bp::GUS promoter fragment. The class of basic Helix Loop Helix transcription factors are known to bind G-boxes (Toledo-Ortiz *et al.* 2003), whereas the JERE motif is recognized by AP2/ERF domain transcription factors (Menke *et al.* 1999).

Sequence analysis of the *tps23* promoter revealed two additional MeJA responsive elements in the 1.2 kb promoter fragment. The CGTCA motif is localized at -658 bp before the start codon, and the TGACG element (Rouster *et al.* 1997) is complementary to the first one, but localized in opposite direction on the minus strand. This sequence motif is missing in the 600 bp promoter fragment and could explain the loss of promoter activity after jasmonic acid treatment. Thus, there might be two distinct induction pathways for TPS23. The first pathway regulates via the induction of jasmonic acid and the second through mechanical wounding. This second pathway might be independent from JA. Nevertheless, it is still possible that the endogenous jasmonic acid induced in response to mechanical wounding of the plants activates the promoter of *tps23*. In addition, TPS10 is only found in induced leaves of *Zea mays* (Köllner *et al.* 2004) while TPS23 is synthesized in both herbivore-induced shoots and roots (Rasmann *et al.* 2005). The results confirm the idea of distinct signaling transduction pathways for *tps10* and *tps23* which utilize different cues for induction.

With the identification of crucial promoter elements, more transcription factor candidates could be tested in binding assays. So far, band shift assays revealed no binding of the G-box binding factor TF8 to the promoters of *tps10* and *tps23*. The transcription factor *tf23* is also

annotated as bHLH and is highly induced after herbivore attack. This factor would be an interesting candidate for further binging analysis because several G-boxes are present throughout the promoters of both terpene synthases. Annotated as an ethylene responsive element, the transcription factor *tf30* might serve as a binding protein for the JERE motif localized in the promoter of *tps23*. Although deletion analysis indicated that this element is not crucial for *tps23* expression, secondary effects with other binding factors or secondary structures cannot be excluded.

One has to keep in mind that the promoter deletion analyses were conducted with maize promoters in Arabidopsis plants. Conclusions have to be drawn carefully, because differences in the defense regulation of the two plant species cannot be ruled out.

### 4.5.3 The promoters of *tps10* and *tps23* respond to mechanical damage and herbivore attack

The sequence analysis revealed a WUN-motif in the promoter of *tps10* (-1097 bp and -1088 bp) and in the promoter of *tps23* (-692 – -684 bp). Deletion of a fragment containing the WUN-motif resulted in an inactive promoter of *tps10*. Because this motif was found to regulate the signaling pathway after wounding (Matton *et al.* 1993), the promoter sequences for this motif were compared between different maize lines.

The promoter sequences of *tps10* were compared between the maize lines Delprim, OH7B, MS71, and B73 (Fig.4.6). The lines Delprim, OH7B and B73 are able to produce TPS10 specific volatiles after herbivore damage, while MS71 does not. The WUN motif is present in all four lines regardless of the ability to produce TPS10-specific volatiles. Overall, the results suggest that the WUN motif is an important regulatory sequence in the promoter of *tps10* but not responsible for the ability to express TPS10 in the lines investigated here.

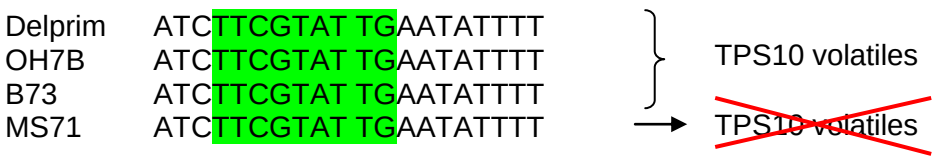



**Fig.4.6: Sequence analysis of the WUN motif of *tps10* promoter in different maize lines.** Sequence is shown from -1304 to -1296 upstream of the start codon. The WUN motif is highlighted in green. Maize line MS71 is not able to produce TPS10 specific volatile, although it possesses a complete WUN motif in its *tps10* promoter.

Promoter fragments of *tps23* are active up to -400 bp, indicating that the WUN-motif is not crucial for this promoter. It rather seems that the WUN-motif has a general activating role for *tps23*. The WUN-motif was compared between the maize lines to investigate potential correlations between the motif and gene activity (Fig.4.7). These maize lines were selected because they differ in their ability to produce (*E*)-ß-caryophyllene. The European maize line Delprim is able to produce this volatile terpene, while the American maize line B73 seems to have lost this ability (Köllner *et al.* 2008). The lines NC358, Du101, and F476 possess a functional TPS23 enzyme while CML247, OH7B, and MS71 are not able to produce (*E*)-ß-caryophyllene after herbivore attack (Degen *et al.* 2004). With the exception of Du101 and NC358, no differences in the WUN-motif between these maize lines were found. The single nucleotide exchange in those two lines does not seem to affect caryophyllene biosynthesis.


**Fig.4.7: Sequence analysis of the *tps23* promoter of different maize lines.** Promoter sequences were amplified from genomic DNA, cloned and sequenced. The sequence comparison from -697 to -689 upstream of the start codon is shown. The WUN motif is marked in green, bold letters indicate a nucleotide exchange.

Sequence comparisons among the promoters of the lines also revealed the presence of the JERE, G-box, CGTCA, and CAAT-boxes in the same position range (data not shown). Therefore, loss of (*E*)-ß-caryophyllene production is not likely due to differences in the *cis*-elements of this promoter fragment, but probably due to the loss of other factors in the signaling cascade.

# 5. Outlook

The aim of this project was to identify herbivore-regulated components of the cellular signal transduction network by microarray hybridization. This technique successfully identified a group of transcription factors with herbivore- induced alterations in gene expression. There are, however, some limitations associated with this technique since it does not identify constitutively expressed genes or factors that are activated or de-activated by mechanisms other than gene expression. An alternative approach is the identification of signal transduction components by molecular mapping. While these methods provide additional information about the function of the signal transduction components, they will not identify factors with redundant function. The combination of both methods might generate a complete overview of the plant responses after herbivory.

In continuation of this project, the investigation of transcription factors with overexpressing lines and knockout maize lines might elucidate their functions. Due to the apparent conservation of these pathways between maize and other plants, homologous transcription factors in *Arabidopsis thaliana* or *Nicotiana tabacum* could provide further information while making use of more accessible transformation systems. Another valuable resource are maize transposon knockout plants that are currently developed by several public outlets. We are constantly checking these resources for knockouts of the candidate genes identified in this study.

Further promoter deletion analysis will clarify the role of the *cis*-acting elements identified in the promoters of *tps10* and *tps23*. In the background of an Arabidopsis COI1 mutant, the effects of JA-mediated pathways can be evaluated. A transient expression system of transcription factors and promoter fragments which was established in tobacco could serve as an alternative method to identify potential targets (Van Der Linde *et al.* 2011).

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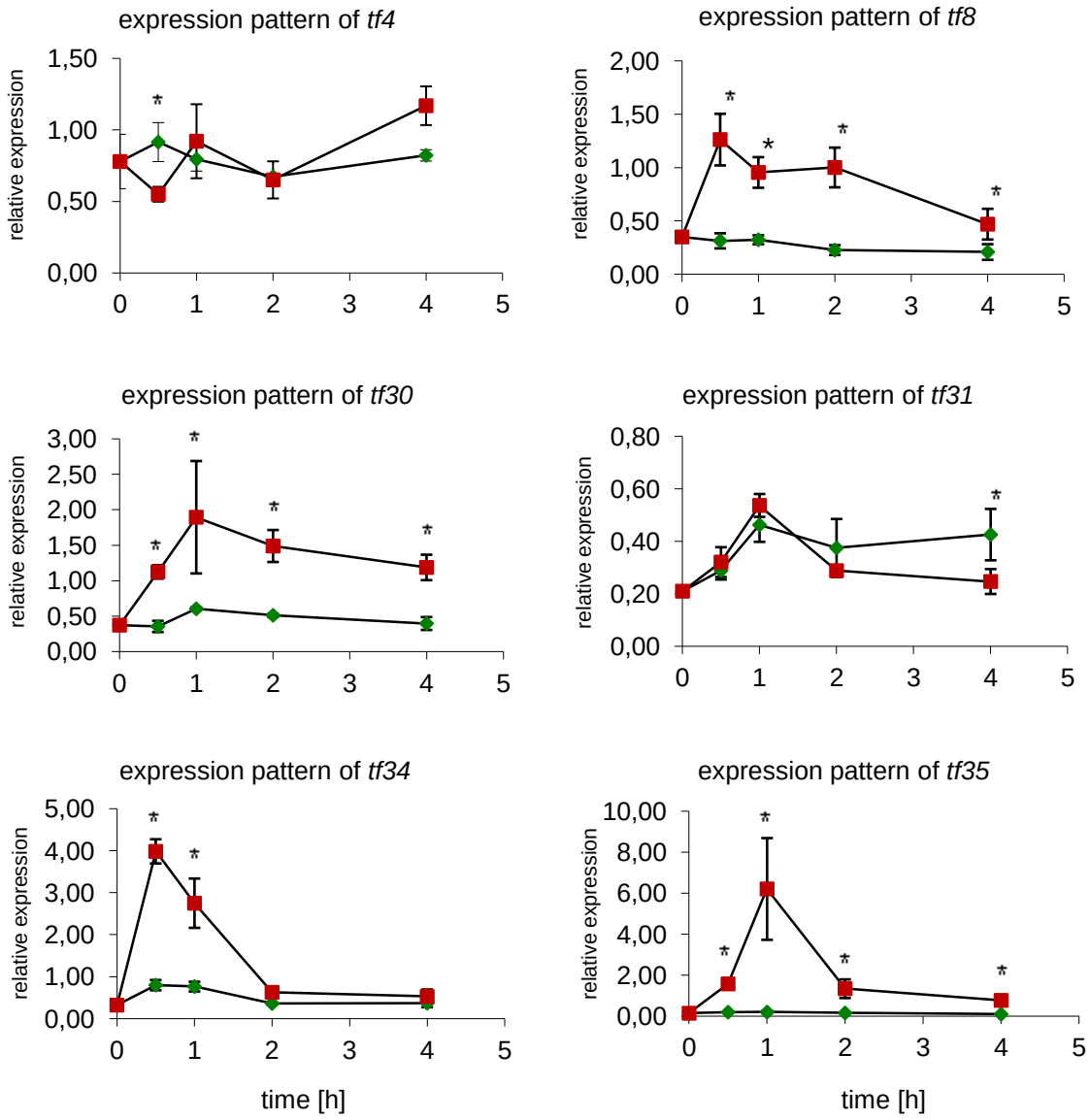
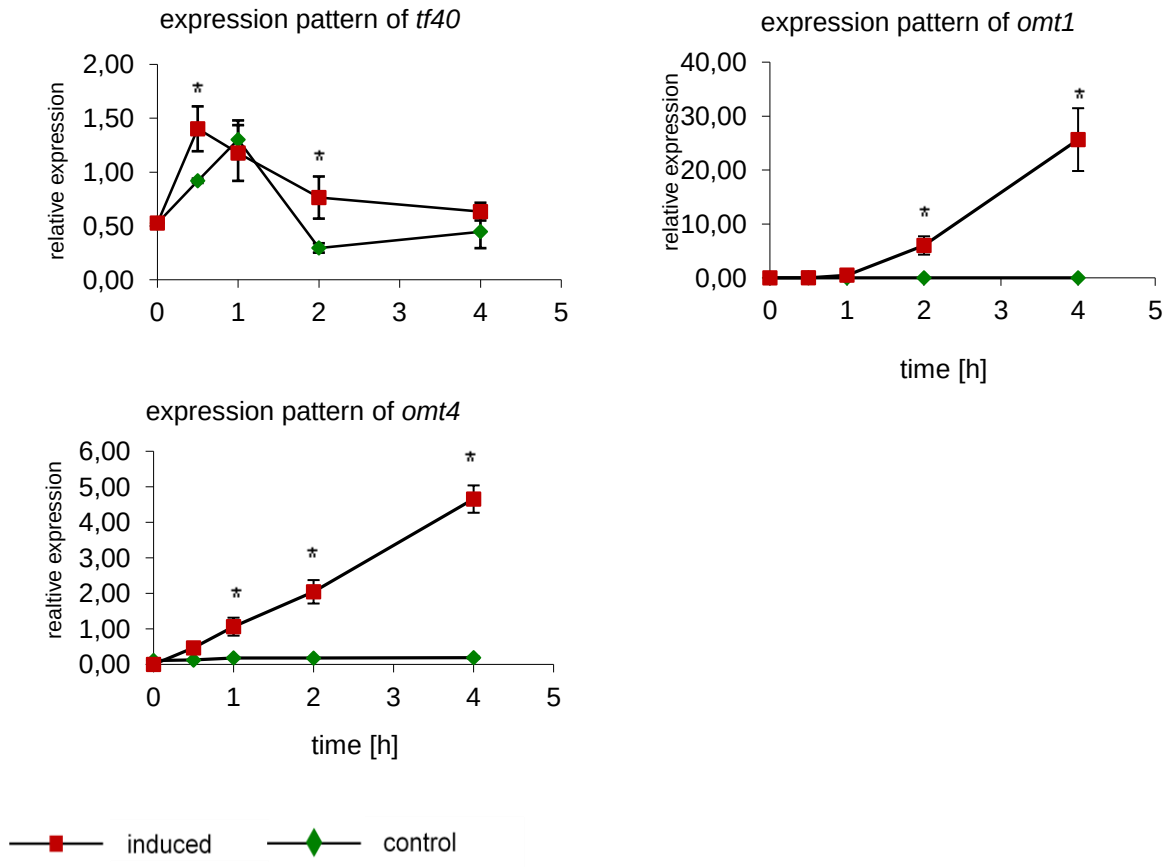
# 7. Appendix

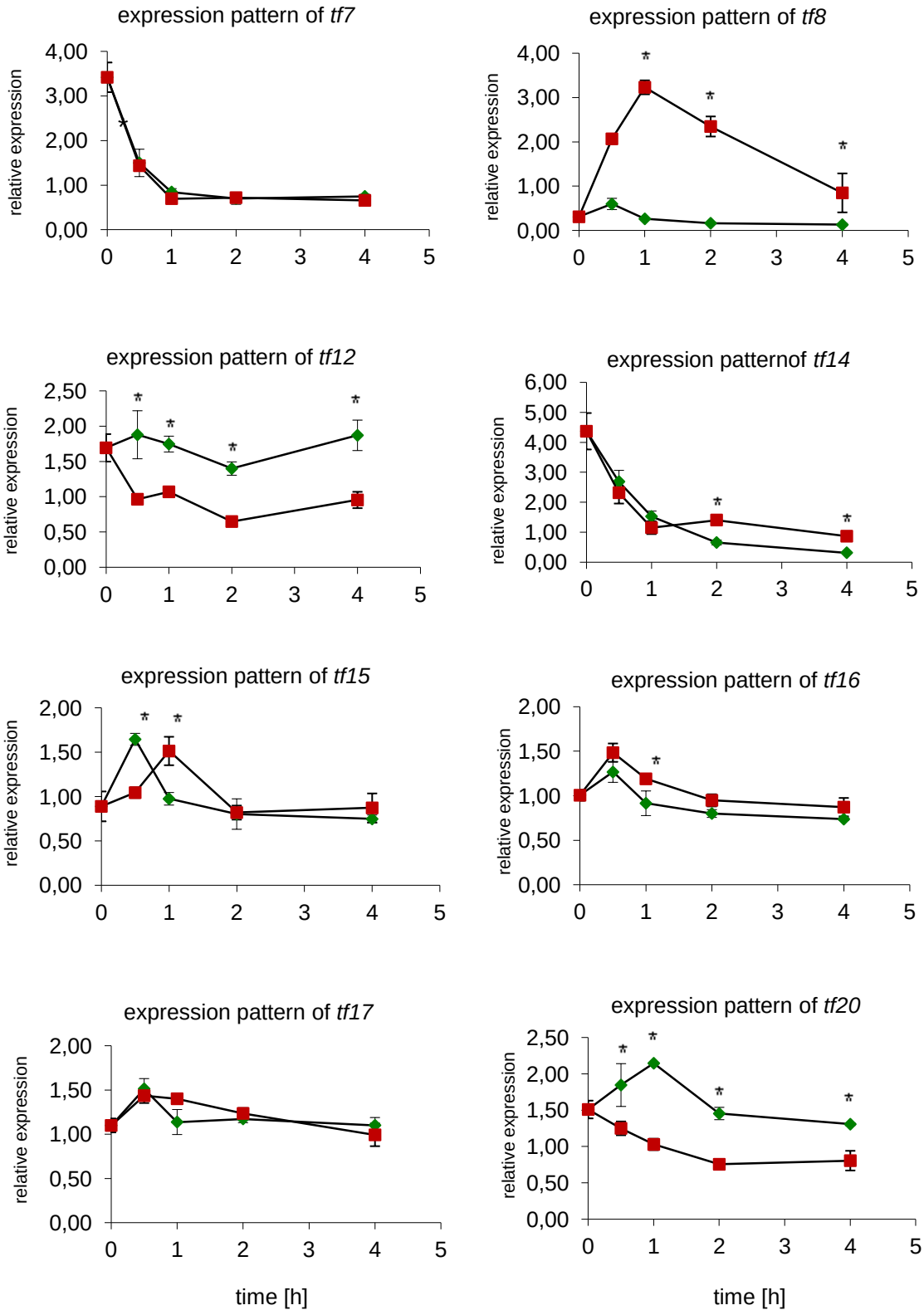
## 7.1 QRT-PCR of the plant material treated with 30 min herbivore feeding

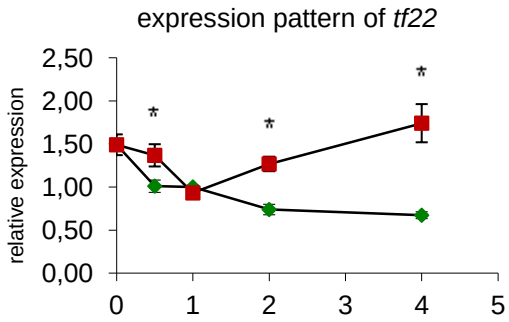


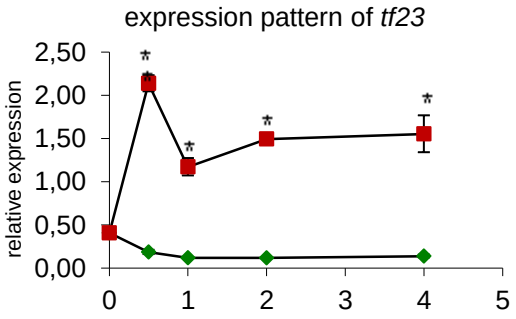


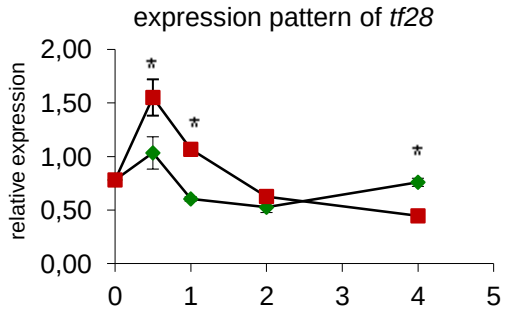

**Relative expression pattern of further transcription factors and terpene synthases tested after 30 min herbivore feeding.** Plants were treated with *S. littoralis* caged for 30 min on a single leaf. Material was harvested after: 0 h,0.5 h, 1 h, 2 h, and 4 h. Means and standard error are shown (n=4). The relative expression levels were calculated as described in 2.4.9. Two-Way ANOVA was used to calculate statistical differences with time as factor one and treatment as second variable. * indicate significant differences between treatments within time points ($p<0.05$).

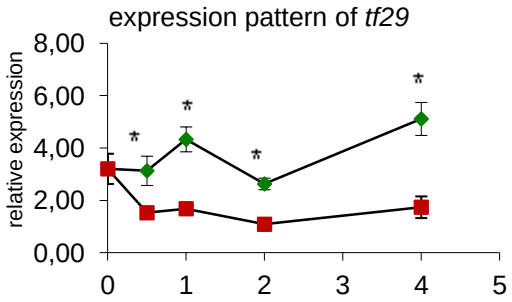
## 7.2 QRT-PCR of plant material treated with continuous feeding

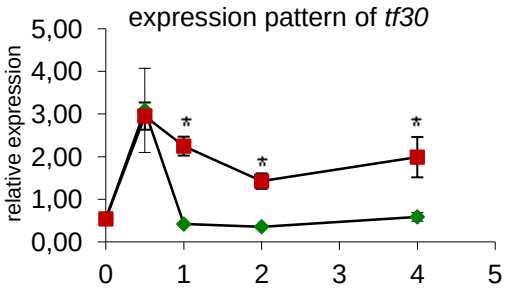


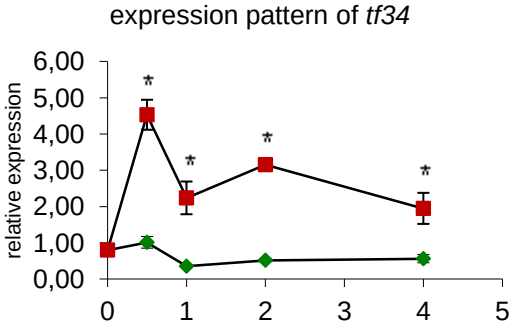

expression pattern of *tf22*
relative expression
2,50
2,00
1,50
1,00
0,50
0,00
0
1
2
3
4
5

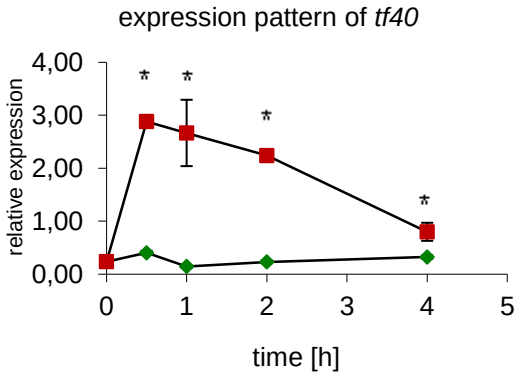

expression pattern of *tf23*
relative expression
2,50
2,00
1,50
1,00
0,50
0,00
0
1
2
3
4
5

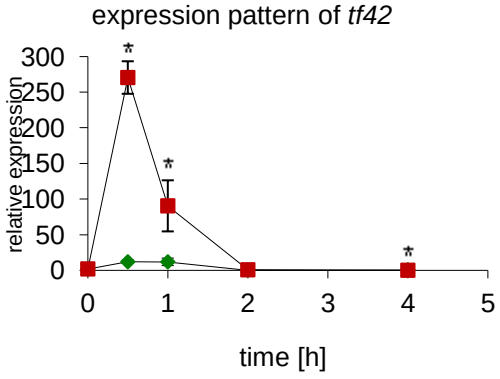

expression pattern of *tf28*
relative expression
2,00
1,50
1,00
0,50
0,00
0
1
2
3
4
5

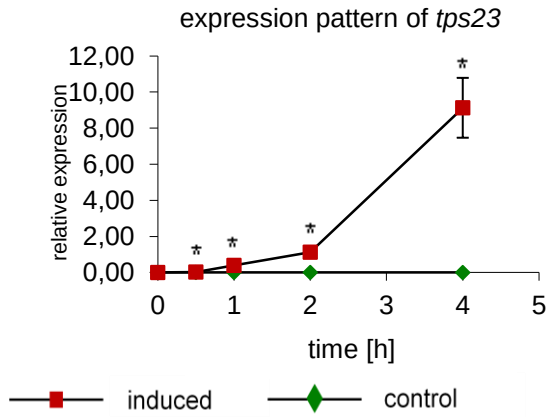

expression pattern of *tf29*
relative expression
8,00
6,00
4,00
2,00
0,00
0
1
2
3
4
5


expression pattern of *tf30*
relative expression
5,00
4,00
3,00
2,00
1,00
0,00
0
1
2
3
4
5


expression pattern of *tf34*
relative expression
6,00
5,00
4,00
3,00
2,00
1,00
0,00
0
1
2
3
4
5

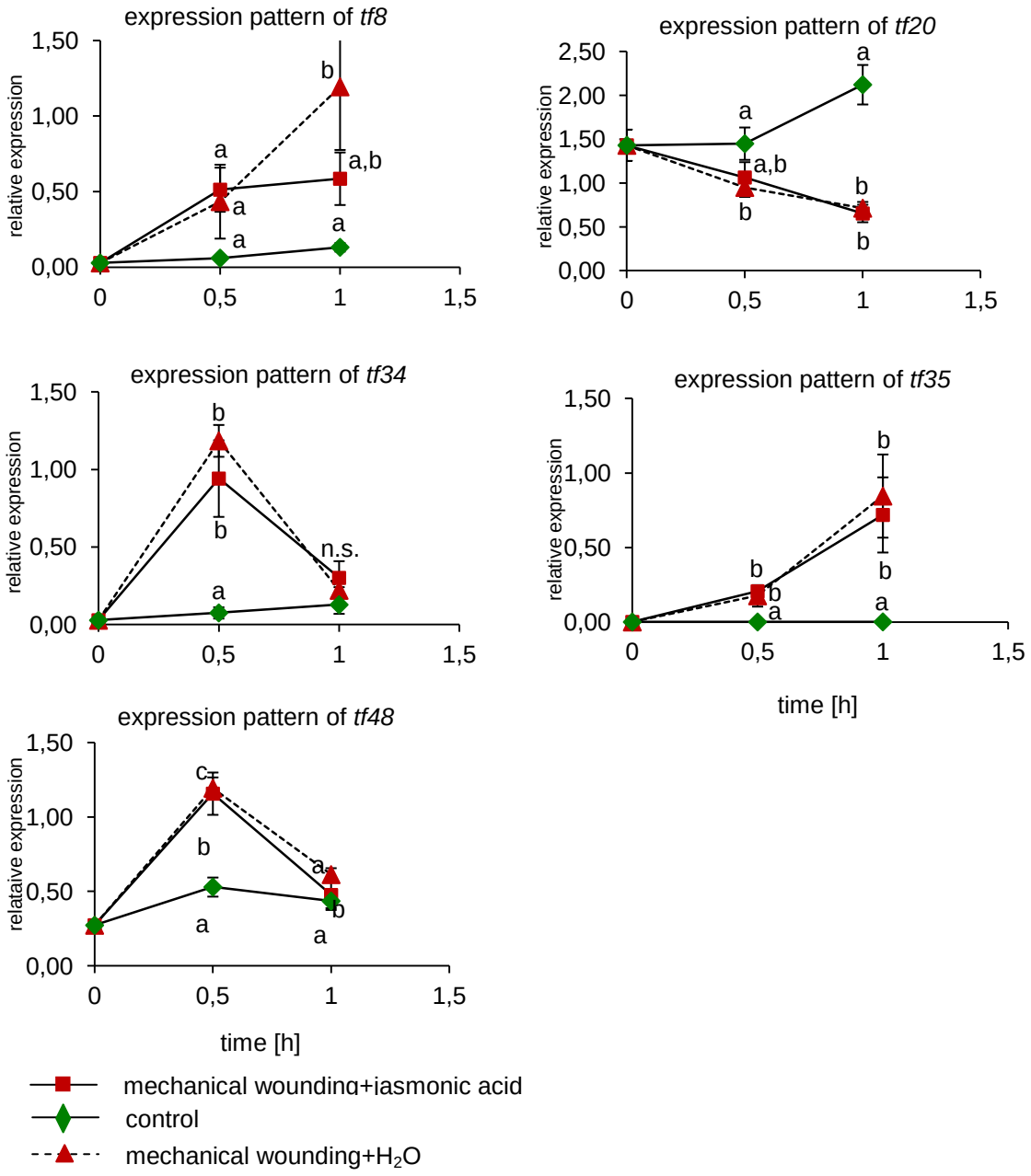

expression pattern of *tf40*
relative expression
4,00
3,00
2,00
1,00
0,00
0
1
2
3
4
5
time [h]


expression pattern of *tf42*
relative expression
300
250
200
150
100
50
0
0
1
2
3
4
5
time [h]



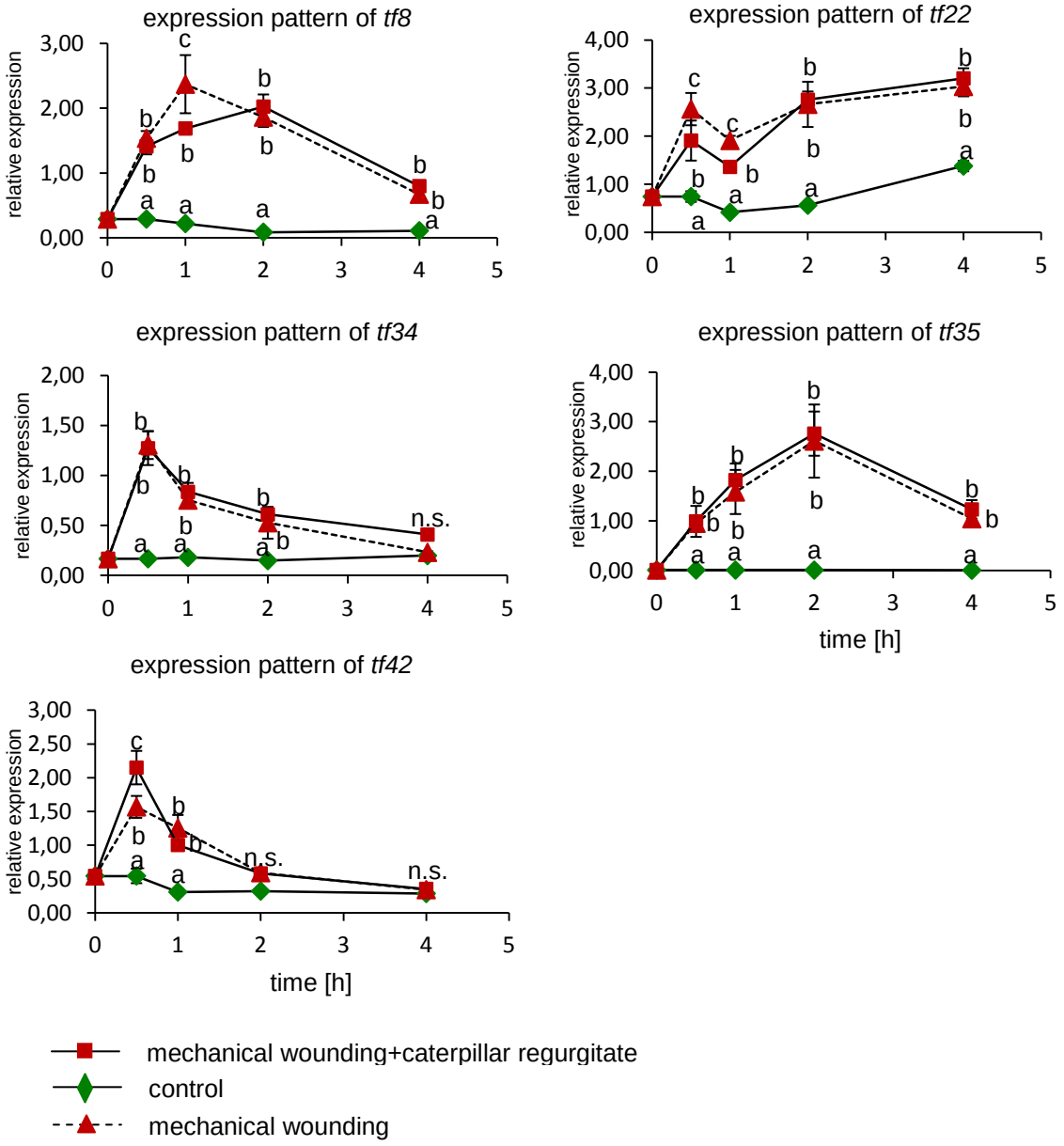

**Relative expression pattern of further genes tested after continuous herbivore feeding.** Expression pattern is shown over a time period of 4 h. Delprim maize leaves were treated with the caterpillar larvae *S. littoralis* until leaf material was harvested. Induced expression pattern is marked with a red square, control points with a green diamond. Expression was calculated against the housekeeping genes. Standard error (n=3) is shown for each measurement. Two-Way ANOVA was used to test significant differences with $p<0.05$ defined as significant for the treatment within the time points (*).

## 7.3 QRT-PCR of plant material induced with jasmonic acid




**Expression profile of further transcription factors and *tps23* after induction with jasmonic acid.** Plants were cut and put into water or water containing jasmonic acid, respectively. The induction time was set to 1 hour to analyze early transcriptional changes. The relative expression was calculated as the expression of the housekeeping gene HG2. Means and standard errors are shown (n=3). Two-Way ANOVA was performed with time as the first variable and treatment as second factor. Different letters indicate significant differences between treatments within time points ($p<0.05$).

## 7.4 QRT-PCR of mechanical treated plant material (Mecworm)




**QRT-PCR analysis of further transcription factors after mechanical induction with and without caterpillar regurgitate.** Plants were treated with mechanical damage and mechanical damage plus the addition of caterpillar regurgitate. Means and standard errors are shown (n=4). The relative expression was calculated as described in 2.5.9. Two-Way ANOVA was performed with time as the first variable and treatment as second factor. Different letters indicate significant differences between treatments within time points ($p<0.05$).

## 7.5 DNA sequences of expressed transcription factors

**>*tf1*- Delprim**

ATGACAGCGCAGAACCCGCCCACAGGACAGGACACACAGAGCCGAGCCACCCCACCCA
CCATCGGCGACCAGCAGCCAGCCGCGGGAGCGAGCTGTTTAAAGACACCGAGTCGGAGT
CGGACGGAGGACTGGCAGGCACAACCGAAGCCACCGCTTCTAGTTCTCGGGTTCATCGC
CAGCAATCCAGACCACATAATGGGACTGCCGGTGACGAGGAGGAGGGAGAGGGACGCG
GAGGCGGAGCTGGACCTGCCGCCGGGGTTCCGGTTCCACCCCACCGACGACGAGCTGGT
GGAGCACTACCTGTGCCGCAAGGCGGCGGGGCAGCGCCTCCCCGTGCCCATCATCGCCG
AGGTGGACCTGTACAGGTTCGACCCCTGGGACCTGCCGGAGCGCGCGCTCTTCGGGGCC
CGGGAGTGGTACTTCTTCACGCCCAGGGACCGCAAGTACCCCAACGGCTCCCGCCCCAA
CCGCGCCGCCGGCGACGGATACTGGAAGGCCACCGGCGCCGACAAGCCCGTCGCGCCGC
GCGGCGCCCGCACGCTCGGGATCAAGAAGGCGCTCGTCTTCTACGCCGGCAAGGCGCCG
CGCGGGGTCAAGACGGACTGGATCATGCACGAGTACAGGCTCGCTGACGCCGGCCGCCG
CGCCAAGAAAGGGTCGCTCAGGGTAAGTTTCTACACACACAAAAAAAAGAGGGGTGAA
CGAGGAATTTTTTAG

**>*tf8*- Delprim**

ATGAAACACCACCACCACCACCACCACCACGGTGGTCTGGTTCCGCGTGGTTCCCATGGC
GGATCCGAATTCATGGAGTTTGACCTGCTGAATTACAGCCCGGAAGCGCAGCTTGAGCT
GATGACCACGATGCTCCAGCTGGAGCAGCTAACTGCGCTCGACGGCCATCAGTTTCCGA
CGATGGCGCCTGTCTCGCCGCCGATATCCCCGATGCAAACCCATCATGCAGGTCACAGCT
TGTCGCCTCCGCCACACATGTCGGCGACGACGACGACCACCACCACCGGGTACCCAGAG
CAGTACACGCCGGCGGCGGCCGTGTACGGCGCCACCGCTACCGGCCTCGAGCACCTCCA
GGACTACGCGCTGCCCCACGGCGACATGTAA

**>*tf20* - Delprim**

ATGAAACACCACCACCACCACCACCACCACGGTGGTCTGGTTCCGCGTGGTTCCCATGGC
GGATCCGAATTCATGAGTTTTAGGACTCGTCATGTTCCGTCTGCTCCTCAAACTGTTGAG
GCTGCAAAACTTCAATCTTCTGGTGCTAGCTTCAATGAATCTATTGGATTCTCAGAGGTC
TTGCAAGGTCAAGAAATTTCTCGGGCAGTTCCTATGTTCCAAGGAATGATGTCTGAGGCT
TGTTCACTAAAAGGAGGATATGGGCTGCATAGTTATATGCGTACCCCAGTTGCTGTTACT
GGATTGTCAGCCACAACTCAAGAGTGTTCTCTCACACTATCTACTCCGCCAGGAGCACAA
GTTCCTTCTGTCTACCCTGATAATATTTTTAACCGAACTGTGGTTCGACAGCTTGGACTGG
CAAGCAAGTTTGATGGTGGAGCTACAAATGCCCAGCAGTCTGTCCCATTTGATAGGCCG

AGGGAAATTTGGAGCAAGCCACAGCATGAAATATCTGATCAAACGAAAATGGATCACTT
TGAGACTAGAAGAGCTTCAGCACCTGGAGATGATGCTGCTAGGCATGGGTCTGGTGGAG
AGGTGGTTCGCAAAACTAGCTGCAGACTTTTTGGTTTCTCGTTGACTGAGAAGATCTTGC
CAGCAGATGATGATGGCATCAAGGAAGTGACCTATGAGCCTGAGTGCCAGAATCCACGG
ATGCTGGACCTGTTCGGGTACAACTGCTCAGCCCCAAGTGCTGCTCTTCCAGCTCTGTGT
GCTGCCCCCTTTGGAATGTGA

**>*tf22*- Delprim**

ATGAAACACCACCACCACCACCACCACCACGGTGGTCTGGTTCCGCGTGGTTCCCATGGC
GGATCCGAATTCATGCAGCTGGGGAAGACCGCCGTCGCCGGCGTCGGCGCCACCAAGGA
GGAGGCGATGGACATGGCCACCTCGCACACGCACTCCCACTCCCAATCACACTCGCACT
CGTGGGGCGAGACGCGCACGCCAGAGTCGGAGATCGTGGACAACGACCCGTTCCCGGA
GCTGGACTCGTTCCCGGCGTTCCAGGACCCGGCGATGATGATGACGGTGCCCAAGGAGG
AGCAGGTGGACGGCTGCAGCGCCAAGAGCGGCAACCTGTTCGTGGACCTCAGCTACGAC
GACATCCAGGGCATGTACAGCGGCCTCGACATGCTGCCGCCGCCCGGGGAGGACTTCTA
CTCCTCGCTCTTCGCGTCTCCCAGGGTCAAGGGGAACCAGCCCGCCGGAGCCGCCGGGTT
GGGACAGTTCTGA

## 7.6 Maize genes involved in the metabolism regulated by herbivory

**Tab.7. 1: 0.5 h after feeding induction**

| MZ-number | Annotation | fold expression (log10) | p-value | Abbreviation |
|---|---|---|---|---|
| **MZ00000384** | NA | 1.002215099 | 0.01782142 | |
| **MZ00000817** | hypothetical protein {Arabidopsis thaliana} | 1.225074771 | 0.01970904 | |
| **MZ00001133** | putative LHY protein {Oryza sativa} | -1.138721789 | 0.00983245 | TF41 |
| **MZ00001172** | protein kinase domain containing protein {Zea mays} | 1.750609659 | 0.0082661 | |
| **MZ00003452** | putative glutathione transporter {Zea mays} | 1.3412105 | 9.98E-06 | |
| **MZ00003946** | Putative cytochrome P450 {Oryza sativa} | 1.092928293 | 0.02645534 | |
| **MZ00004193** | putative bZIP protein HY5 {Oryza sativa} | -1.058351385 | 0.0153649 | TF44 |
| **MZ00004233** | frataxin {Zea mays} | 1.008195964 | 0.03720526 | |
| **MZ00004875** | NA | 1.432468124 | 0.00013116 | |
| **MZ00005052** | hypothetical protein {Zea mays} | 1.317170145 | 0.00350547 | |
| **MZ00005095** | hypothetical protein {Zea mays} | 1.125868895 | 0.00406344 | |
| **MZ00005101** | PRAS-rich protein {Zea mays} | 1.638643656 | 1.78E-06 | |
| **MZ00005245** | NPK1-related protein kinase-like protein {Oryza sativa} | 1.861273913 | 1.93E-07 | TF9 |
| **MZ00005265** | putative helix-loop-helix DNA-binding protein {Oryza sativa} | 1.85600835 | 1.17E-05 | TF23 |
| **MZ00006071** | auxin Efflux Carrier family protein {Zea mays} | -1.020020493 | 0.00161051 | |
| **MZ00007257** | OSJNBa0088A01.13 {Oryza sativa} | -1.15282516 | 0.00105839 | |
| **MZ00007425** | unknown protein {Oryza sativa} | -1.076852341 | 0.00016534 | |
| **MZ00012919** | bZIP transcription factor family protein {Zea mays} | 1.34531873 | 0.00470068 | |
| **MZ00013307** | hypothetical protein {Zea mays} | -1.427738471 | 0.00554345 | |
| **MZ00013411** | ADP-ribosylation factor-like protein 8B {Zea mays} | 1.821458597 | 6.69E-05 | |
| **MZ00014137** | transcription factor-like {Oryza sativa} | 1.066733794 | 0.02577085 | TF45 |
| **MZ00014229** | pathogenesis-related protein 10 {Zea mays} | -1.887100155 | 0.00376567 | |
| **MZ00014822** | ribulosebisphosphate carboxylase {Zea | 1.473387654 | 0.00313702 | |

| | | | | |
|---|---|---|---|---|
| | mays} | | | |
| **MZ00015015** | putative heat-shock protein {Oryza sativa} | 1.38318122 | 0.00812735 | |
| **MZ00015033** | senescence-associated protein DH {Zea mays} | 1.103383772 | 0.00027801 | |
| **MZ00015377** | beta-amylase {Zea mays} | 1.244890875 | 0.01641968 | |
| **MZ00015673** | DRE binding factor 1 {Zea mays} | 1.015806977 | 0.0073984 | TF40 |
| **MZ00015910** | glycine-rich protein1 {Zea mays} | -1.026106562 | 0.01411353 | |
| **MZ00016732** | plasma membrane intrinsic protein ZmPIP2-6 {Zea mays} | -1.623668308 | 1.57E-05 | |
| **MZ00016805** | uroporphyrin-III C-methyltransferase {Zea mays} | -1.159692634 | 0.04434959 | |
| **MZ00016998** | EF-hand Ca2+-binding protein CCD1 {Zea mays} | 1.896118036 | 9.47E-06 | |
| **MZ00017211** | hypothetical protein {Zea mays} | 1.483682576 | 0.0250197 | |
| **MZ00017335** | glutamine-fructose-6-phosphate transaminase 2 {Arabidopsis thaliana} | 1.194048277 | 0.00062369 | |
| **MZ00017518** | polcalcin Jun o 2 {Zea mays} | 1.393254036 | 0.01588083 | |
| **MZ00018052** | putative adenosine monophosphate binding protein 1 AMPBP1 {Oryza sativa} | 1.101526338 | 0.00050198 | |
| **MZ00018113** | protein kinase domain containing protein {Zea mays} | 1.60640663 | 0.01505394 | |
| **MZ00018291** | hypothetical protein {Zea mays} | -1.221127323 | 0.00023375 | |
| **MZ00018541** | Putative EREBP-like protein {Oryza sativa} | -1.149462727 | 0.00017592 | TF38 |
| **MZ00018568** | hypothetical protein {Zea mays} | 1.267529382 | 0.00927323 | |
| **MZ00018761** | putative Myb-like DNA-binding protein {Oryza sativa} | -1.485146512 | 4.54E-06 | TF7 |
| **MZ00018836** | hypothetical protein {Zea mays} | 1.126756936 | 0.00206509 | |
| **MZ00018917** | iron-phytosiderophore transporter protein yellow stripe 1 {Zea mays} | 3.392152206 | 0.00409997 | |
| **MZ00019090** | aquaporin {Zea mays} | -1.023032661 | 0.00042113 | |
| **MZ00019110** | hypothetical protein {Zea mays} | -1.221032441 | 2.69E-05 | |
| **MZ00019303** | pyrimidine-specific ribonucleoside hydrolase {Zea mays} | -1.34740209 | 0.00665309 | |
| **MZ00019321** | hypothetical protein {Sorghum bicolor} | -1.237836533 | 0.00245584 | |
| **MZ00019475** | anthranilate N-benzoyltransferase protein 1 | -1.042018924 | 0.04482982 | |

| | | | | |
|---|---|---|---|---|
| | {Zea mays} | | | |
| **MZ00019555** | putative 0-deacetylbaccatin III-10-O-acetyl transferase {Oryza sativa} | 1.261594002 | 0.00010906 | |
| **MZ00019908** | putative acid phosphatase unknown protein {Oryza sativa} | -1.530816677 | 0.00931408 | |
| **MZ00019970** | unknown protein {Zea mays} | 1.257489938 | 3.62E-05 | |
| **MZ00020525** | hypothetical protein {Zea mays} | 1.212590669 | 0.0083607 | |
| **MZ00020536** | LHY protein {Zea mays} | -1.021075306 | 5.31E-06 | |
| **MZ00020619** | transcription factor WRKY12 {Oryza sativa} | 1.561235153 | 0.00013374 | TF34 |
| **MZ00020668** | hypothetical protein {Zea mays} | 1.007334146 | 0.00577678 | |
| **MZ00020958** | NA | 1.585036469 | 0.01654144 | |
| **MZ00021033** | trithorax-like {Oryza sativa} | -1.250706715 | 0.0105825 | |
| **MZ00021339** | NA | 1.020539002 | 0.00251806 | |
| **MZ00021743** | hypothetical protein {Sorghum bicolor} | 1.027060954 | 0.00435665 | |
| **MZ00021951** | adenosine 5'-phosphosulfate reductase-like2 {Zea mays} | -1.29807553 | 0.00647109 | |
| **MZ00021963** | lethal(2)denticleless-like protein {Oryza sativa} | -1.03714112 | 0.00079035 | |
| **MZ00022163** | putative 10-deacetylbaccatin III-10-O-acetyl transferase {Oryza sativa} | 1.654173807 | 0.04682672 | |
| **MZ00022180** | hypothetical protein {Zea mays} | 1.768363096 | 8.24E-06 | |
| **MZ00022294** | putative esterase {Oryza sativa} | 1.069100268 | 0.00137146 | |
| **MZ00022466** | OSJNBa0088H09.11 {Oryza sativa} | 1.271769412 | 9.46E-06 | |
| **MZ00022797** | NA | 1.027799084 | 6.31E-05 | |
| **MZ00023298** | hypothetical protein {Zea mays} | 1.261401763 | 4.88E-06 | |
| **MZ00023353** | calmodulin-related protein 2 {Zea mays} | 1.055719312 | 0.00169022 | |
| **MZ00023386** | 60S ribosomal protein L23 {Zea mays} | -1.292527637 | 0.00613443 | |
| **MZ00023975** | unknown protein {Oryza sativa} | 1.375785473 | 0.00621716 | |
| **MZ00023983** | ribonuclease S homolog {Zea mays} | 1.091699664 | 0.0020865 | |
| **MZ00024496** | hypothetical protein {Zea mays} | 1.026059166 | 0.02300198 | |
| **MZ00024615** | unknown protein {Oryza sativa} | -1.168857089 | 0.00031705 | |
| **MZ00025206** | O-methyltransferase BX7 {Zea mays} | 1.418920537 | 0.00028954 | |
| **MZ00025556** | unknown protein {Oryza sativa} | -1.067536688 | 0.00704987 | |
| **MZ00025614** | hypothetical protein {Zea mays} | 1.10482634 | 0.00815805 | |
| **MZ00025768** | glutathione S-transferase GST 20 {Zea | 1.384472158 | 0.02387482 | |

| | | | | |
|---|---|---|---|---|
| | mays} | | | |
| **MZ00025832** | putative bHLH transcription factor {Arabidopsis thaliana} | -1.341431929 | 0.00089563 | TF32 |
| **MZ00025850** | putative protein kinase {Oryza sativa} | 1.016202897 | 0.03443971 | |
| **MZ00025868** | putative katanin {Oryza sativa} | 1.126236573 | 0.04800696 | |
| **MZ00026418** | putative neutral invertase {Oryza sativa} | 1.219947423 | 0.00180269 | |
| **MZ00026538** | ZIM-motif family protein {Zea mays} | 1.917098985 | 0.002039 | |
| **MZ00026596** | ethylene responsive element binding factor3 {Oryza sativa} | 1.15306929 | 8.59E-05 | TF30 |
| **MZ0002666** | putative NAC-domain protein {Oryza sativa} | 1.155732123 | 0.02909881 | TF1 |
| **MZ00026682** | putative alkaline/neutral invertase {Oryza sativa} | 1.091851629 | 0.00755716 | |
| **MZ00027468** | DNA binding protein {Zea mays} | 1.048388472 | 0.01397215 | |
| **MZ00027872** | proline oxidase {Zea mays} | 1.806996704 | 0.00015112 | |
| **MZ00028262** | NA | 1.633725077 | 0.00983358 | |
| **MZ00028561** | hypothetical protein {Zea mays} | -1.146562714 | 0.00532343 | |
| **MZ00028681** | alcohol dehydrogenase 1 {Zea mays} | 1.570977449 | 0.01461834 | |
| **MZ00029025** | hypothetical protein {Zea mays} | 1.203301308 | 0.00884145 | |
| **MZ00029057** | FIERG2 protein {Oryza sativa} | 1.131378278 | 0.00321772 | |
| **MZ00029180** | OSJNBa0088A01.13 {Oryza sativa} | -1.23416586 | 0.00046556 | |
| **MZ00029487** | hypothetical protein {Zea mays} | 1.161214665 | 6.01E-05 | |
| **MZ00029551** | Zinc-finger protein 1 (WZF1) {Triticum aestivum} | 1.052090047 | 0.01293518 | TF43 |
| **MZ00029722** | physical impedance induced protein2 {Zea mays} | 1.315623111 | 0.00248652 | |
| **MZ00029740** | hypothetical protein {Arabidopsis thaliana} | 1.152982708 | 0.00308533 | |
| **MZ00029892** | putative MtN21 {Oryza sativa} | -1.31039007 | 0.00015174 | |
| **MZ00030027** | putative trehalose-6-phosphate synthase {Oryza sativa} | 1.028281634 | 0.00231345 | |
| **MZ00030030** | 3-oxoacyl-synthase III {Zea mays} | 1.015110039 | 0.04052413 | |
| **MZ00030212** | kinesin like protein {Zea mays} | -1.174172327 | 0.00042761 | |
| **MZ00030358** | hypothetical protein {Oryza sativa} | -1.167560121 | 0.00247419 | |
| **MZ00030756** | Centromere/kinetochore protein zw10 homolog {Arabidopsis thaliana} | -1.581729142 | 0.00048224 | |
| **MZ00031007** | NA | 1.69416465 | 1.78E-08 | |

| | | | | |
|---|---|---|---|---|
| **MZ00031212** | unknown protein {Oryza sativa} | 1.119784234 | 0.00265804 | |
| **MZ00031407** | hypothetical protein {Sorghum bicolor} | -1.822478579 | 0.00420278 | |
| **MZ00031793** | AP2 domain containing protein {Zea mays} | 1.230839803 | 5.86E-06 | |
| **MZ00031823** | NPK1-related protein kinase-like protein {Zea mays} | 1.086242091 | 1.81E-05 | |
| **MZ00031906** | calmodulin-related protein 2 {Zea mays} | 1.33262819 | 0.00210969 | |
| **MZ00032136** | 1-deoxy-D-xylulose 5-phosphate synthase 2 (dxs2) {Zea mays} | 1.131918466 | 0.00263036 | |
| **MZ00032666** | OSJNBa0088A01.13 {Oryza sativa} | -1.305099542 | 0.01337902 | |
| **MZ00032725** | hypothetical protein {Zea mays} | -1.103184019 | 0.00729237 | |
| **MZ00032877** | putative phi-1 {Oryza sativa} | 1.159345203 | 0.0026771 | TF39 |
| **MZ00033310** | MPI {Tripsacum dactyloides} | 1.100159165 | 0.04799923 | |
| **MZ00033435** | putative ethylene-responsive elongation factor EF-Ts precursor {Oryza sativa} | 1.418271131 | 0.01793575 | |
| **MZ00033470** | hypothetical protein {Zea mays} | 1.154101928 | 0.00466612 | |
| **MZ00033517** | putative progesterone 5-beta-reductase {Oryza sativa} | 1.176457328 | 0.04221815 | |
| **MZ00033521** | hypothetical protein {Zea mays} | 1.002698778 | 0.0032547 | |
| **MZ00033715** | ZIM-motif family protein {Zea mays} | 2.156032 | 2.92E-05 | |
| **MZ00034421** | Glucan endo-1,3-beta-glucosidase {Zea mays} | -1.136946409 | 0.0177255 | |
| **MZ00035024** | hypothetical protein {Zea mays} | -1.079513099 | 0.04420718 | |
| **MZ00035095** | putative nucleoid DNA-binding protein cnd41 {Oryza sativa} | 1.078103935 | 0.04323517 | TF47 |
| **MZ00035642** | alcohol dehydrogenase 1 {Zea mays} | -1.119794958 | 0.01046085 | |
| **MZ00035750** | adhesive/proline-rich protein {Zea mays} | 1.026133492 | 0.00095019 | |
| **MZ00036129** | NA | -1.028370541 | 0.0104233 | |
| **MZ00036398** | xyloglucan endotransglycosylase homolog {Zea mays} | 1.220899721 | 0.00052941 | |
| **MZ00036475** | secondary cell wall-related glycosyltransferase {Zea mays} | 1.051556788 | 0.02014676 | |
| **MZ00036572** | NA | 1.354812122 | 0.03661717 | |
| **MZ00036593** | putative Formate dehydrogenase {Oryza sativa} | -1.445495348 | 0.00308184 | |
| **MZ00036791** | hypothetical protein {Zea mays} | 1.562801382 | 0.00374966 | |
| **MZ00036920** | hypothetical protein {Zea mays} | 1.249703526 | 0.00021124 | |

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|---|---|---|---|---|
| **MZ00036928** | hypothetical protein {Zea mays} | 1.195779048 | 0.019425 | |
| **MZ00036929** | hypothetical protein {Zea mays} | 1.223658453 | 0.0245274 | |
| **MZ00037013** | putative Bowman-Birk serine protease inhibitor {Zea mays} | -1.841815786 | 0.00037619 | |
| **MZ00037020** | NA | 1.864973044 | 0.03151926 | |
| **MZ00037034** | hypothetical protein {Oryza sativa} | 1.229175526 | 4.45E-05 | |
| **MZ00037045** | NA | -1.25345424 | 0.00528173 | |
| **MZ00037085** | Bowman-Birk type wound-induced proteinase inhibitor WIP1 {Zea mays} | 1.005014501 | 0.01083856 | |
| **MZ00037126** | ZIM-motif family protein {Zea mays} | 1.493327424 | 0.02917107 | |
| **MZ00037480** | putative acid phosphatase unknown protein {Oryza sativa} | -1.641308245 | 0.00428676 | |
| **MZ00037820** | NA | -1.198127036 | 0.00342806 | |
| **MZ00038115** | INDETERMINATE-related protein {Zea mays} | -1.220321247 | 0.00148355 | |
| **MZ00038372** | fatty acid desaturase {Zea mays} | 1.081983612 | 0.04941197 | |
| **MZ00038498** | NA | 1.086691517 | 0.04581955 | |
| **MZ00038664** | histone H1-like protein {Zea mays} | -1.243520794 | 0.00520754 | |
| **MZ00039123** | hypothetical protein {Zea mays} | -1.093423245 | 0.00270615 | |
| **MZ00039124** | hypothetical protein {Zea mays} | -1.0824228 | 0.00356507 | |
| **MZ00039194** | hypothetical protein {Zea mays} | -1.060646094 | 0.00979065 | |
| **MZ00039195** | 40S ribosomal protein S4 {Zea mays} | -1.124162616 | 0.00763094 | |
| **MZ00039280** | cytokinin oxidase 3 {Zea mays} | 1.011312915 | 0.02978865 | |
| **MZ00039375** | NA | -1.02744543 | 0.00097929 | |
| **MZ00040302** | B73 pathogenesis-related protein 2 and GASA-like protein {Zea mays} | 1.084389599 | 0.03956753 | |
| **MZ00040935** | hypothetical protein {Zea mays} | -1.147147725 | 0.03264779 | |
| **MZ00040938** | hypothetical protein {Zea mays} | -1.147922347 | 0.01300695 | |
| **MZ00041038** | histone H1-like protein {Zea mays} | -1.014901845 | 0.01065092 | |
| **MZ00041326** | putative Bowman-Birk serine protease inhibitor {Oryza sativa} | -1.919720012 | 0.00482553 | |
| **MZ00041327** | putative Bowman-Birk serine protease inhibitor {Zea mays} | -2.468488509 | 0.00039523 | |
| **MZ00041500** | water stress inducible protein {Oryza sativa} | -1.108968869 | 5.15E-05 | |
| **MZ00041802** | zinc finger protein {Oryza sativa} | -2.032905738 | 0.0001848 | TF37 |

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|---|---|---|---|---|
| **MZ00041804** | zinc finger protein {Oryza sativa} | -1.389607547 | 2.05E-05 | TF29 |
| **MZ00042096** | adenosine 5'-phosphosulfate reductase-like1 {Zea mays} | -1.011458317 | 0.01433219 | |
| **MZ00042109** | O-methyltransferase BX7 {Zea mays} | 1.167581162 | 0.03113949 | |
| **MZ00042137** | phi-1-like phosphate-induced protein {Zea mays} | 1.244230396 | 7.09E-05 | |
| **MZ00042142** | NA | 1.582124932 | 0.00388343 | |
| **MZ00042242** | adhesive/proline-rich protein {Zea mays} | 1.41680588 | 0.00142954 | |
| **MZ00042304** | protein kinase domain containing protein {Zea mays} | 1.096680047 | 0.0186087 | |
| **MZ00042553** | N-acetyltransferase {Zea mays} | 1.202222391 | 0.01039437 | |
| **MZ00042739** | WRKY transcription factor {Oryza sativa} | 1.015746416 | 0.00129574 | TF26 |
| **MZ00042797** | putative glutathione transporter {Zea mays} | 1.413729425 | 0.00476571 | |
| **MZ00042953** | chlorophyll a/b binding protein {Oryza sativa} | 1.428389379 | 0.0358288 | |
| **MZ00043103** | IAA24 - auxin-responsive Aux/IAA family member {Zea mays} | 1.365004205 | 6.46E-06 | |
| **MZ00043117** | adhesive/proline-rich protein {Zea mays} | 1.098964733 | 0.00040617 | |
| **MZ00043359** | hypothetical protein {Zea mays} | 1.239677815 | 0.04264502 | |
| **MZ00043640** | cytochrome b561 {Zea mays} | -1.083928526 | 0.03009207 | |
| **MZ00043658** | pathogenesis-related protein 4 {Triticum monococcum} | -1.345400846 | 0.00200967 | |
| **MZ00043659** | defence-related protein {Zea mays} | -1.516810411 | 0.01026011 | |
| **MZ00043777** | hypothetical protein {Oryza sativa} | -1.279854642 | 0.0031413 | |
| **MZ00043886** | chitinase {Zea mays} | -1.222589817 | 0.00363474 | |
| **MZ00044190** | allene oxide synthase 1 {Zea mays} | 1.613732798 | 0.00444464 | |
| **MZ00044271** | proline oxidase {Zea mays} | 1.596989502 | 0.00111567 | |
| **MZ00044780** | NA | -1.140434047 | 0.02047268 | |
| **MZ00045574** | NA | 1.140244664 | 0.02483458 | |
| **MZ00048730** | putative immediate-early fungal elicitor protein {Oryza sativa} | 1.10710032 | 0.0101808 | |
| **MZ00052490** | pathogenesis-related protein 10 {Zea mays} | -1.259092359 | 0.00355347 | |
| **MZ00054907** | putative cytochrome P450 {Oryza sativa} | 1.173847891 | 0.00965439 | |
| **MZ00055183** | alpha-expansin {Oryza sativa} | 1.176149036 | 0.01950251 | |
| **MZ00055932** | Bowman-Birk type trypsin inhibitor {Zea mays} | 1.095542955 | 0.00885029 | |

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|---|---|---|---|---|
| **MZ00056440** | hypothetical protein {Zea mays} | 1.125029317 | 0.00991602 | |
| **MZ00056523** | putative phi-1 {Oryza sativa} | 1.370339469 | 0.01270272 | TF42 |
| **MZ00056629** | OSJNBa0088A01.13 {Oryza sativa} | -1.247555126 | 0.04295964 | |
| **MZ00056647** | hypothetical protein {Zea mays} | 2.082786391 | 3.15E-05 | |
| **MZ00056690** | glucan endo-1,3-beta-glucosidase homolog1 {Zea mays} | -1.565978075 | 0.00243899 | |
| **MZ00056902** | unknown protein {Oryza sativa} | 1.311417811 | 0.03255265 | |
| **MZ00056923** | myb-like protein {Oryza sativa} | -1.08667495 | 0.01856965 | TF12 |
| **MZ00057095** | putative UVB-resistance protein UVR8 {Oryza sativa} | -1.299218025 | 0.01303813 | |
| **MZ00057372** | hypothetical protein {Sorghum bicolor} | 2.21483029 | 0.01145302 | |
| **MZ00057436** | putative ZEITLUPE {Oryza sativa} | 1.870414143 | 0.00705078 | |

**Tab.7. 2: 1 h after feeding induction**

| **MZ-number** | **Annotation** | **fold expression (log10)** | **p-value** | **Abbrevation** |
|---|---|---|---|---|
| **MZ00000390** | NA | 1.283945388 | 0.02054797 | |
| **MZ00000666** | lipoxygenase (LOX4) {Zea mays} | 1.371594955 | 7.07E-05 | |
| **MZ00001172** | protein kinase domain containing protein {Zea mays} | 1.612111385 | 0.00795182 | |
| **MZ00001288** | unknown protein {Oryza sativa} | 1.034227483 | 2.61E-05 | |
| **MZ00001464** | NA | 1.577397957 | 0.00642841 | |
| **MZ00003802** | FIP1 {Zea mays} | 1.124553927 | 0.00063602 | |
| **MZ00003819** | putative ethylene-responsive transcriptional coactivator {Oryza sativa} | -1.217149183 | 6.06E-05 | TF24 |
| **MZ00003857** | splicing factor U2af 38 kDa subunit {Zea mays} | 1.030400938 | 0.00290021 | |
| **MZ00003861** | hypothetical protein {Zea mays} | 1.345203399 | 0.03933033 | |
| **MZ00003912** | OSJNBa0008M17.5 {Oryza sativa} | 1.909888997 | 0.0031783 | |
| **MZ00003954** | probable senescence-related protein {Arabidopsis thaliana} | 1.185543681 | 0.01077074 | |
| **MZ00003984** | POZ domain protein family-like {Oryza sativa} | 1.036304983 | 0.02070894 | |
| **MZ00004356** | metal ion binding protein {Zea mays} | 1.058634555 | 0.00601811 | |
| **MZ00004452** | NA | 1.967087637 | 1.55E-05 | |

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|---|---|---|---|---|
| **MZ00005052** | hypothetical protein {Zea mays} | 1.373818608 | 0.00135476 | |
| **MZ00005095** | hypothetical protein {Zea mays} | 1.672661508 | 7.66E-05 | |
| **MZ00005245** | NPK1-related protein kinase-like protein {Oryza sativa} | 1.308123996 | 3.86E-06 | TF9 |
| **MZ00005265** | putative helix-loop-helix DNA-binding protein {Oryza sativa} | 1.559098533 | 2.82E-05 | TF23 |
| **MZ00005899** | terpene synthase 2 {Zea mays} | 1.108941326 | 0.00158642 | |
| **MZ00006068** | glucose-6-phosphate/phosphate translocator 2 {Zea mays} | 1.200192939 | 0.03239775 | |
| **MZ00007376** | CSLC9 {Oryza sativa} | 1.024910794 | 0.02431587 | |
| **MZ00012674** | zinc finger protein 3 {Zea mays} | 2.082671995 | 2.25E-06 | |
| **MZ00012715** | OSJNBa0016O02.24 {Oryza sativa} | 1.192491009 | 8.16E-06 | |
| **MZ00013127** | putative polyprenyl diphosphate synthase {Oryza sativa} | 1.425803569 | 0.02905149 | |
| **MZ00013368** | OSJNBb0059K02.3 {Oryza sativa} | -1.004493294 | 0.01509806 | |
| **MZ00013411** | ADP-ribosylation factor-like protein 8B {Zea mays} | 2.452564965 | 1.15E-06 | |
| **MZ00013555** | hypothetical protein {Zea mays} | 1.113295208 | 0.02862942 | |
| **MZ00013669** | hypothetical protein {Zea mays} | 1.121622079 | 0.01288449 | |
| **MZ00013836** | S-adenosylmethionine decarboxylase {Oryza sativa} | 2.823038792 | 1.28E-05 | |
| **MZ00014129** | annexin P35 {Zea mays} | 1.112943221 | 0.00303161 | |
| **MZ00014229** | pathogenesis-related protein 10 {Zea mays} | -1.384732145 | 0.01446172 | |
| **MZ00014287** | hypothetical protein {Zea mays} | 1.206862355 | 0.00013999 | |
| **MZ00014350** | pnFL-2 {Zea mays} | 1.062725415 | 0.00298286 | |
| **MZ00014372** | MTN 3 {Zea mays} | 1.976927034 | 0.00690417 | |
| **MZ00014377** | nodulation homolog 1 {Zea mays} | -1.261717145 | 0.01724428 | |
| **MZ00014737** | UDP-glucose-4-epimerase {Zea mays} | 1.22993013 | 0.00029907 | |
| **MZ00014772** | alcohol dehydrogenase 1 {Zea mays} | 2.037565425 | 2.49E-06 | |
| **MZ00014943** | anthranilate synthase alpha 2 subunit {Oryza sativa} | 1.234507649 | 0.00923884 | |
| **MZ00015033** | senescence-associated protein DH {Zea mays} | 1.152786027 | 8.22E-05 | |
| **MZ00015176** | unknown protein {Oryza sativa} | 1.434562773 | 1.72E-05 | |
| **MZ00015354** | putative protein kinase {Oryza sativa} | 1.266495161 | 0.04028384 | |
| **MZ00015377** | beta-amylase {Zea mays} | 1.262178892 | 0.00925194 | |

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|---|---|---|---|---|
| **MZ00015378** | putative chloroplast-targeted beta-amylase {Oryza sativa} | 1.132113694 | 0.03585699 | |
| **MZ00015582** | NA | -1.092305784 | 0.01211844 | |
| **MZ00015918** | MTD1 {Zea mays} | 1.607148225 | 9.52E-06 | |
| **MZ00016344** | membrane related protein {Oryza sativa} | 1.166804609 | 0.00378905 | |
| **MZ00016498** | disease resistance response protein-like {Oryza sativa} | -1.384778856 | 0.00944444 | |
| **MZ00016555** | unknown {Arabidopsis thaliana} | -1.401387587 | 0.03947377 | |
| **MZ00016666** | hypothetical protein {Zea mays} | 1.90760065 | 2.94E-05 | |
| **MZ00016732** | plasma membrane intrinsic protein 2 ZmPIP2-6 {Zea mays} | -1.180412691 | 0.00014935 | |
| **MZ00016998** | EF-hand Ca2+-binding protein CCD1 {Zea mays} | 1.262560009 | 0.00021398 | |
| **MZ00017265** | MtN3-like protein {Arabidopsis thaliana} | 1.221856304 | 0.00151593 | |
| **MZ00017300** | hypothetical protein {Zea mays} | 1.752330241 | 1.09E-05 | |
| **MZ00017310** | zinc finger protein-like {Oryza sativa} | 1.028489903 | 0.00021037 | TF27 |
| **MZ00017335** | glutamine-fructose-6-phosphate transaminase 2 {Arabidopsis thaliana} | 1.475060334 | 4.04E-05 | |
| **MZ00017432** | ULT transcription factor {Zea mays} | 1.195600214 | 1.14E-06 | |
| **MZ00017456** | CBL-interacting protein kinase {Zea mays} | 1.46120518 | 7.19E-06 | |
| **MZ00017547** | putative HAK2 {Oryza sativa} | 1.017351697 | 0.00783223 | |
| **MZ00017664** | putative heterogeneous nuclear ribonucleoprotein A1 {Oryza sativa} | 1.085573828 | 0.04407853 | |
| **MZ00017966** | hypothetical protein {Zea mays} | 1.045616267 | 0.0392025 | |
| **MZ00018113** | protein kinase domain containing protein {Zea mays} | 1.315325787 | 0.02639512 | |
| **MZ00018241** | ribosome-inactivating protein {Zea mays} | 1.469590655 | 0.01597708 | |
| **MZ00018300** | OJ990528_30.9 {Oryza sativa} | -1.217754385 | 9.31E-05 | |
| **MZ00018541** | Putative EREBP-like protein {Oryza sativa} | 1.311906007 | 2.07E-05 | TF38 |
| **MZ00018568** | hypothetical protein {Zea mays} | 2.057352534 | 0.00011444 | |
| **MZ00018741** | putative cytochrome P450 reductase {Oryza sativa} | 1.500747678 | 0.03564088 | |
| **MZ00018761** | putative Myb-like DNA-binding protein {Oryza sativa} | 1.04066563 | 7.01E-05 | TF7 |
| **MZ00018825** | putative transcription factor {Oryza sativa} | 1.186320278 | 0.0136534 | |
| **MZ00018836** | hypothetical protein {Zea mays} | 2.717729317 | 1.42E-07 | |

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|---|---|---|---|---|
| **MZ00018837** | MAPK6 {Oryza sativa} | 1.236381319 | 0.01265904 | |
| **MZ00019122** | deoxyribodipyrimidine photolyase family protein-like {Oryza sativa} | 1.007329577 | 0.01298166 | |
| **MZ00019182** | hypothetical protein {Oryza sativa} | 1.175688268 | 8.60E-05 | |
| **MZ00019244** | putative l-asparaginase {Oryza sativa} | -1.64736429 | 0.0425309 | |
| **MZ00019278** | hypothetical protein {Zea mays} | 1.281599732 | 0.00042927 | |
| **MZ00019292** | hypothetical protein {Zea mays} | 1.222861576 | 0.00041217 | |
| **MZ00019416** | hypothetical protein {Zea mays} | -1.126745108 | 0.04888914 | |
| **MZ00019442** | riboflavin biosynthesis protein ribAB {Zea mays} | 1.364170942 | 0.00525107 | |
| **MZ00019616** | FIP1 {Zea mays} | 1.119114173 | 0.00024829 | |
| **MZ00019632** | calmodulin-like protein {Pennisetum ciliare} | 1.483912516 | 0.00038138 | |
| **MZ00019729** | terpene synthase 2 {Zea mays} | 2.110081091 | 0.00039675 | |
| **MZ00019752** | hypothetical protein {Zea mays} | -1.012347052 | 0.00919395 | |
| **MZ00019821** | long cell-linked locus protein {Zea mays} | 1.10562925 | 0.00960834 | |
| **MZ00019869** | putative phospholipid cytidylyltransferase {Oryza sativa} | 1.102652854 | 0.00316015 | |
| **MZ00019880** | NA | -1.365101661 | 0.00882452 | |
| **MZ00019894** | stem 28 kDa glycoprotein {Zea mays} | 2.152361363 | 0.00252506 | |
| **MZ00019908** | unknown protein {Oryza sativa} | -1.14481807 | 0.02708139 | |
| **MZ00019970** | hypothetical protein {Zea mays} | 1.643084916 | 7.92E-07 | |
| **MZ00020105** | hypothetical protein {Zea mays} | 1.280143412 | 0.00370592 | |
| **MZ00020210** | hypothetical protein {Zea mays} | 1.972645072 | 3.63E-05 | |
| **MZ00020230** | epoxide hydrolase 2 {Zea mays} | 1.804424994 | 0.00386692 | |
| **MZ00020243** | AT3g52870/F8J2_40 {Arabidopsis thaliana} | 1.035209885 | 0.0334502 | |
| **MZ00020448** | OSJNBa0072K14.9 {Oryza sativa} | 1.403011903 | 0.01409396 | |
| **MZ00020466** | ATSWI3A {Zea mays} | 1.108646789 | 0.00938197 | |
| **MZ00020525** | hypothetical protein {Zea mays} | 1.400286469 | 0.00174502 | |
| **MZ00020668** | hypothetical protein {Zea mays} | 1.496873511 | 0.00012698 | |
| **MZ00020968** | putative lipase class 3 family protein {Oryza sativa} | 1.508826516 | 0.00343915 | |
| **MZ00021254** | OSJNBa0065B15.8 {Oryza sativa} | 1.510637757 | 0.04090632 | |
| **MZ00021379** | putative centromere protein {Oryza sativa} | 1.214169153 | 9.16E-05 | |
| **MZ00021385** | putative cytochrome P450 reductase {Oryza sativa} | 1.287843366 | 0.00198669 | |
| **MZ00021537** | hypothetical protein {Zea mays} | 1.063738542 | 0.00974371 | |

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|---|---|---|---|---|
| **MZ00021587** | cell wall invertase {Zea mays} | 1.512509917 | 0.01280814 | |
| **MZ00021860** | hypothetical protein {Zea mays} | 1.047594001 | 0.00651296 | |
| **MZ00021878** | putative transposase {Zea mays} | 1.102355582 | 0.00892014 | |
| **MZ00022163** | putative 10-deacetylbaccatin III-10-O-acetyl transferase {Oryza sativa} | 2.718399527 | 0.00164784 | |
| **MZ00022294** | putative esterase {Oryza sativa} | 1.152777866 | 0.00035921 | |
| **MZ00022380** | unknown protein {Oryza sativa} | 1.56001253 | 0.03149321 | |
| **MZ00022582** | peroxidase 1 {Zea mays} | 1.115187766 | 0.00077015 | |
| **MZ00022690** | hypothetical protein {Zea mays} | 1.195249585 | 0.00263689 | |
| **MZ00022994** | allene oxide synthase 1{Zea mays} | 1.403238039 | 3.53E-06 | |
| **MZ00023013** | unknown protein {Oryza sativa} | 1.042821796 | 0.00490058 | |
| **MZ00023027** | starch phosphorylase 2 precursor {Zea mays} | 1.108487039 | 0.01001447 | |
| **MZ00023228** | dihydroflavonol-4-reductase {Zea mays} | 1.088088549 | 0.01178162 | |
| **MZ00023318** | putative prephenate dehydratase {Oryza sativa} | 1.438070495 | 6.39E-06 | |
| **MZ00023327** | putative sialin {Oryza sativa} | 1.643781238 | 0.04215142 | |
| **MZ00023353** | calmodulin-related protein 2 {Zea mays} | 1.054071243 | 0.0008588 | |
| **MZ00023367** | Metallothionein-like protein type 2 {Zea mays} | -1.154877051 | 0.00818746 | |
| **MZ00023404** | S-adenosylmethionine decarboxylase proenzyme {Zea mays} | 1.629622925 | 0.04374811 | |
| **MZ00023441** | S-adenosylmethionine synthetase 1 {Zea mays} | 1.270714834 | 0.00636249 | |
| **MZ00023501** | pnFL-2 {Zea mays} | 1.222604249 | 0.02241659 | |
| **MZ00023529** | hypothetical protein {Zea mays} | -1.011090527 | 0.0291208 | |
| **MZ00023975** | unknown protein {Oryza sativa} | 1.357257807 | 0.00380023 | |
| **MZ00023983** | ribonuclease S homolog {Zea mays} | 1.348549183 | 0.00017676 | |
| **MZ00024219** | expressed protein {Oryza sativa} | 1.217143239 | 0.01751258 | |
| **MZ00024302** | hypothetical protein {Asparagus officinalis} | 1.994609619 | 0.00186067 | |
| **MZ00024626** | ETTIN-like auxin response factor {Triticum aestivum} | 1.273105681 | 7.67E-06 | TF20 |
| **MZ00024934** | beta-glucosidase {Musa acuminata} | 1.281155629 | 0.0285818 | |
| **MZ00025068** | hypothetical protein {Zea mays} | 1.036389328 | 0.01519457 | |
| **MZ00025407** | polyamine oxidase1 {Zea mays} | 1.287782744 | 0.00324827 | |
| **MZ00025614** | hypothetical protein {Zea mays} | 2.226268668 | 1.07E-05 | |
| **MZ00025698** | MATE family protein {Zea mays} | 1.143548408 | 0.0066219 | |

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|---|---|---|---|---|
| **MZ00025768** | glutathione S-transferase GST 20 {Zea mays} | 1.835870959 | 0.00260985 | |
| **MZ00025872** | hypothetical protein {Zea mays} | 1.461184682 | 0.00127812 | |
| **MZ00026064** | hypothetical protein {Zea mays} | 1.33130622 | 0.00212193 | |
| **MZ00026277** | hypothetical protein {Zea mays} | 1.137972273 | 0.00147281 | |
| **MZ00026471** | anthranilate synthase alpha 1 subunit {Oryza sativa} | 2.021441239 | 0.00038029 | |
| **MZ00026538** | ZIM-motif family protein {Zea mays} | 2.940955093 | 2.11E-05 | |
| **MZ00026661** | putative NAC-domain protein {Oryza sativa} | 1.388006535 | 0.00667882 | TF1 |
| **MZ00026936** | kelch repeat-containing F-box-like {Oryza sativa} | 1.843083594 | 0.00010782 | |
| **MZ00027105** | putative Bowman-Birk serine protease inhibitor {Oryza sativa} | 2.417900238 | 9.50E-07 | |
| **MZ00027775** | putative branched-chain alpha-keto acid decarboxylase E1 beta subunit {Oryza sativa} | 1.482827774 | 0.00065103 | |
| **MZ00028024** | phosphatase subunit g4-1 {Zea mays} | 1.0955425 | 0.04574018 | |
| **MZ00028203** | hypothetical protein {Zea mays} | 1.267265703 | 0.00069567 | |
| **MZ00028357** | CBL-interacting protein kinase{Zea mays} | 1.92912251 | 1.96E-07 | TF14 |
| **MZ00028712** | putative thioredoxin {Oryza sativa} | 1.145237639 | 2.24E-05 | |
| **MZ00028745** | surfeit locus protein 2 containing protein {Zea mays} | 1.041294892 | 0.00316561 | |
| **MZ00028821** | putative plastidic phosphoglucomutase {Oryza sativa} | 1.366750839 | 0.03769162 | |
| **MZ00028873** | putative mitochondrial carrier protein {Oryza sativa} | 1.036433503 | 3.19E-06 | |
| **MZ00028934** | heavy-metal associated domain containing protein {Zea mays} | -1.125135879 | 0.00036736 | |
| **MZ00029020** | aldose reductase {Zea mays} | 1.00128915 | 0.01748418 | |
| **MZ00029084** | hypothetical protein {Zea mays} | -1.454682251 | 0.01461623 | |
| **MZ00029120** | hypothetical protein {Zea mays} | -1.223869948 | 0.03174235 | |
| **MZ00029180** | OSJNBa0088A01.13 {Oryza sativa} | 2.055566334 | 1.16E-06 | |
| **MZ00029195** | putative phosphoribosyl pyrophosphate synthase {Oryza sativa} | 1.121328523 | 0.00837507 | |
| **MZ00029209** | putative molybdenum cofactor biosynthesis protein A {Oryza sativa} | 1.069362721 | 0.03204676 | |
| **MZ00029217** | hypothetical protein {Zea mays} | 1.205969411 | 0.00166739 | |
| **MZ00029560** | phytocystatin {Actinidia deliciosa;} | 2.15324457 | 0.00082834 | |

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|---|---|---|---|---|
| **MZ00029568** | ZIM-motif family protein {Zea mays} | 1.236126614 | 0.00034215 | |
| **MZ00029614** | NA | 1.1828159 | 0.00033281 | |
| **MZ00030493** | ethylene-responsive transcription factor 3 {Zea mays} | 1.0290928 | 0.00055539 | |
| **MZ00030505** | putative GTP-binding protein ERG {Oryza sativa} | 1.522171526 | 0.00361779 | |
| **MZ00030552** | catalytic/hydrolase {Zea mays} | 1.58166467 | 0.0038112 | |
| **MZ00030705** | putative protein {Arabidopsis thaliana} | -1.060547377 | 0.01990202 | |
| **MZ00030776** | calcium binding EF-hand protein {Zea mays} | -1.005686155 | 0.02811677 | |
| **MZ00030874** | receptor-like kinase {Zea mays} | 1.118536292 | 0.0030828 | |
| **MZ00030879** | chaperone protein dnaJ 11 {Zea mays} | 1.993290211 | 7.95E-05 | |
| **MZ00030891** | VQ motif family protein {Zea mays} | -1.15284514 | 0.03456738 | |
| **MZ00030973** | putative NAC-domain protein {Oryza sativa} | 1.228642896 | 0.00054843 | |
| **MZ00031002** | NA | 1.081530113 | 0.00127147 | |
| **MZ00031039** | hypothetical protein {Zea mays} | 1.031826621 | 0.00112108 | |
| **MZ00031103** | probable integral membrane protein {Oryza sativa} | 1.014615406 | 0.02251413 | |
| **MZ00031189** | putative genetic modifier {Oryza sativa} | 1.208632916 | 0.00664902 | |
| **MZ00031225** | At3g54650/T5N23_10 {Arabidopsis thaliana} | 1.204296929 | 0.00773626 | |
| **MZ00031356** | unknown protein {Oryza sativa} | 1.658705941 | 7.41E-05 | |
| **MZ00031823** | NPK1-related protein kinase-like protein {Zea mays} | 1.361725316 | 5.83E-07 | |
| **MZ00031832** | glutathione transferase {Hordeum vulgare subsp. vulgare} | 1.680984351 | 4.92E-05 | |
| **MZ00031906** | calmodulin-related protein 2 {Zea mays} | 1.550046777 | 0.0003066 | |
| **MZ00032043** | anthranilic acid methyltransferase 3 {Zea mays} | 1.32976498 | 0.00210084 | |
| **MZ00032061** | ADP-glucose pyrophosphorylase large subunit {Zea mays} | 1.465354027 | 0.00175227 | |
| **MZ00032136** | 1-deoxy-D-xylulose 5-phosphate synthase 2 (dxs2) {Zea mays} | 2.440654849 | 7.70E-07 | |
| **MZ00032170** | putative centromere protein {Oryza sativa} | 1.985916131 | 0.00130496 | |
| **MZ00032240** | indole-3-glycerol phosphate synthase {Zea mays} | 1.672229808 | 0.00023867 | |
| **MZ00032294** | transferase, tranferring glykosyl groups {Zea mays } | 1.043999485 | 5.68E-05 | |

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|---|---|---|---|---|
| **MZ00032358** | hypothetical protein {Zea mays} | 1.222266689 | 0.01935675 | |
| **MZ00032391** | putative tocopherol polyprenyltransferase {Oryza sativa} | 1.329069463 | 0.00689361 | |
| **MZ00032415** | putative RNA recognition motif (RRM)-containing protein {Oryza sativa} | 1.073694857 | 0.00030667 | |
| **MZ00032666** | OSJNBa0088A01.13 {Oryza sativa} | 2.047911387 | 0.00027915 | |
| **MZ00032709** | hydrolase, alpha/beta fold family-like {Oryza sativa} | 1.499271698 | 0.03191198 | |
| **MZ00032756** | DEAD/DEAH box helicase-like {Oryza sativa} | 1.164009341 | 0.01197905 | |
| **MZ00032999** | indole-3-glycerol phosphate lyase {Zea mays} | 1.215371277 | 0.01163255 | |
| **MZ00033042** | hypothetical protein {Zea mays} | 1.38304137 | 0.00011616 | |
| **MZ00033225** | hypothetical protein {Zea mays} | -1.047186897 | 0.03503323 | |
| **MZ00033310** | MPI {Tripsacum dactyloides} | 2.352504023 | 0.00019555 | |
| **MZ00033313** | histone H2A {Saccharomyces cerevisiae} | -1.145249522 | 0.01776911 | |
| **MZ00033383** | hypothetical protein {Zea mays} | 1.075793107 | 0.0040306 | |
| **MZ00033390** | DNA binding protein {Zea mays} | 1.96697149 | 1.57E-07 | |
| **MZ00033551** | Chloroplast 30S ribosomal protein S12 {Zea mays} | 1.510108354 | 0.0229258 | |
| **MZ00033552** | psaC gene {Zea mays} | 1.175663107 | 0.00223934 | |
| **MZ00033637** | 3-N-debenzoyl-2-deoxytaxol N-benzoyltransferase {Zea mays} | 2.037004599 | 0.00012992 | |
| **MZ00033715** | hypothetical protein {Oryza sativa} | 2.525061974 | 2.14E-06 | |
| **MZ00034220** | p53 binding protein-like {Oryza sativa} | 1.053557067 | 0.00381158 | |
| **MZ00034292** | S-adenosylmethionine synthetase 1 {Oryza sativa} | 1.171875086 | 0.03257128 | |
| **MZ00034308** | natterin 3 precursor {Thalassophryne nattereri} | 1.788825543 | 0.00369945 | |
| **MZ00034328** | putative branched-chain alpha keto-acid dehydrogenase E1 alpha subunit {Arabidopsis thaliana} | 1.453173361 | 0.00088584 | |
| **MZ00034331** | 2-oxoglutarate-dependent oxygenase {Zea mays} | 1.039943233 | 0.00087375 | |
| **MZ00034354** | putative RNA-binding protein {Oryza sativa} | 1.237627075 | 0.0198947 | |
| **MZ00034379** | unknown protein {Oryza sativa} | 1.228736771 | 0.03987185 | |
| **MZ00034402** | allene oxide synthase 1{Zea mays} | 1.517704882 | 9.24E-05 | |

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|---|---|---|---|---|
| **MZ00034412** | xyloglucan endotransglycosylase homolog {Zea mays} | 1.314451747 | 0.01393762 | |
| **MZ00034828** | NAD(P)H-quinone oxidoreductase chain 5 {Zea mays} | 1.440580128 | 0.00391932 | |
| **MZ00034831** | NAD(P)H-quinone oxidoreductase chain I {Zea mays} | 1.474552195 | 0.00813793 | |
| **MZ00034833** | NAD(P)H-quinone oxidoreductase chain K {Zea mays} | 1.424660392 | 0.02963362 | |
| **MZ00034834** | Apocytochrome f precursor {Zea mays} ^\|^GB\|CAA60298.1\|902234\|ZMA86563 cyt-TRUNCATED- | 1.67830938 | 0.00412018 | |
| **MZ00034838** | PSI P700 apoprotein A1 {Zea mays} | 1.107333632 | 0.00408091 | |
| **MZ00034839** | Photosystem I P700 chlorophyll A apoprotein A2 (PsaB) (PSI-B) {Zea mays} | 1.293290796 | 0.00485007 | |
| **MZ00034840** | psaC gene {Zea mays} | 1.055290493 | 0.00423838 | |
| **MZ00034841** | psaI gene {Zea mays} | 1.722333399 | 0.0009648 | |
| **MZ00034843** | Photosystem Q(B) protein {Zea mays} | 1.311383428 | 0.02994731 | |
| **MZ00034845** | Photosystem II 44 kDa reaction center protein {Zea mays} | 2.698661677 | 9.57E-06 | |
| **MZ00034846** | Photosystem II D2 protein {Zea mays} | 1.011636158 | 0.00437641 | |
| **MZ00034847** | cytochrome b559 alpha chain {Oryza sativa} | 1.161035732 | 0.031754 | |
| **MZ00034848** | cytochrome b559 beta chain {Oryza sativa} | 1.388158936 | 0.00833179 | |
| **MZ00034849** | photosystem II phosphoprotein psbH {Zea mays} | 1.313356163 | 0.03218212 | |
| **MZ00034851** | Photosystem II reaction center J protein {Zea mays} | 1.790096826 | 0.00083462 | |
| **MZ00034856** | Ribulose bisphosphate carboxylase large chain precursor {Zea mays} | 2.873669082 | 0.00012187 | |
| **MZ00034865** | ribosomal protein L33 {Zea mays} | 1.145953078 | 0.02387387 | |
| **MZ00034866** | ribosomal protein L36 {Oryza sativa} | 1.187284713 | 0.0102146 | |
| **MZ00034867** | DNA-directed RNA polymerase alpha chain {Zea mays} | 1.672580203 | 0.00543532 | |
| **MZ00034871** | Chloroplast 30S ribosomal protein S11 {Zea mays} | 1.78226719 | 0.00127735 | |
| **MZ00034872** | photosystem II subunit T {Narcissus elegans} | 2.262354172 | 0.0002624 | |
| **MZ00034873** | chloroplast 30S ribosomal protein S14 {Zea | 1.1616309 | 0.00066217 | |

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|---|---|---|---|---|
| | mays} | | | |
| **MZ00034874** | ribosomal protein S15 {Saccharum officinarum} | 1.285204464 | 0.00033142 | |
| **MZ00034881** | Chloroplast 30S ribosomal protein S4 {Zea mays} | 1.313624596 | 0.00896407 | |
| **MZ00034884** | NA | 1.158495359 | 0.01454772 | |
| **MZ00035054** | putative zinc finger protein {Oryza sativa} | 1.48720279 | 0.03209545 | |
| **MZ00035057** | NA | 1.133754204 | 0.00435236 | |
| **MZ00035071** | NA | 1.050473757 | 0.01624994 | |
| **MZ00035114** | phospho-2-dehydro-3-deoxyheptonate aldolase 1 {Zea mays} | 1.16485242 | 0.00012713 | |
| **MZ00035366** | Alanine aminotransferase 2 {Panicum miliaceum} | 1.087174227 | 0.03855972 | |
| **MZ00035453** | hypothetical protein {Zea mays} | 1.257113946 | 0.00022239 | |
| **MZ00035506** | hypothetical protein {Zea mays} | 2.400747194 | 0.00109718 | |
| **MZ00035543** | hypothetical protein {Zea mays} | -1.49922424 | 0.02218476 | |
| **MZ00035555** | putative senescence-associated protein {Pisum sativum} | 1.564696139 | 0.00468348 | |
| **MZ00035606** | phosphoglycerate mutase {Zea mays} | 1.21897855 | 0.01659736 | |
| **MZ00035637** | NA | 1.515364506 | 0.03228395 | |
| **MZ00035640** | non-photosynthetic NADP-malic enzyme {Zea mays} | 1.440170074 | 0.01796981 | |
| **MZ00035685** | NA | 1.015336271 | 0.04670126 | |
| **MZ00035703** | BLE1 protein {Oryza sativa} | -2.299274466 | 0.01335693 | |
| **MZ00035708** | putative senescence-associated protein {Pisum sativum} | 1.752899753 | 0.02869505 | |
| **MZ00035715** | putative senescence-associated protein {Pisum sativum} | 1.248414714 | 0.02925646 | |
| **MZ00035731** | putative senescence-associated protein {Pisum sativum} | 2.117231965 | 0.00162205 | |
| **MZ00035752** | probable cytochrome P450 monooxygenase {Zea mays} | 1.106080406 | 0.03558492 | |
| **MZ00035753** | hypothetical protein {Zea mays} | 2.44659364 | 0.00022346 | |
| **MZ00035770** | putative senescence-associated protein {Pisum sativum} | 1.58566971 | 0.019657 | |
| **MZ00035787** | unnamed protein product {Kluyveromyces | 2.344711357 | 0.01282742 | |

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|---|---|---|---|---|
| | lactis NRRL Y-1140} | | | |
| **MZ00035813** | putative zinc finger protein | 1.053917829 | 0.02734094 | |
| **MZ00035825** | unnamed protein product | 2.112581184 | 0.01905008 | |
| **MZ00035833** | unnamed protein product | 1.972376292 | 0.00081464 | |
| **MZ00035834** | unnamed protein product | 1.942359748 | 0.00364203 | |
| **MZ00035840** | putative senescence-associated protein {Pisum sativum} | 1.662696715 | 0.01051349 | |
| **MZ00035844** | unnamed protein product | 2.238306542 | 0.00061687 | |
| **MZ00035848** | hypothetical protein {Oryza sativa} | 1.395434545 | 0.00154134 | |
| **MZ00035860** | GRAB1 protein {Triticum sp.} | 1.024494015 | 0.01022381 | |
| **MZ00035947** | putative NAC-domain protein {Oryza sativa} | 1.60998083 | 9.97E-06 | TF22 |
| **MZ00035980** | NAC-like protein {Zea mays} | 1.135388343 | 0.00118448 | |
| **MZ00036019** | putative NAC-domain protein {Oryza sativa} | 1.595205937 | 5.76E-07 | TF51 |
| **MZ00036046** | triacylglycerol lipase like protein {Zea mays} | 1.113995786 | 0.00047973 | |
| **MZ00036073** | lichenase-2 {Zea mays} | 1.174966934 | 0.01802089 | |
| **MZ00036084** | mitochondrial 2-oxoglutarate/malate carrier {Zea mays} | 1.052232967 | 0.01485252 | |
| **MZ00036109** | VTC2 {Zea mays} | 1.273763672 | 0.01041465 | |
| **MZ00036162** | rRNA promoter binding protein {Rattus norvegicus} | 1.46208632 | 0.01325462 | |
| **MZ00036167** | hypothetical protein {Sorghum bicolor} | 1.375199353 | 0.03189078 | |
| **MZ00036200** | NA | 1.050032387 | 0.04696438 | |
| **MZ00036203** | histone one (H1) 101 {Zea mays} | 2.081158338 | 0.00056666 | |
| **MZ00036205** | putative senescence-associated protein {Pisum sativum} | 1.656698754 | 0.00773435 | |
| **MZ00036243** | granule bound starch synthase 2a precursor {Zea mays} | 1.496744711 | 0.00659298 | |
| **MZ00036263** | ribosomal protein L3 {Triticum aestivum} | 1.08633943 | 0.00230476 | |
| **MZ00036264** | putative senescence-associated protein {Pisum sativum} | 1.822211512 | 0.00884855 | |
| **MZ00036265** | unnamed protein product | 2.057588987 | 0.04180248 | |
| **MZ00036295** | unnamed protein product | 2.731276682 | 0.00017084 | |
| **MZ00036308** | unnamed protein product | 2.067413012 | 0.02079413 | |
| **MZ00036332** | Sucrose-Phosphate Synthase {Zea mays} | -1.071567807 | 0.03737248 | |
| **MZ00036448** | NA | 1.0929174 | 0.00495925 | |
| **MZ00036449** | S-adenosylmethionine decarboxylase 2 {Zea | 1.979322835 | 0.00638583 | |

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| | mays} | | | |
| **MZ00036454** | putative auxin efflux carrier (PIN1c) {Zea mays} | 2.045271689 | 0.0014535 | |
| **MZ00036455** | hypothetical protein {Zea mays} | 1.97766129 | 0.01019146 | |
| **MZ00036457** | alanine aminotransferase 2 {Zea mays} | 1.197484877 | 0.04131038 | |
| **MZ00036460** | LOL3 {Zea mays} | 1.972315037 | 0.00538262 | |
| **MZ00036485** | nicotianamine synthase 3 {Zea mays} | 2.123606012 | 0.00044426 | |
| **MZ00036498** | hypothetical protein {Sorghum bicolor} | 1.522914588 | 0.0259925 | |
| **MZ00036513** | putative senescence-associated protein {Pisum sativum} | 1.862190258 | 0.00706775 | |
| **MZ00036519** | putative fructose-bisphosphate aldolase {Oryza sativa} | 1.751127213 | 0.04497906 | |
| **MZ00036530** | unnamed protein product | 1.571360192 | 0.04585194 | |
| **MZ00036531** | hypothetical protein {Oryza sativa} | 1.032160685 | 0.00956812 | |
| **MZ00036584** | NA | 2.337368374 | 1.31E-07 | |
| **MZ00036593** | putative Formate dehydrogenase, mitochondrial precursor {Oryza sativa} | -1.760714531 | 0.00032591 | |
| **MZ00036758** | hypothetical protein {Zea mays} | 1.365868883 | 1.79E-05 | |
| **MZ00036778** | putative chloroplast-targeted beta-amylase {Oryza sativa} | 2.200249039 | 0.0002554 | |
| **MZ00036791** | OSJNBa0079A21.19 {Oryza sativa} | 2.023074532 | 0.00024511 | |
| **MZ00036819** | putative senescence-associated protein {Pisum sativum} | 1.816533685 | 0.00371414 | |
| **MZ00036829** | putative senescence-associated protein {Pisum sativum} | 1.448834749 | 0.01487503 | |
| **MZ00036845** | unnamed protein product | 1.718543049 | 0.02186395 | |
| **MZ00036847** | Ac1147 {Rattus norvegicus} | 1.589239801 | 0.01601009 | |
| **MZ00036849** | zinc finger protein 7 {Zea mays} | 1.074150196 | 0.03513485 | |
| **MZ00036918** | CDH1-D {Gallus gallus} | 1.837356235 | 0.02726923 | |
| **MZ00036934** | unnamed protein product | 2.551219889 | 0.00051638 | |
| **MZ00037011** | NA | 1.009418981 | 0.01122824 | |
| **MZ00037037** | unnamed protein product | 1.586973978 | 0.02819656 | |
| **MZ00037085** | Bowman-Birk type wound-induced proteinase inhibitor WIP1 {Zea mays} | 2.449247951 | 2.32E-06 | |
| **MZ00037115** | OSJNBb0059K02.4 {Oryza sativa} | 1.016379381 | 3.52E-05 | |
| **MZ00037253** | subtilisin/chymotrypsin inhibitor {Zea mays} | 1.002151325 | 0.04928815 | |

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|---|---|---|---|---|
| **MZ00037281** | lichenase 2 {Zea mays} | 1.071845496 | 0.02822171 | |
| **MZ00037304** | terpene synthase 2 {Zea mays} | 2.047985944 | 7.84E-05 | |
| **MZ00037403** | alanine aminotransferase {Zea mays} | 1.17656431 | 0.04541594 | |
| **MZ00037469** | dehydrin {Zea mays} | 1.173895068 | 0.00718839 | |
| **MZ00037470** | glutathione S-transferase:ISOTYPE=IV {Zea mays} | -1.013658351 | 0.01327121 | |
| **MZ00037600** | hypothetical protein {Zea mays} | 2.958693279 | 1.37E-07 | |
| **MZ00037902** | UDP-glucose-4-epimerase {Zea mays} | 1.00335287 | 0.00679671 | |
| **MZ00038047** | adenine nucleotide translocator {Zea mays} | 1.215160816 | 0.04819532 | |
| **MZ00038068** | plasma membrane intrinsic protein2 {Zea mays} | 1.520175078 | 0.01824837 | |
| **MZ00038276** | catalytic/hydrolase {Zea mays} | 1.23163918 | 0.00024122 | |
| **MZ00038457** | ferredoxin-1 {Zea mays} | -1.106050548 | 0.03001737 | |
| **MZ00038646** | ubiquitin-like protein 5 {Zea mays} | 1.189879144 | 0.03871616 | |
| **MZ00038776** | hypothetical protein {Zea mays} | 1.024193973 | 0.01034773 | |
| **MZ00038794** | elongation factor 1alpha {Zea mays} | 1.183934964 | 0.0020084 | |
| **MZ00039156** | hypothetical protein {Zea mays} | 1.053561032 | 0.01248237 | |
| **MZ00039234** | glyceraldehyde-3-phosphate dehydrogenase {Zea mays} | 1.0047173 | 0.0240705 | |
| **MZ00039285** | alpha-zein protein {Zea mays} | 2.081110772 | 0.00350721 | |
| **MZ00039367** | hypothetical protein {Zea mays} | 1.379724837 | 0.0495681 | |
| **MZ00039711** | phosphoglucomutase 2 {Zea mays} | 1.714834307 | 0.03606689 | |
| **MZ00039722** | hypothetical protein {Zea mays} | 1.071785258 | 0.01239221 | |
| **MZ00039734** | beta-glucosidase {Zea mays} | 1.161789806 | 0.0019116 | |
| **MZ00039764** | Bowman-Birk type wound-induced proteinase inhibitor WIP1 {Zea mays} | 1.689514344 | 0.00071951 | |
| **MZ00039805** | hypothetical protein {Zea mays} | 1.648433435 | 0.00014518 | |
| **MZ00039846** | NAC1 transcription factor {Zea mays} | 1.4951973 | 0.00021314 | |
| **MZ00040036** | pyruvate,orthophosphate dikinase {Zea mays} | 1.121827126 | 0.03904921 | |
| **MZ00040075** | Granule-bound starch synthase precursor {Zea mays} | 1.418209135 | 0.03455696 | |
| **MZ00040271** | S-adenosylmethionine decarboxylase 2 {Zea mays} | 1.756260576 | 0.02526966 | |
| **MZ00040277** | putative cytochrome B5 {Oryza sativa} | 1.500549536 | 3.95E-05 | |
| **MZ00040289** | putative casein kinase I {Oryza sativa} | 1.146119451 | 0.02344848 | |
| **MZ00040294** | alcohol dehydrogenase 1 (adh1) {Zea mays} | -1.256672256 | 0.01302296 | |

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|---|---|---|---|---|
| **MZ00040327** | amino acid carrier {Zea mays} | 1.052384531 | 0.03160973 | |
| **MZ00040437** | MYB transcription factor {Zea mays} | 1.076011466 | 0.00349677 | |
| **MZ00040479** | ATP synthase beta subunit {Saccharum officinarum} | 4.544642147 | 1.53E-05 | |
| **MZ00040486** | Ribulose bisphosphate carboxylase large chain precursor {Zea mays} | 1.908224477 | 0.00157497 | |
| **MZ00040525** | putative ATP synthase beta chain {Oryza sativa} | 3.993841648 | 4.35E-05 | |
| **MZ00040654** | glutathione S-transferase GST 25 {Zea mays} | 1.133561637 | 0.00079982 | |
| **MZ00040799** | psaI gene {Zea mays} | 1.691581287 | 0.01875791 | |
| **MZ00040800** | Photosystem II reaction center I protein {Triticum aestivum} | 1.275611 | 0.04520172 | |
| **MZ00040806** | Chloroplast 50S ribosomal protein L23 {Zea mays} | 2.540319317 | 0.04844961 | |
| **MZ00040807** | ribosomal protein L33 {Zea mays} | 1.033648273 | 0.02523624 | |
| **MZ00040842** | strongly similar to NP_195589.2 splicing factor | 1.673406712 | 0.02429822 | |
| **MZ00041005** | subtilisin-chymotrypsin inhibitor homolog1 {Zea mays} | 1.071580564 | 0.03621874 | |
| **MZ00041163** | hypothetical protein {Zea mays} | 1.037888725 | 3.28E-05 | |
| **MZ00041326** | putative Bowman-Birk serine protease inhibitor {Zea mays} | -1.494711493 | 0.01281047 | |
| **MZ00041327** | putative Bowman-Birk serine protease inhibitor {Zea mays} | -1.835149134 | 0.00206329 | |
| **MZ00041372** | xyloglucan endo-transglycosylase/hydrolase (xth1) {Zea mays} | 1.395480882 | 0.00184888 | |
| **MZ00041665** | UDP-glucose-4-epimerase {Zea mays} | 1.227136386 | 0.00259668 | |
| **MZ00041671** | 60S ribosomal protein L13a {Zea mays} | 1.553188404 | 3.60E-05 | |
| **MZ00041708** | unknown protein {Oryza sativa} | -1.298762583 | 0.0041991 | |
| **MZ00041802** | zinc finger protein {Oryza sativa} | -1.388768717 | 0.00204068 | TF37 |
| **MZ00041945** | translational initiation factor eIF-4A {Zea mays} | 1.476509001 | 0.00859072 | |
| **MZ00042040** | small multi-drug export protein {Zea mays} | 1.42644296 | 3.00E-05 | |
| **MZ00042137** | phi-1-like phosphate-induced protein {Zea mays} | 1.431577512 | 6.89E-06 | |
| **MZ00042324** | ribosome-inactivating protein {Zea mays} | 1.314396472 | 0.00546222 | |

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|---|---|---|---|---|
| **MZ00042472** | unknown protein {Oryza sativa} | 1.231514922 | 0.00542327 | |
| **MZ00042545** | amino acid transport protein {Zea mays} | 1.257388074 | 0.00221837 | |
| **MZ00042564** | transducin {Oryza sativa} | 1.209766028 | 0.0414948 | |
| **MZ00042678** | ribosome-inactivating protein {Zea mays} | 1.687783842 | 0.01531937 | |
| **MZ00042739** | WRKY transcription factor {Oryza sativa} | 1.287648034 | 7.67E-05 | TF26 |
| **MZ00042841** | Histone H2A {Zea mays} | 1.752637372 | 0.01824991 | |
| **MZ00042953** | chlorophyll a/b binding protein {Oryza sativa} | 1.474493885 | 0.02031815 | |
| **MZ00043103** | IAA24 - auxin-responsive Aux/IAA family member {Zea mays} | 1.346996393 | 2.84E-06 | |
| **MZ00043393** | 2-oxoglutarate-dependent oxygenase {Zea mays} | 1.639466238 | 1.45E-05 | |
| **MZ00043400** | hypothetical protein {Asparagus officinalis} | 1.857301079 | 2.63E-05 | |
| **MZ00043484** | cysteine protease 1 {Zea mays} | 1.19870677 | 0.03749325 | |
| **MZ00043526** | unknown protein {Oryza sativa} | 1.459866856 | 0.00030876 | |
| **MZ00043539** | transmembrane 9 superfamily protein member 4 {Zea mays} | 2.012963009 | 0.00048569 | |
| **MZ00043988** | hypothetical protein {Zea mays} | -1.330528902 | 0.00185394 | |
| **MZ00044104** | unknown protein {Oryza sativa} | 1.393725382 | 0.00053211 | |
| **MZ00044126** | hypothetical protein {Zea mays} | 1.861114031 | 0.00038173 | |
| **MZ00044135** | hypothetical protein {Zea mays} | 1.106562177 | 1.63E-05 | |
| **MZ00044190** | allene oxide synthase 1 {Zea mays} | 2.40482948 | 8.46E-05 | |
| **MZ00044413** | benzoxazinone synthesis BX9 {Zea mays} | 1.084818665 | 0.04468022 | |
| **MZ00044555** | putative phosphoribosyl pyrophosphate synthase {Oryza sativa} | 1.273373219 | 0.00105759 | |
| **MZ00046581** | beta-amylase {Zea mays} | 1.172624746 | 6.33E-06 | |
| **MZ00046685** | unknown protein {Oryza sativa} | 1.200878543 | 0.00058811 | |
| **MZ00046697** | putative peptidyl-prolycis-trans isomerase protein {Oryza sativa} | 1.07355831 | 0.0056298 | |
| **MZ00046814** | zeaxanthin epoxidase {Zea mays} | 1.160342049 | 0.006663 | |
| **MZ00046924** | mitochondrial transcription termination factor-like {Oryza sativa} | 1.06888442 | 0.04287812 | |
| **MZ00046986** | unknown protein {Oryza sativa} | 1.256543668 | 0.00076368 | |
| **MZ00047586** | putative root hairless 1 {Oryza sativa} | 1.589256026 | 0.00272862 | |
| **MZ00047697** | unknown protein {Oryza sativa} | 1.098830369 | 0.0001109 | |
| **MZ00047756** | IrgB-like family protein {Zea mays} | 1.87547375 | 0.03497623 | |

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|---|---|---|---|---|
| **MZ00047903** | hypothetical protein {Zea mays} | 1.017055501 | 0.00240156 | |
| **MZ00048363** | putative sialin {Oryza sativa} | 1.424518949 | 0.00333418 | |
| **MZ00048364** | beta-amylase {Zea mays} | 2.077666631 | 2.88E-05 | |
| **MZ00048444** | Myb factor protein {Oryza sativa} | 1.931871565 | 0.00022486 | TF28 |
| **MZ00048483** | ZIM-motif family protein {Zea mays} | 2.028045873 | 0.00082304 | |
| **MZ00048497** | putative ATP synthase gamma chain 1, chloroplast (H(+)-transporting two-sector ATPase/F(1)-ATPase/ATPC1) {Oryza sativa} | 1.104324531 | 0.02589263 | |
| **MZ00048814** | putative nucleoid DNA-binding protein cnd41 {Oryza sativa} | 1.630870608 | 0.00547833 | |
| **MZ00049082** | von Willebrand factor type A domain containing protein {Zea mays} | 1.081249464 | 0.00012647 | |
| **MZ00050411** | LOB domain protein 11 {Zea mays} | 1.202533332 | 0.00274949 | |
| **MZ00052267** | putative senescence-associated protein {Pisum sativum} | 2.305749457 | 0.00274858 | |
| **MZ00052283** | hypothetical protein {Zea mays} | 1.664694247 | 0.00076009 | |
| **MZ00054822** | phospho-2-dehydro-3-deoxyheptonate aldolase 1 {Zea mays} | 1.037114826 | 0.00034495 | |
| **MZ00054907** | putative cytochrome P450 {Oryza sativa} | 1.444210825 | 0.00129733 | |
| **MZ00054995** | hypothetical protein {Zea mays} | 1.129921377 | 0.00028563 | |
| **MZ00055184** | putative senescence-associated protein {Pisum sativum} | 1.370242333 | 0.00824871 | |
| **MZ00055463** | esterase {Zea mays} | 1.874727155 | 4.29E-07 | |
| **MZ00055884** | hypothetical protein {Zea mays} | 1.314444877 | 7.05E-08 | |
| **MZ00055932** | Bowman-Birk type trypsin inhibitor {Zea mays} | 1.232359054 | 0.00226953 | |
| **MZ00056629** | OSJNBa0088A01.13 {Oryza sativa} | 1.871600301 | 0.00274666 | |
| **MZ00056644** | disease resistance response protein-like {Oryza sativa} | -1.10469911 | 0.00763107 | |
| **MZ00056647** | hypothetical protein {Zea mays} | 2.395220087 | 2.83E-06 | |
| **MZ00056690** | glucan endo-1,3-beta-glucosidase homolog1 {Zea mays} | -1.020114018 | 0.01949473 | |
| **MZ00056859** | myb-related protein-like {Oryza sativa} | 1.01087786 | 0.02310255 | |
| **MZ00057095** | putative UVB-resistance protein UVR8 {Oryza sativa} | -1.057543077 | 0.02392993 | |
| **MZ00057165** | OSJNBa0039C07.4 {Oryza sativa} | 1.239777368 | 0.02144499 | |

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|---|---|---|---|---|
| **MZ00057252** | probable ring finger protein - barley {Hordeum vulgare} | 1.180631224 | 0.02183747 | |
| **MZ00057436** | putative ZEITLUPE {Oryza sativa} | 3.060342811 | 6.89E-05 | |

**Tab.7. 3: 2 h after feeding induction**

| MZ-number | Annotation | fold expression (log10) | p-value | Abbrevation |
|---|---|---|---|---|
| **MZ00000390** | NA | 1.03023686 | 0.04988142 | |
| **MZ00000418** | transferase {Zea mays} | 1.373511474 | 0.00068188 | |
| **MZ00001464** | NA | 2.361058379 | 0.0002537 | |
| **MZ00003912** | OSJNBa0008M17.5 {Oryza sativa} | 1.858015327 | 0.00329458 | |
| **MZ00003937** | putative UOS1 {Oryza sativa} | 1.286657337 | 0.03894326 | |
| **MZ00004418** | TGF-beta receptor-interacting protein 1 {Phaseolus vulgaris} | 1.091491534 | 0.16466971 | |
| **MZ00004465** | anthranilic acid methyltransferase 1 {Zea mays} | 1.953334566 | 0.09519435 | |
| **MZ00004614** | glucose-6-phosphate/phosphate translocator 2 {Zea mays} | 1.014436622 | 0.00134676 | |
| **MZ00005352** | NA | 1.023726633 | 0.06403457 | |
| **MZ00005405** | farnesyl pyrophosphate synthase1 {Zea mays} | 1.87367602 | 0.00037421 | |
| **MZ00005471** | putative tyrosine/dopa decarboxylase {Oryza sativa} | 1.277068191 | 0.00077685 | |
| **MZ00005511** | hypothetical protein {Zea mays} | 1.19741694 | 0.00066932 | |
| **MZ00005899** | terpene synthase 2 {Zea mays} | 2.445964131 | 5.77E-07 | |
| **MZ00005958** | indole-3-glycerol phosphate lyase {Zea mays} | 2.144543334 | 0.00237136 | |
| **MZ00012674** | zinc finger protein 3 {Zea mays} | 1.302183953 | 0.00020717 | |
| **MZ00012854** | putative zinc transporter {Oryza sativa} | 1.009181101 | 0.27292594 | |
| **MZ00013037** | pyruvate,orthophosphate dikinase {Zea mays} | 1.054684327 | 0.09088338 | |
| **MZ00013112** | Phospholipid-transporting ATPase 1 {Arabidopsis thaliana} | 1.066196225 | 0.00066572 | |
| **MZ00013321** | hypothetical protein {Sorghum bicolor} | 1.078840592 | 5.34E-05 | |
| **MZ00013411** | ADP-ribosylation factor-like protein 8B {Zea mays} | 1.772779 | 2.92E-05 | |
| **MZ00013555** | hypothetical protein {Zea mays} | 1.387785261 | 0.00782457 | |
| **MZ00013725** | DRE-binding protein 4 {Zea mays} | 1.431889465 | 0.00355558 | |

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|---|---|---|---|---|
| **MZ00013773** | UDP-glucose 6-dehydrogenase {Zea mays} | 1.410818771 | 0.00070133 | |
| **MZ00013836** | S-adenosylmethionine decarboxylase {Oryza sativa} | 2.668290682 | 1.82E-05 | |
| **MZ00013840** | phospho-2-dehydro-3-deoxyheptonate aldolase 1 {Zea mays} | 1.798847947 | 0.00022038 | |
| **MZ00013841** | phospho-2-dehydro-3-deoxyheptonate aldolase 1 {Zea mays} | 1.354861127 | 0.01272741 | |
| **MZ00013846** | lipoxygenase11 {Zea mays} | 1.665138179 | 0.15612374 | |
| **MZ00013941** | profilin A {Zea mays} | -1.123587087 | 0.0146436 | |
| **MZ00014008** | Farnesyl pyrophosphate synthetase {Zea mays} | 1.159666733 | 0.01844409 | |
| **MZ00014027** | glycine hydroxymethyltransferase {Arabidopsis thaliana} | 1.374526933 | 0.00021777 | |
| **MZ00014072** | light-inducible protein ATLS1 {Arabidopsis thaliana} | -1.095767662 | 0.05327683 | |
| **MZ00014307** | Cytochrome P450 71C2 {Zea mays} | 1.70239388 | 0.00474709 | |
| **MZ00014377** | nodulation homolog 1 {Zea mays} | -1.303107325 | 0.01284684 | |
| **MZ00014943** | anthranilate synthase alpha 2 subunit {Oryza sativa} | 1.209071744 | 0.00915593 | |
| **MZ00015021** | polyphenol oxidase {Saccharum hybrid cultivar} | 1.15465864 | 0.00250256 | |
| **MZ00015105** | indole synthase {Zea mays} | 1.030830422 | 0.01214453 | |
| **MZ00015138** | UDP-glucuronic acid decarboxylase {Oryza sativa} | 1.201321097 | 0.0011263 | |
| **MZ00015154** | cylicin-1 {Zea mays} | 1.131634848 | 0.00588923 | |
| **MZ00015218** | hypothetical protein {Zea mays} | 1.113226298 | 0.00315424 | |
| **MZ00015279** | macrophage migration inhibitory factor {Zea mays} | -1.013855835 | 0.14618563 | |
| **MZ00015502** | vacuolar sorting receptor homolog {Zea mays} | 1.352260391 | 0.00260728 | |
| **MZ00015504** | blue fluorescent1 {Zea mays} | 1.428410541 | 0.00079352 | |
| **MZ00015505** | putative fruit protein {Oryza sativa} | 1.630659685 | 0.03466756 | |
| **MZ00015701** | lipoxygenase {Zea mays} | 2.581695148 | 0.00051602 | |
| **MZ00016249** | probable hydroxymethylglutaryl-CoA reductase (NADPH2) {Oryza sativa} | 1.539376405 | 0.00299231 | |
| **MZ00016498** | disease resistance response protein-like | -1.251673213 | 0.01472235 | |

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|---|---|---|---|---|
| | {Oryza sativa} | | | |
| **MZ00016835** | nucleotide pyrophosphatase/phosphodiesterase {Zea mays} | 1.492979993 | 0.00034351 | |
| **MZ00016876** | putative cell division protein FtsH3 {Oryza sativa} | 1.067788439 | 0.00805575 | |
| **MZ00016940** | unknown protein {Oryza sativa} | 1.002783573 | 0.35891415 | |
| **MZ00017092** | hypothetical protein {Zea mays} | 1.617888668 | 0.05015276 | |
| **MZ00017211** | hypothetical protein {Zea mays} | 1.550151642 | 0.01108802 | |
| **MZ00017245** | ABC family1 {Zea mays} | 1.230093808 | 0.17593178 | |
| **MZ00017265** | MtN3-like protein {Arabidopsis thaliana} | 1.387075724 | 0.00045726 | |
| **MZ00017300** | hypothetical protein {Zea mays} | 1.045359846 | 0.00106156 | |
| **MZ00017335** | glutamine-fructose-6-phosphate transaminase 2 {Arabidopsis thaliana} | 1.106680174 | 0.00046455 | |
| **MZ00017386** | hypothetical protein {Oryza sativa} | -1.127725041 | 0.00470713 | |
| **MZ00017392** | flavonoid 3-monooxygenase {Zea mays} | 1.368355694 | 0.03466701 | |
| **MZ00017522** | Putative serine/threonine kinase {Oryza sativa} | 1.131462373 | 0.12184173 | |
| **MZ00017601** | hydroperoxide lyase {Zea mays} | 1.215532646 | 2.08E-05 | |
| **MZ00017814** | putative alcohol dehydrogenase {Oryza sativa} | -1.017998925 | 0.03574206 | |
| **MZ00017989** | hypothetical protein {Sorghum bicolor} | 1.423193812 | 0.1475606 | |
| **MZ00018016** | Putative transporter {Oryza sativa} | 1.008044236 | 0.01600165 | |
| **MZ00018189** | hypothetical protein {Zea mays} | 1.060194828 | 0.22352922 | |
| **MZ00018193** | beta-expansin 1a {Zea mays} | -1.059161246 | 0.00060302 | |
| **MZ00018234** | OSJNBb0085F13.14 {Oryza sativa} | 1.020119199 | 0.03142899 | |
| **MZ00018241** | ribosome-inactivating protein {Zea mays} | 2.566665061 | 0.00026059 | |
| **MZ00018258** | hypothetical protein {Zea mays} | 1.145522492 | 0.0719273 | |
| **MZ00018280** | OSJNBa0019K04.6 {Oryza sativa} | 1.092957667 | 0.07619123 | |
| **MZ00018568** | hypothetical protein {Zea mays} | 2.336558636 | 2.66E-05 | |
| **MZ00018741** | putative cytochrome P450 reductase {Oryza sativa} | 2.154914042 | 0.00433498 | |
| **MZ00018836** | hypothetical protein {Zea mays} | 1.26210382 | 0.00034168 | |
| **MZ00018952** | hypothetical protein {Oryza sativa} | -1.108451485 | 0.01277162 | |
| **MZ00019196** | senescence-associated protein DH {Zea mays} | 1.3692118 | 5.90E-05 | |
| **MZ00019277** | unknown protein {Oryza sativa} | -1.01309242 | 0.02812032 | |
| **MZ00019475** | anthranilate N-benzoyltransferase protein 1 | 1.307470694 | 0.00817859 | |

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|---|---|---|---|---|
| | {Zea mays} | | | |
| **MZ00019560** | putative AMP deaminase {Oryza sativa} | 1.843768023 | 7.88E-05 | |
| **MZ00019701** | hypothetical protein {Oryza sativa} | 2.278043903 | 0.0001613 | |
| **MZ00019729** | terpene synthase 2 {Zea mays} | 2.546889179 | 5.76E-05 | |
| **MZ00019894** | stem 28 kDa glycoprotein {Zea mays} | 2.410031229 | 0.00090632 | |
| **MZ00019908** | hypothetical protein {Zea mays} | -1.045638506 | 0.03687567 | |
| **MZ00020111** | 4-coumarate--CoA ligase 4CL1 {Lolium perenne} | 1.006469385 | 0.00983614 | |
| **MZ00020230** | epoxide hydrolase 2 {Zea mays} | 1.715044275 | 0.0046751 | |
| **MZ00020495** | Probable disease resistance protein {Arabidopsis thaliana} ^\|^GB\|CAB38788.1\|4490297\|ATF17M5 putat-TRUNCATED- | 1.026662725 | 0.00333622 | |
| **MZ00020968** | putative lipase class 3 family protein {Oryza sativa} | 2.090846466 | 0.00021577 | |
| **MZ00021254** | OSJNBa0065B15.8 {Oryza sativa} | 1.636843291 | 0.02582368 | |
| **MZ00021385** | putative cytochrome P450 reductase {Oryza sativa} | 1.026286532 | 0.00784386 | |
| **MZ00021997** | putative auxin-regulated protein {Oryza sativa} | 1.166719003 | 0.00416705 | |
| **MZ00022163** | putative 10-deacetylbaccatin III-10-O-acetyl transferase {Oryza sativa} | 2.795284145 | 0.00112124 | |
| **MZ00022180** | hypothetical protein {Zea mays} | 1.461594647 | 1.89E-05 | |
| **MZ00022380** | hypothetical protein {Sorghum bicolor} | 1.66586002 | 0.02069314 | |
| **MZ00022582** | peroxidase 1 {Zea mays} | 1.047218026 | 0.00106451 | |
| **MZ00022994** | allene oxide synthase 1 {Zea mays} | 1.865077821 | 1.06E-07 | |
| **MZ00023013** | unknown protein {Oryza sativa} | 1.171634486 | 0.00186209 | |
| **MZ00023027** | starch phosphorylase 2 precursor {Zea mays} | 1.048303355 | 0.01212634 | |
| **MZ00023087** | hypothetical protein {Zea mays} | 1.26569152 | 0.00012539 | |
| **MZ00023228** | dihydroflavonol-4-reductase {Zea mays} | 1.056075907 | 0.01229024 | |
| **MZ00023293** | MCB2 protein {Hordeum vulgare subsp. vulgare} | -1.045847437 | 0.00349516 | |
| **MZ00023318** | putative prephenate dehydratase {Oryza sativa} | 1.483733745 | 3.58E-06 | |
| **MZ00023441** | S-adenosylmethionine synthetase 1 {Zea mays} | 1.567118066 | 0.00125196 | |

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|---|---|---|---|---|
| **MZ00023501** | pnFL-2 {Zea mays} | 1.33327923 | 0.01265398 | |
| **MZ00023547** | putative aminotransferase class-III {Oryza sativa} | 1.742252391 | 0.0123728 | |
| **MZ00023952** | vacuolar proton pump homolog1 {Zea mays} | 1.009359434 | 0.34530679 | |
| **MZ00023983** | ribonuclease S homolog {Zea mays} | 1.145738995 | 0.00060099 | |
| **MZ00024039** | photosystem I reaction center subunit III {Zea mays} | 1.616016643 | 0.22302104 | |
| **MZ00024196** | superoxide dismutase {Zea mays} | 1.47353444 | 9.49E-05 | |
| **MZ00024204** | putative C-4 sterol methyl oxidase {Oryza sativa} | 1.257850194 | 0.04459984 | |
| **MZ00024350** | anthranilate synthase component II {Zea mays} | 2.327282998 | 0.00358114 | |
| **MZ00024351** | anthranilate synthase component II {Zea mays} | 1.465293952 | 0.00089003 | |
| **MZ00024600** | S-like RNase {Triticum aestivum} | 1.005051476 | 0.00013909 | |
| **MZ00024662** | putative indole-3-glycerol phosphate synthase {Oryza sativa} | 1.176295043 | 0.00089011 | |
| **MZ00024753** | putative angio-associated migratory cell protein {Oryza sativa} | 1.194788081 | 0.16552594 | |
| **MZ00024904** | OSJNBa0058K23.19 {Oryza sativa} | 1.397660148 | 0.00151183 | |
| **MZ00025169** | DEAD box RNA helicase {Zea mays} | 1.227198799 | 0.03618211 | |
| **MZ00025171** | DEAD box RNA helicase1 {Zea mays} | 1.157403615 | 0.00051684 | |
| **MZ00025289** | cytidine deaminase2 {Zea mays} | 1.790277357 | 0.02487384 | |
| **MZ00025407** | polyamine oxidase1 (pao1) {Zea mays} | 1.664314353 | 0.00037069 | |
| **MZ00025580** | OSJNBa0058G03.5 {Oryza sativa} | 1.080026156 | 0.07692816 | |
| **MZ00025708** | ZIM-motif family protein {Zea mays} | 1.131402858 | 0.00286847 | |
| **MZ00025768** | glutathione S-transferase GST 20 {Zea mays} | 2.1001018 | 0.00079211 | |
| **MZ00025895** | farnesyl-pyrophosphate synthetase {Oryza sativa} | 1.906928244 | 0.00476959 | |
| **MZ00025944** | glutathione S-transferase GST 10 {Zea mays} | -1.008378342 | 0.07490153 | |
| **MZ00026004** | glucose-6-phosphate/phosphate translocator 2 {Zea mays} | 1.042467121 | 0.23435668 | |
| **MZ00026277** | hypothetical protein {Zea mays} | 1.519029522 | 0.00010354 | |
| **MZ00026471** | anthranilate synthase alpha 1 subunit {Oryza sativa} | 2.859966877 | 1.10E-05 | |
| **MZ00026538** | ZIM-motif family protein {Zea mays} | 1.380001549 | 0.00865806 | |

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|---|---|---|---|---|
| **MZ00026661** | putative NAC-domain protein {Oryza sativa} | 1.269517381 | 0.00999369 | TF1 |
| **MZ00026684** | hypothetical protein {Zea mays} | 1.077745834 | 0.00159198 | |
| **MZ00026739** | putative lipase {Arabidopsis thaliana} | 2.26447486 | 0.03384457 | |
| **MZ00027030** | 12-oxo-phytodienoic acid reductase8 {Zea mays} | 1.342701039 | 0.02357186 | |
| **MZ00027037** | OSJNBa0008M17.5 {Oryza sativa} | 2.694023971 | 0.01666961 | |
| **MZ00027073** | hypothetical protein {Zea mays} | 1.286337591 | 0.08322685 | |
| **MZ00027387** | cinnamyl alcohol dehydrogenase1 {Zea mays} | 1.543096669 | 0.00444697 | |
| **MZ00027416** | autophagy-related 12 {Zea mays} | 1.26397244 | 0.05916287 | |
| **MZ00027491** | Cytochrome P450 71C4 {Zea mays} | 1.234304683 | 0.02707684 | |
| **MZ00027637** | chloride channel {Zea mays} | 1.12853167 | 0.00081646 | |
| **MZ00028221** | putative phosphoethanolamine methyltransferase {Oryza sativa} | 1.114589694 | 0.02651546 | |
| **MZ00028790** | hypothetical protein {Zea mays} | 1.043993089 | 0.00318289 | |
| **MZ00028898** | hypothetical protein {Zea mays} | 1.391299979 | 0.0006231 | |
| **MZ00029195** | putative phosphoribosyl pyrophosphate synthase {Oryza sativa} | 2.560977534 | 6.02E-06 | |
| **MZ00029519** | OSJNBa0008M17.5 {Oryza sativa} | 1.558536958 | 0.00333745 | |
| **MZ00029560** | phytocystatin {Actinidia deliciosa} | 2.808226321 | 6.41E-05 | |
| **MZ00029584** | arogenate dehydrogenase {Zea mays} | 1.296479229 | 1.36E-05 | |
| **MZ00029594** | sesquiterpene cyclase {Zea mays} | 1.605835591 | 9.10E-06 | |
| **MZ00029629** | histone deacetylase {Zea mays} | 1.773627052 | 0.00677565 | |
| **MZ00029916** | hypothetical protein {Zea mays} | 1.119383857 | 0.00074939 | |
| **MZ00029921** | anthranilic acid methyltransferase 1 {Zea mays} | 1.27577375 | 0.07055959 | |
| **MZ00030298** | sucrose-phosphatase {Zea mays} | 1.285520188 | 2.22E-05 | |
| **MZ00030501** | terpene synthase {Zea mays} | 1.316340614 | 0.00018751 | |
| **MZ00030642** | chemocyanin {Zea mays} | 1.114132022 | 0.00269918 | |
| **MZ00030744** | integral membrane protein DUF6 containing protein {Zea mays} | 1.175017063 | 0.01859008 | |
| **MZ00030829** | aldo-keto reductase/ oxidoreductase {Zea mays} | 1.631060743 | 0.00398554 | |
| **MZ00031225** | At3g54650/T5N23_10 {Arabidopsis thaliana} | 1.130579468 | 0.00986646 | |
| **MZ00031356** | unknown protein {Oryza sativa} | 1.590638565 | 8.93E-05 | |
| **MZ00031477** | hypothetical protein {Zea mays} | 1.036987982 | 0.00035747 | |
| **MZ00031624** | putative prephenate dehydratase {Oryza | 1.124857295 | 0.00043053 | |

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|---|---|---|---|---|
| | sativa} | | | |
| **MZ00031736** | terpene synthase10 {Zea mays} | 2.478956434 | 0.00139642 | |
| **MZ00031748** | hypothetical protein {Zea mays} | 1.100082514 | 0.01356034 | |
| **MZ00031832** | glutathione transferase {Hordeum vulgare subsp. vulgare} | 1.578120101 | 7.31E-05 | |
| **MZ00031957** | unknown protein {Oryza sativa} | 1.004907218 | 0.00168799 | |
| **MZ00032043** | anthranilic acid methyltransferase 3 {Zea mays} | 1.33487533 | 0.00173148 | |
| **MZ00032136** | 1-deoxy-D-xylulose 5-phosphate synthase 2 (dxs2) {Zea mays} | 3.227763457 | 2.18E-08 | |
| **MZ00032170** | putative centromere protein {Oryza sativa} | 1.944509146 | 0.00129221 | |
| **MZ00032240** | indole-3-glycerol phosphate synthase {Zea mays} | 2.034400307 | 3.00E-05 | |
| **MZ00032999** | indole-3-glycerol phosphate lyase {Zea mays} | 1.563299031 | 0.0019546 | |
| **MZ00033310** | MPI {Tripsacum dactyloides} | 3.01765026 | 1.39E-05 | |
| **MZ00033551** | Chloroplast 30S ribosomal protein S12 {Zea mays} | 2.293633708 | 0.00147481 | |
| **MZ00033552** | psaC gene {Zea mays} | 1.427344874 | 0.00040398 | |
| **MZ00033637** | 3-N-debenzoyl-2-deoxytaxol N-benzoyltransferase {Zea mays} | 1.974223767 | 0.00014116 | |
| **MZ00033688** | pyruvate,orthophosphate dikinase {Zea mays} | 1.556751962 | 0.17929047 | |
| **MZ00034236** | vacuolar sorting receptor homolog1 {Zea mays} | 1.272306222 | 0.00144763 | |
| **MZ00034292** | S-adenosylmethionine synthetase 1 {Oryza sativa} | 1.101136222 | 0.0387964 | |
| **MZ00034295** | methionine synthase {Zea mays} | 2.307220428 | 3.28E-06 | |
| **MZ00034298** | seed specific protein of balanced nutritional quality {Amaranthus hypochondriacus} | 1.362589081 | 0.00856829 | |
| **MZ00034308** | natterin 3 precursor {Thalassophryne nattereri} | 1.723248995 | 0.00409385 | |
| **MZ00034331** | 2-oxoglutarate-dependent oxygenase {Zea mays} | 1.03500533 | 0.00075819 | |
| **MZ00034402** | allene oxide synthase {Zea mays} | 1.671836552 | 2.88E-05 | |
| **MZ00034828** | NAD(P)H-quinone oxidoreductase chain 5 {Zea mays} | 1.508385378 | 0.00243565 | |
| **MZ00034831** | NAD(P)H-quinone oxidoreductase chain I | 1.188448296 | 0.02334139 | |

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|---|---|---|---|---|
| | {Zea mays} | | | |
| **MZ00034832** | NAD(P)H-quinone oxidoreductase chain J {Zea mays} | 1.312867972 | 0.02494666 | |
| **MZ00034833** | NAD(P)H-quinone oxidoreductase chain K {Zea mays} | 2.179723534 | 0.00208898 | |
| **MZ00034834** | Apocytochrome f precursor {Zea mays}^|^GB|CAA60298.1|902234|ZMA86563 cyt-TRUNCATED- | 1.704495188 | 0.00318348 | |
| **MZ00034838** | PSI P700 apoprotein A1 {Zea mays} | 2.784546574 | 5.88E-07 | |
| **MZ00034839** | Photosystem I P700 chlorophyll A apoprotein A2 {Zea mays} | 2.086225666 | 8.50E-05 | |
| **MZ00034840** | psaC gene {Zea mays} | 1.48064752 | 0.00025438 | |
| **MZ00034841** | psaI gene {Zea mays} | 2.201212435 | 9.34E-05 | |
| **MZ00034842** | photosystem I subunit IX {Oryza nivara} | 2.27378194 | 0.00955403 | |
| **MZ00034843** | Photosystem Q(B) protein {Zea mays} | 1.633766858 | 0.00832835 | |
| **MZ00034845** | Photosystem II 44 kDa reaction center protein {Zea mays} | 2.854597088 | 4.13E-06 | |
| **MZ00034846** | Photosystem II D2 protein {Zea mays} | 1.818045758 | 2.52E-05 | |
| **MZ00034847** | cytochrome b559 alpha chain {Oryza sativa} | 1.775936741 | 0.00233617 | |
| **MZ00034848** | cytochrome b559 beta chain {Oryza sativa} | 1.606566149 | 0.00277161 | |
| **MZ00034849** | photosystem II phosphoprotein psbH {Zea mays} | 2.438270573 | 0.00052747 | |
| **MZ00034850** | Photosystem II reaction center I protein {Triticum aestivum} | 2.054908102 | 0.00190159 | |
| **MZ00034851** | Photosystem II reaction center J protein {Zea mays} | 2.142328229 | 0.00014564 | |
| **MZ00034853** | photosystem II L protein {Oryza sativa} | 1.187725187 | 0.00697087 | |
| **MZ00034854** | NA | 2.050272742 | 0.00272595 | |
| **MZ00034855** | photosystem II protein N {Oryza sativa} | 2.02867509 | 0.00540431 | |
| **MZ00034856** | Ribulose bisphosphate carboxylase large chain precursor {Zea mays} | 3.708092123 | 7.59E-06 | |
| **MZ00034857** | Chloroplast 30S ribosomal protein S12 {Zea mays} | 2.38414342 | 0.00187299 | |
| **MZ00034858** | Chloroplast 50S ribosomal protein L14 {Zea mays}ribosomal protein L14 {Zea mays} ^-TRUNCATED- | 1.865715686 | 0.02070231 | |

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|---|---|---|---|---|
| **MZ00034859** | Chloroplast 50S ribosomal protein L16 {Zea mays} | 2.252885787 | 0.03994905 | |
| **MZ00034860** | ribosomal protein L2 {Zea mays} | 2.099443546 | 0.11249719 | |
| **MZ00034862** | Chloroplast 50S ribosomal protein L22 {Zea mays} | 2.981569473 | 0.0411925 | |
| **MZ00034863** | Chloroplast 50S ribosomal protein L23. {Zea mays} ^\|^PIR\|S01396\|R5ZM23 ribosomal protein L23 - maize chloroplast {Zea mays} ^\|^GB\|BAD27383.1\|49659602\|AP006714 ribosomal protein L23 {Saccharum officinarum;}-TRUNCATED- | 2.426050952 | 0.05597254 | |
| **MZ00034865** | ribosomal protein L33 {Zea mays} | 1.326255597 | 0.00969839 | |
| **MZ00034866** | ribosomal protein L36 {Oryza sativa} | 2.30907383 | 4.47E-05 | |
| **MZ00034867** | DNA-directed RNA polymerase alpha chain {Zea mays} | 2.178472896 | 0.00066476 | |
| **MZ00034871** | Chloroplast 30S ribosomal protein S11 {Zea mays} | 2.053424775 | 0.00033218 | |
| **MZ00034872** | photosystem II subunit T {Narcissus elegans} | 2.705007934 | 3.96E-05 | |
| **MZ00034873** | Chloroplast 30S ribosomal protein S14 {Zea mays} | 1.156380639 | 0.00057142 | |
| **MZ00034874** | ribosomal protein S15 {Saccharum officinarum} | 2.058579357 | 2.42E-06 | |
| **MZ00034877** | Chloroplast 30S ribosomal protein S18 {Zea mays} | 2.002648333 | 0.00181047 | |
| **MZ00034878** | ribosomal protein S19 {Zea mays} | 1.988382211 | 0.03254884 | |
| **MZ00034879** | Chloroplast 30S ribosomal protein S2 {Zea mays} | 1.997499065 | 0.01274782 | |
| **MZ00034880** | Chloroplast 30S ribosomal protein S3 {Zea mays} | 2.834132874 | 0.00551188 | |
| **MZ00034881** | Chloroplast 30S ribosomal protein S4 {Zea mays} | 2.792795774 | 1.45E-05 | |
| **MZ00034882** | Chloroplast 30S ribosomal protein S7 {Zea mays} | 2.44499997 | 0.08955369 | |
| **MZ00034883** | Chloroplast 30S ribosomal protein S8 {Zea mays} | 1.834970735 | 0.08675822 | |
| **MZ00034895** | hypothetical protein {Zea mays} | 2.155866354 | 0.13762338 | |

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|---|---|---|---|---|
| **MZ00034901** | NA | 1.041764824 | 0.02735304 | |
| **MZ00034902** | NA | 1.310040741 | 0.01478759 | |
| **MZ00034904** | NA | 1.458630883 | 0.00261811 | |
| **MZ00034910** | NA | 1.489061889 | 0.0431608 | |
| **MZ00034930** | lipoxygenase10 {Zea mays} | 1.124129713 | 0.00242893 | |
| **MZ00035055** | lipoxygenase6 {Zea mays} | 1.049963052 | 0.00588982 | |
| **MZ00035057** | hypothetical protein {Sorghum bicolor} | 1.703244145 | 0.00014203 | |
| **MZ00035114** | phospho-2-dehydro-3-deoxyheptonate aldolase 1 {Zea mays} | 1.112711835 | 0.00015787 | |
| **MZ00035119** | putative senescence-associated protein {Pisum sativum} | 1.078421948 | 0.06953704 | |
| **MZ00035213** | prpol {Zea mays} | 1.057014741 | 0.01829625 | |
| **MZ00035259** | putative senescence-associated protein {Pisum sativum} | 1.506943662 | 0.00363069 | |
| **MZ00035364** | ABA- and ripening-inducible-like protein {Zea mays} | 1.090715747 | 0.25096348 | |
| **MZ00035373** | AER {Zea mays} | 1.296724162 | 0.00016459 | |
| **MZ00035374** | methionine synthase {Zea mays} | 1.973657913 | 1.84E-06 | |
| **MZ00035394** | putative senescence-associated protein {Pisum sativum} | 1.735292879 | 0.00095714 | |
| **MZ00035414** | synthase proteolipid subunit,ATP {Spinacia sp.} | 2.105032338 | 0.2767487 | |
| **MZ00035506** | hypothetical protein {Zea mays} | 2.610852895 | 0.00046109 | |
| **MZ00035555** | putative senescence-associated protein {Pisum sativum} | 2.013258584 | 0.00060866 | |
| **MZ00035616** | pyruvate,orthophosphate dikinase {Zea mays} | 1.105201782 | 0.55002025 | |
| **MZ00035637** | NA | 2.674661284 | 0.00080415 | |
| **MZ00035685** | NA | 2.082256523 | 0.00047532 | |
| **MZ00035702** | NA | 1.927259588 | 0.00308432 | |
| **MZ00035704** | NA | 1.093259361 | 0.01590859 | |
| **MZ00035708** | putative senescence-associated protein {Pisum sativum} | 1.638762142 | 0.03516077 | |
| **MZ00035715** | putative senescence-associated protein {Pisum sativum} | 2.149019892 | 0.00082668 | |
| **MZ00035720** | hypothetical protein {Zea mays} | 1.550246251 | 0.00015237 | |
| **MZ00035731** | putative senescence-associated protein {Pisum | 1.862421144 | 0.00347306 | |

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| | sativum} | | | |
| **MZ00035752** | probable cytochrome P450 monooxygenase {Zea mays} | 1.776277849 | 0.00197458 | |
| **MZ00035753** | hypothetical protein {Zea mays} | 2.362359758 | 0.00025024 | |
| **MZ00035770** | putative senescence-associated protein {Pisum sativum} | 2.265850802 | 0.00184994 | |
| **MZ00035787** | unnamed protein product | 2.602140335 | 0.00605042 | |
| **MZ00035813** | putative zinc finger protein | 1.22852734 | 0.01096484 | |
| **MZ00035825** | unnamed protein product | 2.523691105 | 0.00607011 | |
| **MZ00035828** | putative senescence-associated protein {Pisum sativum} | 1.685101641 | 0.00102647 | |
| **MZ00035833** | unnamed protein product | 2.277198937 | 0.00019668 | |
| **MZ00035834** | unnamed protein product | 2.105099096 | 0.00174862 | |
| **MZ00035835** | unnamed protein product | 1.466083263 | 0.00612952 | |
| **MZ00035840** | putative senescence-associated protein {Pisum sativum} | 1.906894424 | 0.00387732 | |
| **MZ00035842** | carbonic anhydrase {Zea mays} | 1.119621929 | 0.33733191 | |
| **MZ00035844** | unnamed protein product | 2.010759187 | 0.00121774 | |
| **MZ00035848** | Hypothetical protein {Oryza sativa Zea mays} | 1.183254307 | 0.00425262 | |
| **MZ00035981** | NAD-dependent epimerase/dehydratase family protein {Zea mays} | 1.43966079 | 0.00323953 | |
| **MZ00035987** | hypothetical protein {Oryza sativa} | 1.483413721 | 0.00506518 | |
| **MZ00035997** | lipoxygenase6 {Zea mays} | 1.529627126 | 0.00345538 | |
| **MZ00036078** | hypothetical protein {Zea mays} | 1.091621379 | 1.19E-05 | |
| **MZ00036098** | metallothionein-like protein {Zea mays} | -1.013899956 | 0.32926996 | |
| **MZ00036151** | putative senescence-associated protein {Pisum sativum} | 1.254159615 | 0.00567947 | |
| **MZ00036162** | rRNA promoter binding protein {Rattus norvegicus} | 1.843663789 | 0.00267149 | |
| **MZ00036167** | hypothetical protein {Sorghum bicolor} | 2.258290515 | 0.00138824 | |
| **MZ00036171** | UDP-glucose 6-dehydrogenase {Zea mays} | 1.363534355 | 0.00056812 | |
| **MZ00036200** | NA | 1.835061841 | 0.0017198 | |
| **MZ00036203** | histone one (H1) 101 {Zea mays} | 2.101125169 | 0.00043311 | |
| **MZ00036205** | putative senescence-associated protein {Pisum sativum} | 1.89849751 | 0.00272458 | |
| **MZ00036223** | putative senescence-associated protein {Pisum | 1.57220368 | 0.00046902 | |

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|---|---|---|---|---|
| | sativum} | | | |
| **MZ00036242** | putative senescence-associated protein {Pisum sativum} | 1.478318745 | 0.03563985 | |
| **MZ00036243** | granule bound starch synthase 2a precursor (GBSS2a) {Zea mays} | 1.094694143 | 0.03137115 | |
| **MZ00036244** | unnamed protein product | 1.004911815 | 0.00479287 | |
| **MZ00036264** | putative senescence-associated protein {Pisum sativum} | 1.873646486 | 0.0065148 | |
| **MZ00036265** | unnamed protein product | 1.966699518 | 0.04593108 | |
| **MZ00036281** | NA | 1.506155728 | 0.00426289 | |
| **MZ00036282** | putative senescence-associated protein {Pisum sativum} | 1.592934397 | 0.00868318 | |
| **MZ00036291** | putative senescence-associated protein {Pisum sativum} | 1.586983509 | 8.55E-05 | |
| **MZ00036295** | unnamed protein product | 2.422442263 | 0.00040533 | |
| **MZ00036305** | putative senescence-associated protein {Pisum sativum} | 1.788881631 | 0.00604369 | |
| **MZ00036306** | putative senescence-associated protein {Pisum sativum} | 1.179195899 | 0.01808718 | |
| **MZ00036308** | unnamed protein product | 2.337353837 | 0.00944129 | |
| **MZ00036310** | putative senescence-associated protein {Pisum sativum} | 1.524420782 | 0.00140849 | |
| **MZ00036349** | hypothetical protein {Zea mays} | -1.462407949 | 0.22449326 | |
| **MZ00036382** | putative senescence-associated protein {Pisum sativum} | 1.641639011 | 0.01431298 | |
| **MZ00036442** | GR1a protein {Zea mays} | -1.136685438 | 0.04741771 | |
| **MZ00036454** | putative auxin efflux carrier (PIN1c) {Zea mays} | 1.575126155 | 0.00748912 | |
| **MZ00036455** | hypothetical protein {Zea mays} | 1.858269238 | 0.01278453 | |
| **MZ00036485** | nicotianamine synthase 3 {Zea mays} | 1.840102697 | 0.00118929 | |
| **MZ00036498** | hypothetical protein {Sorghum bicolor} | 1.675552124 | 0.01425941 | |
| **MZ00036513** | putative senescence-associated protein {Pisum sativum} | 2.190952853 | 0.00202693 | |
| **MZ00036530** | unnamed protein product | 2.901123628 | 0.00107926 | |
| **MZ00036531** | hypothetical protein {Oryza sativa} | 1.008471784 | 0.00961719 | |
| **MZ00036538** | subtilisin/chymotrypsin inhibitor {Zea mays} | 1.195270515 | 0.00786864 | |

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|---|---|---|---|---|
| **MZ00036544** | probable cytochrome P450 monooxygenase {Zea mays} | 1.395566362 | 0.00077366 | |
| **MZ00036635** | hypothetical protein {Zea mays} | 1.345974808 | 0.02378928 | |
| **MZ00036754** | hypothetical protein {Zea mays} | 2.521828061 | 0.00346663 | |
| **MZ00036758** | hypothetical protein {Zea mays} | 1.14114505 | 8.51E-05 | |
| **MZ00036768** | putative senescence-associated protein {Pisum sativum} | 1.713283174 | 0.00029757 | |
| **MZ00036791** | hypothetical protein {Zea mays} | 1.425780091 | 0.00328259 | |
| **MZ00036819** | putative senescence-associated protein {Pisum sativum} | 1.76285171 | 0.00391167 | |
| **MZ00036829** | putative senescence-associated protein {Pisum sativum} | 1.829644036 | 0.00306785 | |
| **MZ00036845** | unnamed protein product | 2.677675051 | 0.00112489 | |
| **MZ00036847** | Ac1147 {Rattus norvegicus} | 2.273354409 | 0.00136262 | |
| **MZ00036916** | NA | 2.712528549 | 0.00075519 | |
| **MZ00036918** | CDH1-D {Gallus gallus} | 2.635988843 | 0.00291371 | |
| **MZ00036934** | unnamed protein product | 2.459725572 | 0.00058132 | |
| **MZ00036948** | NA | -1.092872771 | 0.10983161 | |
| **MZ00036957** | protein phosphatase 2C isoform gamma {Zea mays} | 1.000833318 | 0.45243199 | |
| **MZ00037011** | hypothetical protein {Sorghum bicolor} | 1.648072715 | 0.00026833 | |
| **MZ00037032** | beta-glucosidase aggregating factor precursor {Zea mays} | 1.042936523 | 0.52779442 | |
| **MZ00037037** | unnamed protein product | 2.508856965 | 0.00151149 | |
| **MZ00037070** | polyamine oxidase1 {Zea mays} | 1.882864467 | 0.00893681 | |
| **MZ00037083** | metallothionein-like protein {Zea mays} | -1.30986033 | 0.26800897 | |
| **MZ00037085** | Bowman-Birk type wound-induced proteinase inhibitor WIP1 {Zea mays} | 3.145357742 | 1.01E-07 | |
| **MZ00037127** | hypothetical protein {Zea mays} | 1.283188616 | 0.00871686 | |
| **MZ00037226** | putative Regulatory protein NPR1 {Oryza sativa} | 1.158551478 | 0.02019668 | |
| **MZ00037253** | subtilisin/chymotrypsin inhibitor {Zea mays} | 1.341218552 | 0.01083495 | |
| **MZ00037304** | terpene synthase 2 {Zea mays} | 2.478170865 | 9.15E-06 | |
| **MZ00037445** | NA | 2.012765459 | 0.06455987 | |
| **MZ00037482** | putative senescence-associated protein {Pisum sativum} | 1.196111214 | 0.03836735 | |

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|---|---|---|---|---|
| **MZ00037636** | 2-oxoglutarate-dependent oxygenase {Zea mays} | 1.300747818 | 0.05385622 | |
| **MZ00038613** | PseuodARR-B transcription factor {Zea mays} | 1.010471674 | 0.00796261 | |
| **MZ00038794** | elongation factor 1alpha {Zea mays} | 1.880044664 | 2.85E-05 | |
| **MZ00038859** | hypothetical protein {Zea mays} | 1.393594349 | 0.00110408 | |
| **MZ00039037** | plastid-specific 30S ribosomal protein 3 {Zea mays} | -1.109421309 | 0.08519377 | |
| **MZ00039051** | putative potassium transporter {Oryza sativa} | 1.141033632 | 0.10016461 | |
| **MZ00039088** | 1,4-alpha-glucan branching enzyme {Zea mays} | 1.272853793 | 0.00250618 | |
| **MZ00039164** | inositol phosphatase-like protein {Oryza sativa} | 1.203209221 | 0.20528438 | |
| **MZ00039285** | alpha-zein protein {Zea mays} | 2.06370811 | 0.00318572 | |
| **MZ00039489** | Bowman-Birk type wound-induced proteinase inhibitor {Zea mays} | 1.171174207 | 0.07264903 | |
| **MZ00039593** | NA | 1.299125433 | 0.19897827 | |
| **MZ00039598** | blue fluorescent1 {Zea mays} | 1.02023615 | 0.00446823 | |
| **MZ00039734** | beta-glucosidase {Zea mays} | 1.539320025 | 0.00015339 | |
| **MZ00039764** | Bowman-Birk type wound-induced proteinase inhibitor WIP1 {Zea mays} | 2.785896639 | 4.82E-06 | |
| **MZ00039805** | hypothetical protein {Zea mays} | 1.044672424 | 0.00455325 | |
| **MZ00039806** | anthranilate synthase component II {Zea mays} | 1.372195418 | 0.10902343 | |
| **MZ00039973** | ribosomal protein L2 {Saccharum officinarum} | 1.281628918 | 0.28746312 | |
| **MZ00040003** | NA | 1.743584142 | 0.00545019 | |
| **MZ00040009** | W22 ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit {Zea mays} | 1.17171518 | 0.33207763 | |
| **MZ00040034** | germin-like protein {Zea mays} | -1.11057651 | 0.12083606 | |
| **MZ00040075** | Granule-bound starch synthase precursor {Zea mays} | 1.125875028 | 0.07774499 | |
| **MZ00040188** | photosystem II protein K {Oryza sativa} | 1.188031134 | 0.18562822 | |
| **MZ00040243** | hypothetical protein {Zea mays} | 1.106538341 | 0.14931719 | |
| **MZ00040343** | prephenate dehydratase {Ipomoea trifida} | 1.112203562 | 0.00216773 | |

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|---|---|---|---|---|
| **MZ00040479** | coupling factor beta-subunit and coupling factor epsilon subunit {Zea mays} | 3.822815669 | 6.92E-05 | |
| **MZ00040486** | Ribulose bisphosphate carboxylase large chain precursor {Zea mays} | 2.733285584 | 5.74E-05 | |
| **MZ00040508** | NA | 1.554799983 | 0.00531562 | |
| **MZ00040525** | coupling factor beta-subunit and coupling factor epsilon subunit {Zea mays} | 3.671220342 | 7.94E-05 | |
| **MZ00040527** | ribosomal protein L2 {Zea mays} | 2.540899268 | 0.03867241 | |
| **MZ00040628** | myb-related gene Zm1 {Zea mays} | -1.27109151 | 0.01837966 | |
| **MZ00040654** | glutathione S-transferase GST 25 {Zea mays} | 1.854784425 | 6.03E-06 | |
| **MZ00040686** | sesquiterpene cyclase {Zea mays} | 1.145045375 | 0.00142632 | |
| **MZ00040778** | Late embryogenesis abundant protein {Zea mays} | -1.139368541 | 0.01569762 | |
| **MZ00040799** | psaI gene {Zea mays} | 2.230967347 | 0.00308213 | |
| **MZ00040800** | Photosystem II reaction center I protein {Triticum aestivum} | 1.942170688 | 0.00426513 | |
| **MZ00040803** | NA | 1.964366004 | 0.00591802 | |
| **MZ00040806** | Chloroplast 50S ribosomal protein L23 {Zea mays} | 2.11583341 | 0.08656297 | |
| **MZ00040807** | ribosomal protein L33, chloroplast {Zea mays} | 1.4412571 | 0.00317229 | |
| **MZ00040840** | hypothetical protein {Oryza sativa} | 1.502598241 | 0.00429305 | |
| **MZ00040842** | strongly similar to NP_195589.2 splicing factor | 2.401907649 | 0.00244596 | |
| **MZ00041005** | subtilisin/chymotrypsin inhibitor {Zea mays} | 1.923266389 | 0.00086624 | |
| **MZ00041019** | gibberellin responsive2 {Zea mays} | -1.838835982 | 0.08294999 | |
| **MZ00041271** | lipoxygenase {Zea mays} | 2.505159931 | 1.66E-06 | |
| **MZ00041304** | glutaredoxin homolog1 {Zea mays} | 2.024433968 | 0.15610566 | |
| **MZ00041326** | putative Bowman-Birk serine protease inhibitor {Zea mays} | -1.011123658 | 0.0677727 | |
| **MZ00041462** | putative LHY protein {Oryza sativa} | 1.173702164 | 0.09398768 | |
| **MZ00041612** | Nonspecific lipid-transfer protein precursor {Zea mays} | -1.010754305 | 0.12150455 | |
| **MZ00041682** | pyruvate, orthophosphate dikinase1 {Zea mays} | 1.461197038 | 0.00067066 | |
| **MZ00041721** | ADP-ribosylation factor GTPase-activating | 1.021027131 | 0.00450159 | |

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|---|---|---|---|---|
| | protein {Zea mays} | | | |
| **MZ00041757** | early light-induced protein {Zea mays} | -1.326550517 | 0.01909108 | |
| **MZ00041768** | putative zinc finger protein {Zea mays} | 1.876859616 | 0.00674281 | |
| **MZ00042158** | ripening-related protein {Zea mays} | 1.288863788 | 1.26E-05 | |
| **MZ00042245** | O-succinylhomoserine sulfhydrylase {Zea mays} | 1.348953347 | 0.00021578 | |
| **MZ00042324** | ribosome-inactivating protein {Zea mays} | 2.192584792 | 7.35E-05 | |
| **MZ00042472** | unknown protein {Oryza sativa} | 1.399418899 | 0.00192199 | |
| **MZ00042564** | transducin {Oryza sativa} | 1.243124141 | 0.03349451 | |
| **MZ00042637** | phosphoenolpyruvate carboxylase {Zea mays} | 1.425763064 | 0.00813485 | |
| **MZ00042678** | ribosome-inactivating protein {Zea mays} | 1.898939795 | 0.00680879 | |
| **MZ00042841** | Histone H2A {Zea mays} | 2.564840296 | 0.00138606 | |
| **MZ00042873** | S-adenosylmethionine synthetase 1 {Zea mays} | 1.229118789 | 0.01383571 | |
| **MZ00042935** | Bowman-Birk type wound-induced proteinase inhibitor {Zea mays} | 1.693144719 | 0.00062321 | |
| **MZ00042953** | chlorophyll a/b binding protein {Oryza sativa} | 2.437134414 | 0.00062186 | |
| **MZ00042981** | hypothetical protein {Zea mays} | 1.210135134 | 0.06125176 | |
| **MZ00043035** | chitinase {Zea mays} | 1.08489003 | 0.01839433 | |
| **MZ00043120** | glycogen synthase kinase-3 MsK-3 {Zea mays} | 1.224967912 | 0.20131319 | |
| **MZ00043160** | hypothetical protein {Zea mays} | 1.269621672 | 0.1367847 | |
| **MZ00043232** | putative glycine-rich protein {Oryza sativa} | 1.290025949 | 0.00063507 | |
| **MZ00043311** | patatin-like protein {Sorghum bicolor} | 1.006969191 | 0.05401471 | |
| **MZ00043393** | 2-oxoglutarate-dependent oxygenase {Zea mays} | 1.900113408 | 2.34E-06 | |
| **MZ00043436** | hypothetical protein {Zea mays} | -1.516879775 | 0.09696187 | |
| **MZ00043437** | 36.4 kDa proline-rich protein {Zea mays} | -1.270344591 | 0.39887341 | |
| **MZ00043517** | allene oxide cyclase {Zea mays} | 1.031104822 | 0.04933524 | |
| **MZ00043695** | hypothetical protein {Zea mays} | 1.076869941 | 0.28161283 | |
| **MZ00043885** | farnesyl-pyrophosphate synthetase {Oryza sativa} | 1.333004762 | 0.00146245 | |
| **MZ00044190** | allene oxide synthase {Zea mays} | 2.077496591 | 0.00026439 | |
| **MZ00044245** | lipoxygenase6 {Zea mays} | 1.112313827 | 0.00120756 | |
| **MZ00044256** | naringenin 3-dioxygenase {Zea mays} | -1.028395083 | 0.04002628 | |
| **MZ00044555** | putative phosphoribosyl pyrophosphate | 2.84328689 | 2.73E-07 | |

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|---|---|---|---|---|
| | synthase {Oryza sativa} | | | |
| **MZ00045590** | putative senescence-associated protein {Pisum sativum} | 1.764488313 | 0.00297732 | |
| **MZ00046685** | unknown protein {Oryza sativa} | 1.21984965 | 0.00042702 | |
| **MZ00046774** | alpha expansin1 {Zea mays} | 1.235942194 | 0.00035693 | |
| **MZ00046814** | zeaxanthin epoxidase {Zea mays} | 1.07631936 | 0.00918206 | |
| **MZ00047625** | hypothetical protein {Arabidopsis thaliana} | 1.027418035 | 0.33318035 | |
| **MZ00047697** | unknown protein {Oryza sativa} | 1.166447195 | 5.05E-05 | |
| **MZ00048483** | ZIM-motif family protein {Zea mays} | 1.160538777 | 0.0253863 | |
| **MZ00048932** | putative PPR protein {Oryza sativa} | 1.039192736 | 0.00870651 | |
| **MZ00049082** | von Willebrand factor type A domain containing protein {Zea mays} | 1.05442141 | 0.00012978 | |
| **MZ00049092** | G-box binding protein {Oryza sativa} | 1.030464571 | 2.35E-05 | TF21 |
| **MZ00052267** | putative senescence-associated protein {Pisum sativum} | 2.69681953 | 0.00070173 | |
| **MZ00054821** | putative cellulose synthase, catalytic subunit {Oryza sativa} | 1.021784979 | 0.10730215 | |
| **MZ00054822** | phospho-2-dehydro-3-deoxyheptonate aldolase 1 {Zea mays} | 1.179987378 | 8.69E-05 | |
| **MZ00054897** | glutathione S-transferase GST 25 {Zea mays} | 1.022009763 | 0.0029306 | |
| **MZ00055184** | putative senescence-associated protein {Pisum sativum} | 1.627309067 | 0.00227724 | |
| **MZ00055270** | ripening-related protein {Zea mays} | 1.134046361 | 0.00333059 | |
| **MZ00055448** | hypothetical protein {Zea mays} | 1.429817444 | 0.00181569 | |
| **MZ00055463** | esterase {Zea mays} | 1.628271524 | 1.65E-06 | |
| **MZ00055632** | NA | 1.13429863 | 0.00111829 | |
| **MZ00055932** | Bowman-Birk type trypsin inhibitor {Zea mays} | 1.858499428 | 5.62E-05 | |
| **MZ00056320** | NA | 1.108260008 | 0.12288358 | |
| **MZ00056687** | farnesyl pyrophosphate synthase1 {Zea mays} | 1.368180368 | 0.00848017 | |
| **MZ00056914** | lipid binding protein {Zea mays} | -1.396168321 | 0.00961975 | |
| **MZ00056987** | acyl-desaturase {Zea mays} | 1.49581173 | 0.0024615 | |
| **MZ00057163** | putative dehydration-induced myb-related protein Cpm7 {Oryza sativa} | 1.191934847 | 0.14664984 | |
| **MZ00057436** | putative ZEITLUPE {Oryza sativa} | 1.271767928 | 0.03065219 | |

**Tab.7. 4: 4 h after feeding induction**

| MZ-number | Annotation | fold expression (log10) | p-value | Abbrevation |
|---|---|---|---|---|
| **MZ00000418** | transferase {Zea mays} | 1.647718896 | 0.00010682 | |
| **MZ00000664** | RING finger-like {Oryza sativa} | 1.029575535 | 0.00119236 | TF50 |
| **MZ00001096** | putative multidrug resistance protein {Oryza sativa} | 1.206465531 | 0.01457681 | |
| **MZ00001464** | NA | 1.296340485 | 0.01500009 | |
| **MZ00003835** | nonspecific lipid-transfer protein AKCS9 {Zea mays} | 2.412798892 | 7.43E-06 | |
| **MZ00004337** | O-methyltransferase BX7 {Zea mays} | 1.014204268 | 1.56E-05 | |
| **MZ00004436** | acidic class I chitinase {Zea mays} | 1.437908238 | 6.15E-07 | |
| **MZ00004614** | glucose-6-phosphate/phosphate translocator 2 {Zea mays} | 1.086569521 | 0.00062124 | |
| **MZ00005060** | putative tyrosine/dopa decarboxylase {Oryza sativa} | 1.060656784 | 8.12E-05 | |
| **MZ00005219** | Bowman-Birk type trypsin inhibitor {Zea mays} | 2.100082667 | 2.45E-08 | |
| **MZ00005242** | 4-methyl-5-thiazole monophosphate biosynthesis protein {Zea mays} | 1.085640116 | 0.00042067 | |
| **MZ00005352** | NA | 1.097040333 | 0.04385328 | |
| **MZ00005405** | farnesyl pyrophosphate synthase1 {Zea mays} | 3.009614571 | 2.57E-06 | |
| **MZ00005471** | putative tyrosine/dopa decarboxylase {Oryza sativa} | 2.251851334 | 2.40E-06 | |
| **MZ00005511** | hypothetical protein {Zea mays} | 1.894304158 | 6.41E-06 | |
| **MZ00005543** | lingual lipase-like {Oryza sativa} | 1.147904357 | 0.03654641 | |
| **MZ00005899** | terpene synthase 2 {Zea mays} | 3.07901935 | 2.72E-08 | |
| **MZ00005958** | indole-3-glycerol phosphate lyase {Zea mays} | 2.278405955 | 0.00121973 | |
| **MZ00012674** | zinc finger protein 3{Zea mays} | 2.013439353 | 1.86E-06 | |
| **MZ00012818** | NA | 1.087796896 | 5.94E-05 | |
| **MZ00013037** | pyruvate,orthophosphate dikinase {Zea mays} | 1.244240049 | 0.04504177 | |
| **MZ00013321** | hypothetical protein {Sorghum bicolor} | 1.225292226 | 1.10E-05 | |

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|---|---|---|---|---|
| **MZ00013555** | hypothetical protein {Zea mays} | 2.137020135 | 0.00024802 | |
| **MZ00013773** | UDP-glucose 6-dehydrogenase {Zea mays} | 1.785566767 | 6.63E-05 | |
| **MZ00013816** | adenosine kinase {Zea mays} | 1.476870418 | 1.23E-06 | |
| **MZ00013836** | S-adenosylmethionine decarboxylase {Oryza sativa} | 1.090388287 | 0.01679961 | |
| **MZ00013840** | phospho-2-dehydro-3-deoxyheptonate aldolase 1 {Zea mays} | 2.616442997 | 3.94E-06 | |
| **MZ00013846** | lipoxygenase11 {Zea mays} | 2.774923944 | 0.02267559 | |
| **MZ00013941** | profilin A {Zea mays} | -1.040261611 | 0.01892245 | |
| **MZ00014008** | farnesyl pyrophosphate synthase1 {Zea mays} | 1.416681809 | 0.00485544 | |
| **MZ00014027** | glycine hydroxymethyltransferase {Arabidopsis thaliana} | 2.336426886 | 6.81E-07 | |
| **MZ00014197** | ribonucleoprotein A {Zea mays} | -1.773472715 | 0.03465986 | |
| **MZ00014212** | putative thioredoxin {Oryza sativa} | 1.477468485 | 0.01147305 | |
| **MZ00014229** | pathogenesis-related protein 10 {Zea mays} | 1.304638089 | 0.01517031 | |
| **MZ00014307** | Cytochrome P450 71C2 {Zea mays}^\|^GB\|CAA72208.1\|1870201\|ZMCI31 AC2 cytoc-TRUNCATED- | 2.792136642 | 6.63E-05 | |
| **MZ00014361** | NADP-dependent malic enzyme {Zea mays} | 1.02233304 | 0.02336121 | |
| **MZ00014377** | nodulation homolog 1 {Zea mays} | -1.379055539 | 0.00783907 | |
| **MZ00014624** | hypothetical protein {Zea mays} | 1.480555719 | 1.71E-05 | |
| **MZ00014883** | beta-D-glucan exohydrolase {Zea mays} | -1.286702844 | 0.0052577 | |
| **MZ00014943** | anthranilate synthase alpha 2 subunit {Oryza sativa} | 1.521101771 | 0.00161973 | |
| **MZ00015021** | polyphenol oxidase {Saccharum hybrid cultivar} | 2.698095179 | 5.66E-07 | |
| **MZ00015105** | indole synthase {Zea mays} | 2.898369593 | 1.16E-06 | |
| **MZ00015138** | UDP-glucuronic acid decarboxylase {Oryza sativa} | 1.310454838 | 0.00043916 | |
| **MZ00015154** | cylicin-1 {Zea mays} | 1.035090828 | 0.0085689 | |
| **MZ00015227** | putative Magnaporthe grisea pathogenicity protein {Oryza sativa} | 1.048192452 | 0.00019924 | |
| **MZ00015397** | hypothetical protein {Oryza sativa} | -1.057378026 | 0.01781058 | |
| **MZ00015502** | vacuolar sorting receptor homolog {Zea mays} | 2.340645738 | 1.61E-05 | |

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|---|---|---|---|---|
| **MZ00015504** | blue fluorescent1 {Zea mays} | 3.294858187 | 1.13E-07 | |
| **MZ00015505** | putative fruit protein {Oryza sativa} | 2.464343265 | 0.00280619 | |
| **MZ00015562** | putative C-4 sterol methyl oxidase {Oryza sativa} | 1.146349495 | 5.17E-05 | |
| **MZ00015582** | NA | -1.382495022 | 0.0018843 | |
| **MZ00015701** | lipoxygenase {Zea mays} | 3.426651786 | 2.87E-05 | |
| **MZ00015910** | glycine-rich protein1 {Zea mays} | 1.608130556 | 0.0001958 | |
| **MZ00016101** | putative RAB7A protein (GTP-binding protein) {Oryza sativa} | 1.214100915 | 0.00070002 | TF49 |
| **MZ00016102** | UDP-glucosyltransferase BX8 {Zea mays} | 1.217485779 | 0.00011047 | |
| **MZ00016249** | probable hydroxymethylglutaryl-CoA reductase {Oryza sativa} | 1.055182242 | 0.0236022 | |
| **MZ00016502** | spermidine synthase {Zea mays} | 1.244468942 | 6.64E-06 | |
| **MZ00016732** | plasma membrane intrinsic protein ZmPIP2-6 {Zea mays} | 1.462920291 | 1.09E-05 | |
| **MZ00016835** | nucleotide pyrophosphatase/phosphodiesterase {Zea mays} | 2.171743586 | 6.76E-06 | |
| **MZ00016891** | desiccation-related protein {Zea mays} | 1.00284981 | 0.01941399 | |
| **MZ00017092** | hypothetical protein {Zea mays} | 3.40528207 | 0.00042136 | |
| **MZ00017211** | hypothetical protein {Zea mays} | 2.041112354 | 0.00147243 | |
| **MZ00017265** | MtN3-like protein {Arabidopsis thaliana} | 1.787407692 | 3.35E-05 | |
| **MZ00017300** | hypothetical protein {Zea mays} | 1.519836765 | 2.81E-05 | |
| **MZ00017392** | flavonoid 3-monooxygenase {Zea mays} | 2.3033303 | 0.00126532 | |
| **MZ00017601** | hydroperoxide lyase {Zea mays} | 1.507149055 | 1.52E-06 | |
| **MZ00017669** | ATP-dependent Clp protease ATP-binding subunit precursor {Oryza sativa} | 1.023755915 | 0.00594516 | |
| **MZ00018225** | branched-chain-amino-acid aminotransferase {Zea mays} | 1.61386825 | 5.11E-05 | |
| **MZ00018234** | OSJNBb0085F13.14 {Oryza sativa} | 2.238448389 | 0.00010782 | |
| **MZ00018241** | ribosome-inactivating protein {Zea mays} | 4.00774054 | 2.22E-06 | |
| **MZ00018568** | hypothetical protein {Zea mays} | 4.382704752 | 1.57E-08 | |
| **MZ00018837** | MAPK6 {Oryza sativa} | 1.050730695 | 0.02275596 | |
| **MZ00019117** | chitinase {Zea mays} | 1.46420269 | 1.87E-09 | |
| **MZ00019196** | senescence-associated protein DH {Zea mays} | 1.46074733 | 2.34E-05 | |

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|---|---|---|---|---|
| **MZ00019212** | Cytochrome P450 98A1 {Sorghum bicolor} | 1.271706542 | 5.22E-06 | |
| **MZ00019387** | unknown protein {Oryza sativa} | 1.357516679 | 0.02117362 | |
| **MZ00019475** | anthranilate N-benzoyltransferase protein 1 {Zea mays} | 2.448152777 | 4.23E-05 | |
| **MZ00019533** | putative class I chitinase {Cryptomeria japonica} | 2.474647715 | 1.60E-05 | |
| **MZ00019560** | putative AMP deaminase {Oryza sativa} | 1.853404456 | 5.69E-05 | |
| **MZ00019701** | hypothetical protein {Oryza sativa} | 4.787255698 | 3.80E-08 | |
| **MZ00019729** | terpene synthase 2 {Zea mays} | 3.979099203 | 3.50E-07 | |
| **MZ00019785** | hypothetical protein {Zea mays} | 1.211209862 | 0.01378212 | |
| **MZ00019894** | stem 28 kDa glycoprotein {Zea mays} | 3.881688222 | 7.90E-06 | |
| **MZ00019895** | putative casein kinase {Oryza sativa} | 1.135924211 | 6.10E-06 | |
| **MZ00020111** | 4-coumarate--CoA ligase 4CL1 {Lolium perenne} | 1.771570295 | 0.00010365 | |
| **MZ00020230** | epoxide hydrolase 2 {Zea mays} | 2.455054342 | 0.00023007 | |
| **MZ00020437** | O-methyltransferase ZRP4 {Zea mays} | 1.482863701 | 1.22E-05 | |
| **MZ00020525** | hypothetical protein {Zea mays} | 1.156131212 | 0.00469091 | |
| **MZ00020592** | aluminum-induced protein {Zea mays} | 1.09956014 | 0.01715516 | |
| **MZ00020968** | putative lipase class 3 family protein {Oryza sativa} | 2.882426198 | 6.84E-06 | |
| **MZ00021254** | OSJNBa0065B15.8 {Oryza sativa} | 2.323154923 | 0.0027783 | |
| **MZ00021663** | dehydration-responsive element-binding protein {Zea mays} | 1.151011291 | 0.02685228 | |
| **MZ00021682** | unknown {Oryza sativa} | -1.381465127 | 0.02418672 | |
| **MZ00021951** | adenosine 5'-phosphosulfate reductase-like2 {Zea mays} | 1.05629426 | 0.00968449 | |
| **MZ00021997** | putative auxin-regulated protein {Oryza sativa} | 1.067903291 | 0.00615988 | |
| **MZ00022083** | 1-deoxy-D-xylulose 5-phosphate synthase {Zea mays} | 1.053043025 | 3.49E-05 | |
| **MZ00022163** | putative 10-deacetylbaccatin III-10-O-acetyl transferase {Oryza sativa} | 4.899689512 | 4.25E-06 | |
| **MZ00022180** | hypothetical protein {Zea mays} | 1.764031312 | 1.85E-06 | |
| **MZ00022800** | serine carboxypeptidase K10B2.2 {Zea mays} | 2.031921506 | 6.62E-06 | |
| **MZ00022994** | allene oxide synthase {Zea mays} | 2.643815963 | 1.04E-09 | |

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|---|---|---|---|---|
| **MZ00023013** | unknown protein {Oryza sativa} | 1.776995487 | 3.84E-05 | |
| **MZ00023087** | hypothetical protein {Zea mays} | 1.027214959 | 0.00061337 | |
| **MZ00023228** | dihydroflavonol-4-reductase {Zea mays} | 1.402008269 | 0.00158823 | |
| **MZ00023318** | putative prephenate dehydratase {Oryza sativa} | 1.547390935 | 1.64E-06 | |
| **MZ00023438** | adenosylhomocysteinase {Zea mays} | 2.425651631 | 4.44E-07 | |
| **MZ00023441** | S-adenosylmethionine synthetase 1 {Zea mays} | 2.898485381 | 2.76E-06 | |
| **MZ00023501** | pnFL-2 {Zea mays} | 1.734685259 | 0.00191934 | |
| **MZ00023547** | putative aminotransferase class-III {Oryza sativa} | 1.647437738 | 0.01440386 | |
| **MZ00023983** | ribonuclease S homolog {Zea mays} | 2.668811706 | 6.74E-08 | |
| **MZ00024058** | cortical cell-delineating protein {Zea mays} | 1.350617385 | 5.68E-06 | |
| **MZ00024099** | hypothetical protein {Zea mays} | 1.008994697 | 0.00604603 | |
| **MZ00024166** | Cytochrome P450 71C1 {Zea mays} | 1.190936906 | 6.00E-05 | |
| **MZ00024196** | superoxide dismutase {Zea mays} | 2.573824329 | 1.75E-07 | |
| **MZ00024204** | putative C-4 sterol methyl oxidase {Oryza sativa} | 1.801911567 | 0.00596782 | |
| **MZ00024232** | vacuolar ATP synthase 16 kDa proteolipid subunit {Zea mays} | 1.072665632 | 3.39E-05 | |
| **MZ00024287** | monodehydroascorbate reductase {Oryza sativa} | 1.0840865 | 7.41E-05 | |
| **MZ00024296** | 2-oxoglutarate-dependent oxygenase {Zea mays} | 1.10563189 | 0.00255405 | |
| **MZ00024350** | anthranilate synthase component II {Zea mays} | 2.409350416 | 0.00229962 | |
| **MZ00024351** | anthranilate synthase component II {Zea mays} | 2.01451089 | 3.93E-05 | |
| **MZ00024544** | cold shock protein-1 {Triticum aestivum;} | 1.499160326 | 5.69E-06 | |
| **MZ00024574** | NADH dependent Glutamate Synthase {Oryza sativa} | 1.127233867 | 0.00792172 | |
| **MZ00024618** | putative chorismate mutase precursor {Oryza sativa} | 1.29047541 | 0.00498575 | |
| **MZ00024662** | putative indole-3-glycerol phosphate synthase {Oryza sativa} | 1.389109439 | 0.00016764 | |
| **MZ00024672** | methylenetetrahydrofolate reductase {Zea | 1.728822638 | 7.12E-05 | |

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|---|---|---|---|---|
| | mays} | | | |
| **MZ00025068** | hypothetical protein {Zea mays} | 1.685936725 | 0.00034882 | |
| **MZ00025169** | DEAD box RNA helicase {Zea mays} | 1.183698296 | 0.03741489 | |
| **MZ00025206** | O-methyltransferase BX7 {Zea mays} | 2.134200036 | 1.11E-06 | |
| **MZ00025407** | polyamine oxidase1 (pao1) {Zea mays} | 3.881562411 | 3.34E-08 | |
| **MZ00025508** | lipoxygenase {Zea mays} | 1.010782356 | 0.00575184 | |
| **MZ00025768** | glutathione S-transferase GST 20 {Zea mays} | 3.77124288 | 2.02E-06 | |
| **MZ00025815** | 1,4-alpha-glucan branching enzyme {Zea mays} | 1.036859589 | 0.0149282 | |
| **MZ00025895** | farnesyl-pyrophosphate synthetase {Oryza sativa} | 2.579127864 | 0.00038868 | |
| **MZ00026064** | hypothetical protein {Zea mays} | 1.184553754 | 0.00338943 | |
| **MZ00026065** | Uroporphyrinogen decarboxylase {Zea mays} | -1.106241231 | 0.03380446 | |
| **MZ00026277** | hypothetical protein {Zea mays} | 1.286843129 | 0.00035883 | |
| **MZ00026471** | anthranilate synthase alpha 1 subunit {Oryza sativa} | 4.106031991 | 1.38E-07 | |
| **MZ00026538** | ZIM-motif family protein {Zea mays} | 1.577377563 | 0.00303287 | |
| **MZ00026684** | hypothetical protein {Zea mays} | 1.017309026 | 0.00198065 | |
| **MZ00026717** | membrane protein-like {Oryza sativa} | 1.309573377 | 2.98E-05 | |
| **MZ00026739** | putative lipase {Arabidopsis thaliana} | 3.788609788 | 0.00127186 | |
| **MZ00026889** | unknown protein {Oryza sativa} | 1.050254905 | 4.16E-05 | |
| **MZ00027029** | 12-oxo-phytodienoic acid reductase8 {Zea mays} | 1.760037257 | 2.78E-05 | |
| **MZ00027030** | 12-oxo-phytodienoic acid reductase8 {Zea mays} | 1.677728673 | 0.00575783 | |
| **MZ00027105** | putative Bowman-Birk serine protease inhibitor {Oryza sativa} | 1.080427659 | 0.00141663 | |
| **MZ00027113** | cell death suppressor protein lls1 {Zea mays} | 1.013428417 | 0.03161038 | |
| **MZ00027387** | cinnamyl alcohol dehydrogenase1 {Zea mays} | 3.455374242 | 2.35E-06 | |
| **MZ00027491** | Cytochrome P450 71C4 {Zea mays} | 3.489589549 | 6.03E-06 | |
| **MZ00027637** | chloride channel {Zea mays} | 1.657696416 | 1.81E-05 | |
| **MZ00028098** | NADP-dependent oxidoreductase P1 {Zea mays} | 1.104943201 | 0.0008107 | |
| **MZ00028511** | ferredoxin-1 {Zea mays} | 1.777191667 | 0.00174606 | |
| **MZ00028617** | putative cytochrome P450 {Oryza sativa} | -1.069192553 | 0.03567487 | |

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|---|---|---|---|---|
| **MZ00028806** | OSJNBb0039L24.4 {Oryza sativa} | 1.008487868 | 0.00260146 | |
| **MZ00028898** | hypothetical protein {Zea mays} | 1.162896807 | 0.00202356 | |
| **MZ00029141** | hypothetical protein {Zea mays} | 1.492809751 | 0.0151496 | |
| **MZ00029195** | putative phosphoribosyl pyrophosphate synthase {Oryza sativa} | 2.45294004 | 7.05E-06 | |
| **MZ00029386** | glycoside hydrolase {Zea mays} | 1.954809177 | 7.81E-06 | |
| **MZ00029560** | phytocystatin {Actinidia deliciosa} | 5.654218225 | 1.95E-08 | |
| **MZ00029584** | arogenate dehydrogenase {Zea mays} | 2.620787512 | 2.78E-09 | |
| **MZ00029594** | sesquiterpene cyclase {Zea mays} | 2.273228904 | 1.33E-07 | |
| **MZ00029921** | anthranilic acid methyltransferase 1 {Zea mays} | 1.812580743 | 0.0128333 | |
| **MZ00030045** | elicitor inducible beta-1,3-glucanase-like {Oryza sativa} | 1.20452908 | 0.01864414 | |
| **MZ00030298** | sucrose-phosphatase {Zea mays} | 2.016399959 | 1.09E-07 | |
| **MZ00030501** | terpene synthase {Zea mays} | 1.104756847 | 0.00066751 | |
| **MZ00030570** | hypothetical protein {Zea mays} | 1.123078132 | 0.00010771 | |
| **MZ00030642** | chemocyanin {Zea mays} | 2.322197319 | 2.32E-06 | |
| **MZ00030744** | integral membrane protein DUF6 containing protein {Zea mays} | 1.241663347 | 0.01185062 | |
| **MZ00030829** | aldo-keto reductase/ oxidoreductase {Zea mays} | 2.130167564 | 0.00041614 | |
| **MZ00031013** | PDR-like ABC transporter {Oryza sativa} | 1.035294458 | 0.00529047 | |
| **MZ00031018** | ethylene-responsive transcription factor 4 {Zea mays} | 1.168680405 | 0.00140573 | |
| **MZ00031067** | RING zinc finger protein-like {Zea mays} | 1.020444315 | 9.18E-05 | |
| **MZ00031356** | unknown protein {Oryza sativa} | 1.843466329 | 1.55E-05 | |
| **MZ00031407** | hypothetical protein {Sorghum bicolor} | 1.603643997 | 0.00388671 | |
| **MZ00031476** | putative oxysterol-binding protein {Zea mays} | 1.263785725 | 0.00838334 | |
| **MZ00031477** | hypothetical protein {Zea mays} | 1.328280615 | 2.67E-05 | |
| **MZ00031481** | NA | 1.001796222 | 0.0002705 | |
| **MZ00031624** | putative prephenate dehydratase {Oryza sativa} | 1.191331874 | 0.00020282 | |
| **MZ00031651** | hypothetical protein {Zea mays} | 1.128068735 | 0.00060626 | |
| **MZ00031721** | hypothetical protein {Zea mays} | 1.014749425 | 0.00123222 | |
| **MZ00031736** | terpene synthase10 {Zea mays} | 4.13524189 | 9.78E-06 | |

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|---|---|---|---|---|
| **MZ00031748** | hypothetical protein {Zea mays} | 1.784642927 | 0.00036155 | |
| **MZ00031957** | unknown protein {Oryza sativa} | 2.794228564 | 3.87E-08 | |
| **MZ00031982** | putative naphthoate synthase {Oryza sativa} | -1.157700769 | 0.0022313 | |
| **MZ00032043** | anthranilic acid methyltransferase 3 {Zea mays} | 2.514674154 | 3.60E-06 | |
| **MZ00032136** | 1-deoxy-D-xylulose 5-phosphate synthase 2 (dxs2) {Zea mays} | 3.509334029 | 5.53E-09 | |
| **MZ00032240** | indole-3-glycerol phosphate synthase {Zea mays} | 2.924372824 | 4.27E-07 | |
| **MZ00032974** | putative protein {Oryza sativa} | 1.463064686 | 0.00012928 | |
| **MZ00032999** | indole-3-glycerol phosphate lyase {Zea mays} | 2.095648312 | 0.00013394 | |
| **MZ00033132** | putative pirin {Oryza sativa} | 1.766897353 | 0.00064096 | |
| **MZ00033298** | OSJNBa0094O15.5 {Oryza sativa} | 1.258139749 | 2.42E-05 | |
| **MZ00033310** | MPI {Tripsacum dactyloides} | 4.942795839 | 3.76E-08 | |
| **MZ00033339** | Histidine-rich glycoprotein precursor {Dictyostelium discoideum} | 1.298137318 | 0.01295126 | |
| **MZ00033428** | putative chitinase {Musa acuminata} | 1.032715744 | 0.00026745 | |
| **MZ00033723** | hypothetical protein {Zea mays} | 1.277967278 | 4.51E-06 | |
| **MZ00034292** | S-adenosylmethionine synthetase 1 {Oryza sativa} | 1.731836302 | 0.00254092 | |
| **MZ00034295** | methionine synthase {Zea mays} | 3.685154095 | 9.85E-09 | |
| **MZ00034298** | seed specific protein of balanced nutritional quality {Amaranthus hypochondriacus} | 2.735807896 | 2.27E-05 | |
| **MZ00034300** | chitinase {Zea mays} | 1.672698603 | 0.01447863 | |
| **MZ00034308** | natterin 3 precursor {Thalassophryne nattereri} | 2.736152141 | 7.31E-05 | |
| **MZ00034328** | putative branched-chain alpha keto-acid dehydrogenase E1 alpha subunit {Arabidopsis thaliana} | 1.096548339 | 0.0047625 | |
| **MZ00034331** | 2-oxoglutarate-dependent oxygenase {Zea mays} | 1.895001827 | 1.53E-06 | |
| **MZ00034402** | allene oxide synthase 1 {Zea mays} | 2.203460979 | 1.10E-06 | |
| **MZ00034408** | UDP-glucosyltransferase BX8 {Zea mays} | 1.770840426 | 3.67E-06 | |
| **MZ00034412** | xyloglucan endotransglycosylase homolog {Zea mays} | -1.079653967 | 0.02909091 | |

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|---|---|---|---|---|
| **MZ00034841** | psaI gene {Zea mays} | 1.435163876 | 0.00260033 | |
| **MZ00034843** | Photosystem Q(B) protein {Zea mays} | 1.299706548 | 0.02460417 | |
| **MZ00034849** | photosystem II phosphoprotein psbH {Zea mays} | 1.359253167 | 0.02150718 | |
| **MZ00034856** | Ribulose bisphosphate carboxylase large chain precursor {Zea mays} | 1.509317075 | 0.01083472 | |
| **MZ00034872** | photosystem II subunit T {Narcissus elegans} | 1.066671967 | 0.02925808 | |
| **MZ00034930** | lipoxygenase10 {Zea mays} | 1.821197884 | 2.86E-05 | |
| **MZ00034968** | hypothetical protein {Zea mays} | 1.076881855 | 7.99E-05 | |
| **MZ00035055** | lipoxygenase6 {Zea mays} | 1.975575199 | 2.36E-05 | |
| **MZ00035114** | phospho-2-dehydro-3-deoxyheptonate aldolase 1 {Zea mays} | 1.53183477 | 4.80E-06 | |
| **MZ00035120** | adenosine kinase {Zea mays} | 1.206479286 | 0.00125126 | |
| **MZ00035243** | adenosylhomocysteinase {Zea mays} | 1.310404132 | 0.00024358 | |
| **MZ00035273** | nonspecific lipid-transfer protein AKCS9 {Zea mays} | 1.5566982 | 0.00115757 | |
| **MZ00035373** | AER {Zea mays} | 1.454416719 | 4.21E-05 | |
| **MZ00035374** | methionine synthase {Zea mays} | 4.150849163 | 1.63E-10 | |
| **MZ00035604** | 12-oxo-phytodienoic acid reductase8 {Zea mays} | 1.552010275 | 5.98E-07 | |
| **MZ00035632** | adenosylhomocysteinase {Zea mays} | 1.833118349 | 1.35E-05 | |
| **MZ00035637** | NA | 1.38553636 | 0.03829489 | |
| **MZ00035698** | Thiazole biosynthetic enzyme 1-2 {Zea mays} | -1.238592469 | 0.00420821 | |
| **MZ00035833** | unnamed protein product | 1.043803947 | 0.03181342 | |
| **MZ00035997** | lipoxygenase6 {Zea mays} | 2.361100536 | 7.54E-05 | |
| **MZ00036024** | AER {Zea mays} | 1.148408817 | 5.67E-05 | |
| **MZ00036078** | hypothetical protein {Zea mays} | 1.924555595 | 1.29E-08 | |
| **MZ00036171** | UDP-glucose 6-dehydrogenase {Zea mays} | 2.229600337 | 3.62E-06 | |
| **MZ00036200** | NA | 1.771636514 | 0.00180923 | |
| **MZ00036295** | unnamed protein product | 1.335942472 | 0.01941835 | |
| **MZ00036303** | beta-expansin 1 protein {Zea mays} | 1.025577602 | 0.01427073 | |
| **MZ00036398** | xyloglucan endotransglycosylase homolog {Zea mays} | -1.106608878 | 0.00037272 | |
| **MZ00036485** | nicotianamine synthase 3 {Zea mays} | 1.084554877 | 0.02674138 | |
| **MZ00036530** | unnamed protein product | 1.813587954 | 0.01882393 | |

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| **MZ00036538** | subtilisin/chymotrypsin inhibitor {Zea mays} | 3.650827443 | 1.89E-07 | |
| **MZ00036614** | methionine synthase {Coffea arabica} | 3.005417872 | 3.22E-05 | |
| **MZ00036626** | Asr protein {Zea mays} | -1.051647385 | 0.00972258 | |
| **MZ00036710** | NA | 1.412688237 | 0.00041375 | |
| **MZ00036717** | abscisic stress protein homolog {Zea mays} | 1.020777793 | 0.02372581 | |
| **MZ00036758** | hypothetical protein {Zea mays} | 1.425188233 | 6.72E-06 | |
| **MZ00036774** | O-succinylhomoserine sulfhydrylase {Zea mays} | 1.703850736 | 4.54E-05 | |
| **MZ00036847** | Ac1147 {Rattus norvegicus} | 1.258534232 | 0.03839008 | |
| **MZ00036884** | disease resistance-like protein {Arabidopsis thaliana} | 1.235296364 | 0.00026378 | |
| **MZ00036916** | NA | 1.423860238 | 0.03495645 | |
| **MZ00036918** | CDH1-D {Gallus gallus;} | 1.539952036 | 0.0472115 | |
| **MZ00036940** | tonoplast water channel {Zea mays} | 1.133447104 | 0.00061518 | |
| **MZ00036975** | Asr protein {Zea mays} | -1.186471142 | 0.01189242 | |
| **MZ00037045** | pathogenesis related protein-5 {Zea mays} | 1.297543025 | 0.00155856 | |
| **MZ00037070** | polyamine oxidase1 {Zea mays} | 3.088978537 | 0.00017111 | |
| **MZ00037085** | Bowman-Birk type wound-induced proteinase inhibitor WIP1 {Zea mays} | 5.65932748 | 4.83E-11 | |
| **MZ00037092** | homeobox transcription factor KNOTTED1 (kn1) {Zea mays} | 1.29106848 | 0.00046329 | |
| **MZ00037106** | hypothetical protein {Zea mays} | -1.720936039 | 0.02571698 | |
| **MZ00037127** | hypothetical protein {Zea mays} | 2.554537218 | 2.54E-05 | |
| **MZ00037158** | adenosylhomocysteinase {Zea mays} | 1.639577332 | 6.10E-07 | |
| **MZ00037240** | putative phosphoethanolamine methyltransferase {Oryza sativa} | 1.130183996 | 0.00849243 | |
| **MZ00037253** | subtilisin/chymotrypsin inhibitor {Zea mays} | 3.467529924 | 2.36E-06 | |
| **MZ00037256** | cytochrome P450 monooxygenase CYP71C3v2 {Zea mays} | 1.330953174 | 0.00484051 | |
| **MZ00037263** | annexin P35 {Zea mays} | 1.02662211 | 0.00260273 | |
| **MZ00037304** | terpene synthase 2 {Zea mays} | 3.84179118 | 4.51E-08 | |
| **MZ00037357** | safener induced1 {Zea mays} | 1.560353844 | 0.00061984 | |
| **MZ00037429** | adenosine kinase {Zea mays} | 1.237351476 | 0.00181642 | |
| **MZ00037482** | putative senescence-associated protein {Pisum sativum} | 1.215580094 | 0.0315315 | |
| **MZ00037574** | NA | 1.31540595 | 1.21E-06 | |

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| **MZ00037615** | putative NLI interacting factor {Oryza sativa} | 1.736868267 | 7.84E-07 | TF48 |
| **MZ00037636** | 2-oxoglutarate-dependent oxygenase {Zea mays} | 1.363467578 | 0.03965708 | |
| **MZ00037735** | lipoxygenase11 {Zea mays} | 1.302532528 | 0.00132902 | |
| **MZ00037858** | UDP-glucuronic acid decarboxylase {Oryza sativa} | 1.124100904 | 4.50E-05 | |
| **MZ00038365** | beta-glucosidase aggregating factor precursor {Zea mays} | 1.239380265 | 0.00036756 | |
| **MZ00038776** | hypothetical protein {Zea mays} | 1.302419117 | 0.00147753 | |
| **MZ00038794** | elongation factor 1alpha {Zea mays} | 3.339536678 | 3.30E-08 | |
| **MZ00038859** | hypothetical protein {Zea mays} | 2.213988295 | 1.19E-05 | |
| **MZ00039167** | Putative C-4 sterol methyl oxidase {Oryza sativa} | 2.164065924 | 0.00011494 | |
| **MZ00039459** | putative thioredoxin {Oryza sativa} | 1.213779261 | 2.82E-05 | |
| **MZ00039489** | Bowman-Birk type wound-induced proteinase inhibitor {Zea mays} | 3.342140742 | 6.52E-05 | |
| **MZ00039589** | cytochrome b5 {Oryza sativa} | 1.177676906 | 4.15E-05 | |
| **MZ00039598** | blue fluorescent1 {Zea mays} | 1.642364948 | 7.26E-05 | |
| **MZ00039734** | beta-glucosidase {Zea mays} | 2.191760902 | 3.21E-06 | |
| **MZ00039764** | Bowman-Birk type wound-induced proteinase inhibitor WIP1 {Zea mays} | 4.946218601 | 4.13E-09 | |
| **MZ00039782** | cystatin II {Zea mays} | 1.754947344 | 0.00388596 | |
| **MZ00039805** | hypothetical protein {Zea mays} | 1.460139962 | 0.0002745 | |
| **MZ00039806** | anthranilate synthase component II {Zea mays} | 1.924034011 | 0.0273911 | |
| **MZ00039818** | cytochrome P450 monooxygenase CYP71C3v2 {Zea mays} | 2.06096152 | 0.00574876 | |
| **MZ00040006** | hypothetical protein {Zea mays} | 1.377795851 | 0.01050715 | |
| **MZ00040123** | HSP protein (HSP90-2) {Zea mays} | 1.463121515 | 0.02353243 | |
| **MZ00040243** | hypothetical protein {Zea mays} | 2.677106357 | 0.00209871 | |
| **MZ00040386** | Serine/threonine kinase protein | 1.115811329 | 0.00495188 | |
| **MZ00040420** | CSLE6 - cellulose synthase-like family E {Zea mays} | -1.000659501 | 0.00384163 | |
| **MZ00040469** | hypothetical protein {Sorghum bicolor} | 1.311579979 | 2.22E-05 | |
| **MZ00040479** | coupling factor beta-subunit and coupling factor epsilon subunit {Zea mays} | 1.764906451 | 0.01787083 | |

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| **MZ00040486** | Ribulose bisphosphate carboxylase large chain precursor {Zea mays} | 1.009652592 | 0.04574858 | |
| **MZ00040525** | coupling factor beta-subunit and coupling factor epsilon subunit {Zea mays} | 1.759964033 | 0.01579834 | |
| **MZ00040651** | ribosome-inactivating protein {Zea mays} | 1.16169119 | 0.00034695 | |
| **MZ00040654** | glutathione S-transferase GST 25 {Zea mays} | 4.008690578 | 4.57E-10 | |
| **MZ00040686** | sesquiterpene cyclase {Zea mays} | 1.185829618 | 0.00086881 | |
| **MZ00040837** | dnaK-type molecular chaperone hsc70-2 {Arabidopsis thaliana} | 1.014991123 | 0.04735592 | |
| **MZ00040937** | hypothetical protein {Sorghum bicolor} | 1.147020541 | 0.00025899 | |
| **MZ00040980** | dnaK-type molecular chaperone hsp70 {Oryza sativa} | 1.375815251 | 0.01261521 | |
| **MZ00041005** | subtilisin-chymotrypsin inhibitor homolog1 {Zea mays} | 3.959773934 | 4.86E-07 | |
| **MZ00041019** | gibberellin responsive2 {Zea mays} | -2.716600508 | 0.01344002 | |
| **MZ00041129** | tonoplast water channel {Zea mays} | 1.381561891 | 0.00098186 | |
| **MZ00041213** | putative UDP-glucose dehydrogenase {Sorghum bicolor} | 1.973709909 | 0.0001496 | |
| **MZ00041214** | UDP-glucose 6-dehydrogenase {Zea mays} | 2.421688461 | 9.53E-07 | |
| **MZ00041254** | phospho-2-dehydro-3-deoxyheptonate aldolase 1 {Zea mays} | 1.224644729 | 1.63E-05 | |
| **MZ00041260** | putative 70 kDa peptidylprolyl isomerase {Oryza sativa} | 1.039472436 | 0.0113347 | |
| **MZ00041271** | lipoxygenase {Zea mays} | 4.521047126 | 1.01E-09 | |
| **MZ00041287** | heat shock protein hsp70 {Zea mays} | 1.465548359 | 0.00039756 | |
| **MZ00041335** | legumain-like protease {Zea mays} | -1.198148554 | 0.00116106 | |
| **MZ00041405** | putative phospho-2-dehydro-3-deoxyheptonate aldolase 1 {Oryza sativa} | 1.595995236 | 0.00390226 | |
| **MZ00041439** | dehydrin (dhn2) {Zea mays} | 1.002675913 | 0.0039044 | |
| **MZ00041513** | wound-induced protease inhibitor {Zea mays subsp. parviglumis} | 1.665990925 | 8.15E-06 | |
| **MZ00041530** | IN2-1 protein {Zea mays} | 1.034567658 | 0.04443869 | |
| **MZ00041596** | ZIM-motif family protein {Zea mays} | 1.027619472 | 0.01852564 | |
| **MZ00041601** | beta-glucosidase aggregating factor precursor {Zea mays} | 1.356055442 | 0.02873466 | |
| **MZ00041768** | putative zinc finger protein {Zea mays} | 3.616692105 | 2.31E-05 | |

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|---|---|---|---|---|
| **MZ00041827** | 3-dehydroquinate synthase {Zea mays} | 1.108372983 | 0.04699278 | |
| **MZ00042000** | At5g04080 {Arabidopsis thaliana} | 1.725110889 | 0.00119655 | |
| **MZ00042109** | O-methyltransferase BX7 {Zea mays} | 2.061277542 | 0.00027866 | |
| **MZ00042158** | ripening-related protein {Zea mays} | 1.766710856 | 2.79E-07 | |
| **MZ00042217** | hypothetical protein {Zea mays} | 1.017663782 | 0.00029728 | |
| **MZ00042245** | O-succinylhomoserine sulfhydrylase {Zea mays} | 1.975941173 | 3.55E-06 | |
| **MZ00042324** | ribosome-inactivating protein. {Zea mays} | 3.633688185 | 2.36E-07 | |
| **MZ00042637** | phosphoenolpyruvate carboxylase {Zea mays} | 1.272955991 | 0.01328751 | |
| **MZ00042678** | ribosome-inactivating protein {Zea mays} | 3.638665168 | 2.48E-05 | |
| **MZ00042841** | Histone H2A {Zea mays} | 1.347556855 | 0.0481309 | |
| **MZ00042873** | S-adenosylmethionine synthetase 1 {Zea mays} | 2.254520198 | 0.00012398 | |
| **MZ00042904** | HSP protein (HSP90-2) {Zea mays} | 1.347214915 | 0.00085693 | |
| **MZ00042921** | methionine synthase {Zea mays} | 1.942360533 | 7.22E-06 | |
| **MZ00042935** | Bowman-Birk type wound-induced proteinase inhibitor {Zea mays} | 2.806477643 | 3.53E-06 | |
| **MZ00042940** | hypothetical protein {Zea mays} | -1.038946349 | 0.00095885 | |
| **MZ00042953** | chlorophyll a/b binding protein {Oryza sativa} | 3.703542259 | 8.95E-06 | |
| **MZ00042980** | hypothetical protein {Zea mays} | 2.718403746 | 0.00028633 | |
| **MZ00042981** | hypothetical protein {Zea mays} | 2.869766039 | 0.00023453 | |
| **MZ00043004** | cystatin {Zea mays} | 2.877029847 | 0.00272396 | |
| **MZ00043035** | chitinase {Zea mays} | 2.304194705 | 5.10E-05 | |
| **MZ00043160** | hypothetical protein {Zea mays} | 2.515494427 | 0.00645937 | |
| **MZ00043179** | subtilisin/chymotrypsin inhibitor {Zea mays} | 1.389935228 | 8.58E-05 | |
| **MZ00043232** | putative glycine-rich protein {Oryza sativa} | 2.724001999 | 2.33E-07 | |
| **MZ00043240** | ribonuclease S homolog {Zea mays} | 1.936173351 | 0.00034383 | |
| **MZ00043311** | patatin-like protein {Sorghum bicolor} | 1.086772039 | 0.03507248 | |
| **MZ00043339** | Thiazole biosynthetic enzyme 1-2 {Zea mays} | -1.110096582 | 0.00364068 | |
| **MZ00043393** | 2-oxoglutarate-dependent oxygenase {Zea mays} | 2.480265011 | 7.84E-08 | |
| **MZ00043517** | allene oxide cyclase {Zea mays} | 1.61478242 | 0.00392188 | |
| **MZ00043518** | allene oxide cyclase {Zea mays} | 1.276933426 | 0.000768 | |

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|---|---|---|---|---|
| **MZ00043781** | lipoxygenase {Zea mays} | 1.19008889 | 0.00380615 | |
| **MZ00043784** | trans-cinnamate 4-monooxygenase {Zea mays} | 1.042706134 | 0.00329744 | |
| **MZ00043885** | farnesyl-pyrophosphate synthetase {Oryza sativa} | 1.630982419 | 0.00021638 | |
| **MZ00044135** | hypothetical protein {Zea mays} | 1.187979142 | 4.50E-06 | |
| **MZ00044190** | allene oxide synthase 1 {Zea mays} | 4.078079317 | 1.65E-07 | |
| **MZ00044245** | lipoxygenase6 {Zea mays} | 2.141181888 | 1.68E-06 | |
| **MZ00044413** | benzoxazinone synthesis BX9 {Zea mays} | 1.235658497 | 0.01949316 | |
| **MZ00044555** | putative phosphoribosyl pyrophosphate synthase {Oryza sativa} | 3.80066505 | 5.90E-09 | |
| **MZ00044562** | NA | 1.490490377 | 3.22E-06 | |
| **MZ00044642** | hypothetical protein {Oryza sativa} | 2.051187735 | 5.80E-08 | |
| **MZ00046552** | hypothetical protein {Zea mays} | 1.026512391 | 0.00813629 | |
| **MZ00046592** | glutathione transferase40 {Zea mays} | 1.272607956 | 2.08E-05 | |
| **MZ00047034** | putative arginine methyltransferase {Oryza sativa} | 1.112998783 | 0.03587827 | |
| **MZ00047153** | methylenetetrahydrofolate reductase {Zea mays} | 1.718731981 | 2.64E-05 | |
| **MZ00048571** | acc oxidase {Zea mays} | 1.4146259 | 1.44E-05 | |
| **MZ00048905** | hypothetical protein {Zea mays} | 1.01234542 | 0.00030394 | |
| **MZ00049092** | G-box binding protein {Oryza sativa} | 1.200285945 | 3.47E-06 | TF21 |
| **MZ00049506** | hypothetical protein {Oryza sativa} | 1.554045332 | 0.0130741 | |
| **MZ00052059** | flowering promoting factor-like 1 {Zea mays} | 1.211568258 | 0.00772696 | |
| **MZ00052490** | pathogenesis-related protein 10 {Zea mays} | 1.415478947 | 0.00050066 | |
| **MZ00054816** | adenosylhomocysteinase {Zea mays} | 1.650873179 | 1.74E-06 | |
| **MZ00054822** | phospho-2-dehydro-3-deoxyheptonate aldolase 1 {Zea mays} | 1.041476239 | 0.00021236 | |
| **MZ00054897** | glutathione S-transferase GST 25 {Zea mays} | 3.109945306 | 3.26E-08 | |
| **MZ00054995** | hypothetical protein {Zea mays} | 1.678339411 | 3.37E-06 | |
| **MZ00055013** | methylenetetrahydrofolate reductase {Zea mays} | 1.538239481 | 1.13E-06 | |
| **MZ00055270** | ripening-related protein {Zea mays} | 1.7991641 | 5.49E-05 | |
| **MZ00055448** | hypothetical protein {Zea mays} | 1.782120094 | 0.00023721 | |
| **MZ00055463** | esterase {Zea mays} | 1.661780979 | 9.55E-07 | |

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|---|---|---|---|---|
| **MZ00055932** | Bowman-Birk type trypsin inhibitor {Zea mays} | 2.569479125 | 1.37E-06 | |
| **MZ00056269** | hypothetical protein {Sorghum bicolor} | 1.004733332 | 2.81E-05 | |
| **MZ00056664** | hypothetical protein {Sorghum bicolor} | 1.306314787 | 0.01244828 | |
| **MZ00056687** | farnesyl pyrophosphate synthase1 {Zea mays} | 2.021782258 | 0.00039941 | |
| **MZ00056765** | prefoldin subunit 2 {Zea mays} | -1.179215429 | 0.01330582 | |
| **MZ00056914** | lipid binding protein {Zea mays} | -1.007349915 | 0.04252574 | |
| **MZ00056987** | acyl-desaturase {Zea mays} | 1.264800142 | 0.00628795 | |
| **MZ00057095** | putative UVB-resistance protein UVR8 {Oryza sativa} | 1.035194979 | 0.02070113 | |
| **MZ00057294** | putative dehydration-responsive protein RD22 precursor {Oryza sativa} | 1.907172925 | 0.00151744 | |
| **MZ00057421** | Glyceraldehyde 3-phosphate dehydrogenase {Zea mays} | 1.078073788 | 0.04255359 | |
| **MZ00057436** | putative ZEITLUPE {Oryza sativa} | 1.740651364 | 0.0045763 | |

## 7.7 Transcription factors regulated by herbivory, mechanical damage, and systemic induction in leaves and roots of maize

**Tab.7. 5: Transcription factors identified in roots. Comparison between systemic induction and mechanical damage**

| MZ-number | Annotation | fold expression (log10) | p-value | Abbreviation |
|---|---|---|---|---|
| **MZ00000664** | RING finger-like {Oryza sativa} | -1.17311677 | 0.00256481 | TF50 |
| **MZ00000942** | putative Myb-related transcription factor {Oryza sativa} | -1.11768355 | 0.013915 | |
| **MZ00005189** | RING-H2 zinc finger protein ATL6-like {Oryza sativa} | -1.08860955 | 0.0003481 | |
| **MZ00012674** | zinc finger protein 3 {Zea mays} | -1.07583988 | 0.01514441 | |
| **MZ00013314** | myb-related gene Zm1. {Zea mays} | -1.2089436 | 0.00156514 | |
| **MZ00013458** | putative zinc finger protein ZmZf {Zea mays} | 1.45477385 | 0.00073486 | |
| **MZ00015793** | putative DNA-binding protein PD3 {Oryza sativa} | 1.62217624 | 0.01486775 | |
| **MZ00018661** | F-box protein family {Arabidopsis thaliana} | 1.02444407 | 0.00162727 | |
| **MZ00018825** | putative transcription factor {Oryza sativa} | 1.12985982 | 0.00129396 | |
| **MZ00019229** | twin LOV protein 1 {Arabidopsis thaliana} | 1.0775719 | 0.00291805 | |
| **MZ00020499** | development regulation gene OsNAC4 {Oryza sativa} | -1.22221271 | 0.01218443 | |
| **MZ00021114** | putative F-box protein {Oryza sativa} | 2.00276908 | 0.00586368 | |
| **MZ00022225** | zinc finger (AN1-like)-like protein {Oryza sativa} | -1.19631869 | 0.04278423 | |
| **MZ00022460** | putative Ras-GTPase-activating protein binding protein 1 {Oryza sativa} | -1.20398419 | 0.00162251 | |
| **MZ00024843** | putative zinc finger transcription factor {Oryza sativa} | 1.20573495 | 5.73E-05 | |
| **MZ00025533** | myb-related transcription factor MYB59 {Arabidopsis thaliana} | 1.03666135 | 0.00476553 | |
| **MZ00026127** | development regulation gene OsNAC4 | -1.02172616 | 0.02978254 | |

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|---|---|---|---|---|
| | {Oryza sativa} | | | |
| **MZ00026538** | ZIM-motif family protein {Zea mays} | -1.41036951 | 0.00419174 | |
| **MZ00026661** | putative NAC-domain protein {Oryza sativa} | -2.38974895 | 0.00013525 | TF1 |
| **MZ00028419** | bZIP protein {Oryza sativa} | 1.37423647 | 0.00066664 | |
| **MZ00028904** | myb-related gene Zm38. {Zea mays} | 1.02765764 | 0.00930875 | |
| **MZ00030906** | transcription factor Rap212 {Oryza sativa} | -1.13699108 | 0.00591033 | |
| **MZ00030973** | putative NAC-domain protein {Oryza sativa} | -1.289499 | 9.73E-05 | |
| **MZ00031271** | transcription factor {Oryza sativa} | -1.04920935 | 0.03016695 | |
| **MZ00032440** | putative leucine zipper-containing protein {Oryza sativa} | -1.03465161 | 0.04385328 | |
| **MZ00033157** | Myb-related transcription factor-like protein {Oryza sativa} | 1.00375338 | 0.00733829 | |
| **MZ00033341** | transcription factor Myb3 {Triticum aestivum} | -1.19466639 | 0.00259737 | |
| **MZ00033711** | putative NAC-domain protein {Oryza sativa} | -1.07117436 | 0.00300881 | |
| **MZ00033715** | ZIM-motif family protein {Zea mays} | -1.39199293 | 0.03460359 | |
| **MZ00035860** | GRAB1 protein {Triticum sp.} | -1.0185033 | 0.01178006 | |
| **MZ00035947** | putative NAC-domain protein {Oryza sativa} | -1.01956023 | 0.00138845 | TF22 |
| **MZ00036019** | putative NAC-domain protein {Oryza sativa} | -2.44954618 | 0.00014679 | TF51 |
| **MZ00037166** | putative zinc finger transcription factor {Oryza sativa} | 1.42192839 | 5.77E-05 | |
| **MZ00038922** | WRKY transcription factor {Oryza sativa} | -1.01094044 | 0.00583476 | |
| **MZ00039225** | putative zinc finger protein ZmZf {Zea mays} | 1.3916815 | 0.00070862 | |
| **MZ00040842** | strongly similar to NP_195589.2 splicing factor | -1.82242211 | 0.01655065 | |
| **MZ00041306** | putative ASR2 {Oryza sativa} | -1.2099269 | 0.00401326 | |
| **MZ00041768** | putative zinc finger protein {Zea mays} | -1.87712778 | 1.24E-05 | |
| **MZ00042353** | R2R3 Myb transcription factor MYB- | -1.43425611 | 0.00450982 | |

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|---|---|---|---|---|
| | IF35 {Zea mays} | | | |
| **MZ00042676** | smr domain-containing protein –like {Oryza sativa} | -1.38823076 | 0.00880997 | |
| **MZ00042739** | WRKY transcription factor {Oryza sativa} | -1.20980279 | 0.00117118 | TF26 |
| **MZ00046918** | putative homeodomain protein {Oryza sativa} | -1.05545756 | 0.00014435 | |
| **MZ00049598** | putative bZIP protein {Oryza sativa} | 1.17967009 | 0.00020976 | |
| **MZ00056649** | putative SWIb domain-containing protein {Oryza sativa} | -1.04308183 | 0.01821648 | |
| **MZ00057150** | putative FKBP12 interacting protein {Oryza sativa} | -1.02718293 | 0.00011043 | |
| **MZ00057284** | zinc finger protein family-like {Oryza sativa} | 1.01316243 | 0.03649266 | |

**Tab.7. 6: Transcription factors identified in roots. Comparison between local herbivore damage and mechanical damage**

| MZ number | Annotation | fold expression (log10) | p-value | Abbrevation |
|---|---|---|---|---|
| **MZ00000937** | putative bHLH084 transcription factor {Arabidopsis thaliana} | -1.45459357 | 0.00104639 | |
| **MZ00000942** | putative Myb-related transcription factor {Oryza sativa} | -1.23641091 | 0.00973813 | |
| **MZ00005265** | putative helix-loop-helix DNA-binding protein {Oryza sativa (japonica cultivar-group);} | 1.76936392 | 0.00118141 | TF23 |
| **MZ00012587** | putative ethylene response factor 1 {Oryza sativa} | -1.13552342 | 0.00507723 | |
| **MZ00012674** | zinc finger protein 3 {Zea mays} | 1.10422733 | 0.0154617 | |
| **MZ00013750** | LIM transcription factor homolog {Zea mays} | -1.07140769 | 0.00381153 | |
| **MZ00015793** | putative DNA-binding protein PD3 {Oryza sativa} | 2.10213416 | 0.00439977 | |
| **MZ00018321** | AP2 domain transcription factor EREBP {Oryza sativa} | 2.03570049 | 0.03399623 | |
| **MZ00018515** | putative zinc finger and C2 domain | -1.12721725 | 7.15E-05 | |

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|---|---|---|---|---|
| | protein {Oryza sativa} | | | |
| **MZ00019724** | zinc-finger protein S3574 {Oryza sativa} | 1.06297339 | 0.00287096 | |
| **MZ00022534** | FKF1 {Mesembryanthemum crystallinum} | 1.1901183 | 0.00033774 | |
| **MZ00025599** | putative zinc finger protein {Oryza sativa } | -1.15153203 | 4.81E-05 | |
| **MZ00026726** | similar to nucleoid DNA-binding-like protein {Oryza sativa} | -1.21283829 | 0.00106192 | |
| **MZ00029568** | ZIM-motif family protein {Zea mays} | 1.07886517 | 0.00027794 | |
| **MZ00031271** | transcription factor {Oryza sativa} | 2.30031778 | 0.00040686 | |
| **MZ00033715** | ZIM-motif family protein {Zea mays} | 1.74012163 | 0.01462193 | |
| **MZ00037906** | Radc1 {Oryza sativa} | -1.23534247 | 0.0042087 | |
| **MZ00040702** | R2R3 Myb protein {Zea mays} | -1.54732424 | 0.00029875 | |
| **MZ00041718** | floral organ regulator 2 {Oryza sativa} | -1.07285153 | 0.00272305 | |
| **MZ00043644** | putative EREBP-type transcription factor {Oryza sativa} | 2.02737794 | 0.00339868 | |
| **MZ00043824** | putative WD-40 repeat protein {Oryza sativa} | -1.04729989 | 0.00152939 | |
| **MZ00044166** | floral organ regulator 2 {Oryza sativa} | -1.20193017 | 0.0049003 | |

**Tab.7. 7: Transcription factors identified in systemic induced roots**

| MZ number | Annotation | fold expression (log10) | p-value | Abbrevation |
|---|---|---|---|---|
| **MZ00004381** | bZIP transcription factor-like protein {Arabidopsis thaliana} | -1.14356897 | 0.0116739 | |
| **MZ00014951** | transcriptional activator DEMETER {Arabidopsis thaliana} | 1.03194135 | 0.00033156 | |
| **MZ00017495** | OSE3 {Oryza sativa} | 1.35581577 | 0.00678932 | |
| **MZ00019076** | Hox2b {Zea mays} | 1.04260847 | 0.0003865 | |
| **MZ00021809** | zwh21.1 {Oryza sativa} | -1.09485472 | 0.00644913 | |
| **MZ00022377** | ZIGA2 protein-like {Oryza sativa} | -1.03227658 | 0.00182741 | |
| **MZ00022460** | putative Ras-GTPase-activating protein binding protein 1 {Oryza sativa} | -1.34135467 | 0.0006585 | |
| **MZ00023293** | MCB2 protein {Hordeum vulgare subsp. | 1.1090304 | 0.0012409 | |

| | | | | |
|---|---|---|---|---|
| | Vulgare} | | | |
| **MZ00026127** | development regulation gene OsNAC4 {Oryza sativa} | 1.11467291 | 0.01781558 | |
| **MZ00026870** | RISBZ5 {Oryza sativa} | 1.10551394 | 0.02792086 | |
| **MZ00027941** | putative ATP-binding-cassette protein {Oryza sativa} | 2.30432218 | 0.01084393 | |
| **MZ00028351** | zinc-finger protein S3574 {Oryza sativa} | -1.52392556 | 0.01036772 | |
| **MZ00036053** | SAR DNA binding protein {Oryza sativa} | -1.05992594 | 0.00028416 | |
| **MZ00036067** | OSE3 {Oryza sativa} | 1.13275655 | 0.00188415 | |
| **MZ00036162** | rRNA promoter binding protein {Rattus norvegicus} | -1.87284556 | 0.00771251 | |
| **MZ00039225** | putative zinc finger protein ZmZf {Zea mays} | 1.02017357 | 0.0042214 | |
| **MZ00040842** | strongly similar to NP_195589.2 splicing factor | -2.34866516 | 0.00367576 | |
| **MZ00048943** | putative transcription factor {Oryza sativa} | -1.11201395 | 0.00033161 | |
| **MZ00054846** | WRKY transcription factor 70 {Oryza sativa} | 2.58060619 | 0.00271994 | |

**Tab.7. 8: Transcription factors identified in herbivore-attacked roots**

| MZ number | Annotation | fold expression (log10) | p-value | Abbrevation |
|---|---|---|---|---|
| **MZ00000937** | putative bHLH084 transcription factor {Arabidopsis thaliana} | -1.44819319 | 0.00132125 | |
| **MZ00001769** | myb transcription factor {Hordeum vulgare subsp. Vulgare} | 1.21169365 | 0.00085054 | |
| **MZ00004381** | bZIP transcription factor-like protein {Arabidopsis thaliana} | -1.03848128 | 0.0278384 | |
| **MZ00005189** | RING-H2 zinc finger protein ATL6-like {Oryza sativa} | 1.05349043 | 0.00067154 | |
| **MZ00005265** | putative helix-loop-helix DNA-binding protein {Oryza sativa} | 1.61261607 | 0.00259158 | TF23 |
| **MZ00012674** | zinc finger protein 3 {Zea mays} | 1.99250531 | 0.00056628 | |
| **MZ00015793** | putative DNA-binding protein PD3 | 1.44270659 | 0.03312226 | |

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|---|---|---|---|---|
| | {Oryza sativa} | | | |
| **MZ00017226** | DNA-binding protein RAV2-like {Oryza sativa} | 1.03257487 | 0.00075845 | |
| **MZ00017495** | OSE3 {Oryza sativa} | 1.60672272 | 0.00432566 | |
| **MZ00018321** | AP2 domain transcription factor EREBP {Oryza sativa} | 3.09154154 | 0.0051438 | |
| **MZ00019886** | transcription factor MYC7E {Zea mays} | 1.21347465 | 0.00012983 | |
| **MZ00020499** | development regulation gene OsNAC4 {Oryza sativa} | 1.67398892 | 0.00300613 | |
| **MZ00026127** | development regulation gene OsNAC4 {Oryza sativa} | 1.73215694 | 0.00266655 | |
| **MZ00026538** | ZIM-motif family protein {Zea mays} | 2.31151939 | 0.0002444 | |
| **MZ00026661** | putative NAC-domain protein {Oryza sativa} | 2.55609061 | 0.00012955 | TF2 |
| **MZ00028044** | WRKY-type DNA binding protein {Solanum tuberosum} | 1.57561401 | 0.00536121 | |
| **MZ00028131** | kelch repeat-containing F-box-like {Oryza sativa} | 1.12681359 | 0.00016689 | |
| **MZ00028389** | putative GAMYB-binding protein {Oryza sativa} | 1.09379614 | 0.02579671 | |
| **MZ00031271** | Transcription Factor {Oryza sativa} | 3.21045114 | 4.31E-05 | |
| **MZ00033341** | transcription factor Myb3 {Triticum aestivum} | 1.23358786 | 0.00310482 | |
| **MZ00033715** | ZIM-motif family protein {Zea mays} | 2.66226357 | 0.00157363 | |
| **MZ00035959** | putative homeodomain protein {Oryza sativa} | 1.54528552 | 9.28E-05 | |
| **MZ00035991** | putative chloroplast nucleoid DNA-binding protein cnd41 {Oryza sativa} | 1.05895222 | 0.00751199 | |
| **MZ00036019** | putative NAC-domain protein {Oryza sativa} | 2.14675134 | 0.00058666 | TF51 |
| **MZ00036067** | OSE3 {Oryza sativa} leuzin zipper | 1.49577716 | 0.00054186 | |
| **MZ00040702** | R2R3 Myb protein {Zea mays} | -1.16150608 | 0.00249669 | |
| **MZ00041768** | putative zinc finger protein {Zea mays} | 2.29463039 | 4.00E-06 | |
| **MZ00042353** | R2R3 Myb transcription factor MYB-IF35 {Zea mays} | 1.88808181 | 0.00121086 | |
| **MZ00042739** | WRKY transcription factor {Oryza | 1.18263124 | 0.00201012 | TF26 |

| | | | | |
|---|---|---|---|---|
| | sativa} | | | |
| **MZ00043644** | putative EREBP-type transcription factor {Oryza sativa;} | 1.98563475 | 0.00460597 | |
| **MZ00046918** | putative homeodomain protein {Oryza sativa} | 1.19531442 | 9.01E-05 | |
| **MZ00056566** | zinc finger transcription factor ZF1 {Oryza sativa} | 1.42091009 | 0.00147646 | TF46 |

**Tab.7. 9: Transcription factors identified in mechanical wounded roots**

| MZ number | Annotation | fold expression (log10) | p-value | Abbrevation |
|---|---|---|---|---|
| **MZ00000942** | putative Myb-related transcription factor {Oryza sativa} | 1.23401259 | 0.01833295 | |
| **MZ00004235** | PRLI-interacting factor G-like protein {Oryza sativa } | 1.01257862 | 0.02626641 | |
| **MZ00004381** | bZIP transcription factor-like protein {Arabidopsis thaliana} | -1.52370818 | 0.00681936 | |
| **MZ00013767** | initiation factor (iso)4f p82 subunit {Triticum aestivum} | 1.14695383 | 0.00075967 | |
| **MZ00020499** | development regulation gene OsNAC4 {Oryza sativ} | 2.04519041 | 0.00156283 | |
| **MZ00021114** | putative F-box protein {Oryza sativa} | -2.22404443 | 0.0077869 | |
| **MZ00023973** | putative NAC-domain protein {Oryza sativa} | 1.04455787 | 0.00244106 | |
| **MZ00026127** | development regulation gene OsNAC4 {Oryza sativa} | 2.13639907 | 0.00129392 | |
| **MZ00026538** | ZIM-motif family protein {Zea mays} | 1.38545928 | 0.01087381 | |
| **MZ00026661** | putative NAC-domain protein {Oryza sativa} | 2.48132865 | 0.00032211 | TF1 |
| **MZ00028044** | WRKY-type DNA binding protein {Solanum tuberosum} | 1.46023276 | 0.01327617 | |
| **MZ00028351** | zinc-finger protein S3574 {Oryza sativa} | -1.73644816 | 0.01363055 | |
| **MZ00028419** | bZIP protein {Oryza sativa} | -1.65777426 | 0.00053869 | |
| **MZ00031018** | ethylene-responsive transcription factor 4 {Zea mays} | 1.00709987 | 0.02262177 | |
| **MZ00035959** | putative homeodomain protein {Oryza | 1.49720919 | 0.00023715 | |

| | | | | |
|---|---|---|---|---|
| | sativa} | | | |
| **MZ00036019** | putative NAC-domain protein {Oryza sativa} | 1.93159471 | 0.00218935 | TF51 |
| **MZ00041306** | putative ASR2 {Oryza sativa} | 1.38555034 | 0.00453449 | |
| **MZ00041768** | putative zinc finger protein {Zea mays} | 2.11656395 | 1.67E-05 | |
| **MZ00042353** | R2R3 Myb transcription factor MYB-IF35 {Zea mays} | 1.19742317 | 0.02499708 | |
| **MZ00046918** | putative homeodomain protein {Oryza sativa} | 1.38046222 | 6.20E-05 | |
| **MZ00054846** | WRKY transcription factor 70 {Oryza sativa} | 1.81331771 | 0.04033333 | |
| **MZ00055542** | zinc-finger protein R2931 {Oryza sativa} | 1.09809491 | 0.0006885 | |
| **MZ00056523** | putative phi-1 {Oryza sativa} | 1.49562379 | 0.01697013 | TF42 |
| **MZ00057404** | PHD finger protein-like {Oryza sativa} | 1.02584234 | 0.01008488 | |

**Tab.7. 10: Transcription factors in leaves. Comparison between systemic induction and mechanical damage**

| MZ number | Annotation | fold expression (log10) | p-value | Abbrevation |
|---|---|---|---|---|
| **MZ00000664** | RING finger-like {Oryza sativa} | -1.17021127 | 0.00069659 | TF50 |
| **MZ00001133** | putative LHY protein {Oryza sativa} | -1.54479187 | 0.00029076 | TF41 |
| **MZ00014272** | putative LHY protein {Oryza sativa} | -2.08412602 | 0.02891213 | |
| **MZ00021611** | NAM-like protein {Oryza sativa} | -1.19152825 | 0.0197212 | |
| **MZ00023293** | MCB2 protein {Hordeum vulgare subsp. Vulgare} | -1.10641059 | 0.00319869 | |
| **MZ00030973** | putative NAC-domain protein {Oryza sativa} | -1.14540025 | 0.00049405 | |
| **MZ00032849** | putative phi-1 {Oryza sativa} | 1.09935974 | 0.00190247 | |
| **MZ00041462** | putative LHY protein {Oryza sativa} | -2.00264664 | 0.01398821 | |
| **MZ00056649** | putative SWIb domain-containing protein {Oryza sativa} | -1.20443432 | 0.02147772 | |

**Tab.7. 11: Transcription factors in leaves. Comparison between herbivore induction and mechanical damage**

| MZ number | Annotation | fold expression (log10) | p-value | Abbrevation |
|---|---|---|---|---|
| **MZ00001821** | zinc finger (C3HC4-type RING finger) | -1.0821601 | 0.02187925 | |

| | | | | |
|---|---|---|---|---|
| | protein-like {Oryza sativa} | | | |
| **MZ00012674** | zinc finger protein 3 {Zea mays} | 2.32013829 | 4.13E-04 | |
| **MZ00017617** | putative WD-repeat protein 12 {Oryza sativa} | -1.25582415 | 0.00183641 | |
| **MZ00017641** | DNA binding protein-like {Oryza sativa} | -1.07749508 | 0.00586116 | |
| **MZ00018435** | CDC5 protein {Zea mays} | 2.03854817 | 0.00041144 | |
| **MZ00019167** | DNA-binding protein-like {Oryza sativa} | -1.12845165 | 0.0162055 | |
| **MZ00020099** | putative zinc finger (C3HC4-type RING finger) protein {Oryza sativa} | -1.20289123 | 0.00629871 | |
| **MZ00025599** | putative zinc finger protein {Oryza sativa} | -1.06110654 | 0.03758546 | |
| **MZ00026538** | ZIM-motif family protein {Zea mays} | 1.80812953 | 0.01490771 | |
| **MZ00028904** | myb-related gene Zm38. {Zea mays} | -1.14581193 | 0.01165362 | |
| **MZ00031176** | DNA-binding protein-like protein {Oryza sativa} | -1.15092799 | 0.03580132 | |
| **MZ00031553** | putative HAC13 protein {Oryza sativa} | -1.30267487 | 0.00238518 | |
| **MZ00032076** | putative ZR1 protein {Oryza sativa} | -2.20207462 | 0.00859237 | |
| **MZ00035947** | putative NAC-domain protein {Oryza sativa} | 1.27497329 | 0.01101208 | TF22 |
| **MZ00036019** | putative NAC-domain protein {Oryza sativa} | 1.22392712 | 0.00352567 | TF51 |
| **MZ00037092** | homeobox transcription factor KNOTTED1 (kn1) {Zea mays} | 2.54708663 | 0.01426112 | |
| **MZ00040600** | SBP-domain protein 7 {Zea mays} | -1.00525421 | 0.02227148 | |
| **MZ00041768** | putative zinc finger protein {Zea mays} | 5.08405164 | 2.65E-03 | |
| **MZ00044274** | putative finger transcription factor {Oryza sativa} | -1.25357837 | 0.03216688 | |
| **MZ00044596** | R2R3MYB-domain protein {Zea mays} | -1.05460042 | 0.0039064 | |

**Tab.7. 12: Transcription factors regulated in mechanical damaged leaves**

| MZ number | Annotation | fold expression (log10) | p-value | Abbrevation |
|---|---|---|---|---|
| **MZ00021611** | NAM-like protein {Oryza sativa} | 1.18 | 0.03 | |
| **MZ00028419** | bZIP protein {Oryza sativa} | -1.11 | 0.02 | |
| **MZ00028904** | myb-related gene Zm38. {Zea mays} | 1.15 | 0.02 | |

**Tab.7. 13: Transcription factors regulated in herbivore-damaged leaves**

| MZ number | Annotation | fold expression (log10) | p-value | Abbrevation |
|---|---|---|---|---|
| **MZ00012674** | zinc finger protein 3 {Zea mays} | 2.23317188 | 0.00032993 | |
| **MZ00016101** | putative RAB7A protein (GTP-binding protein) {Oryza sativa} | 1.18925891 | 0.00021631 | TF49 |
| **MZ00017495** | OSE3 {Oryza sativa} | 1.1681705 | 2.05E-02 | |
| **MZ00024412** | EREBP-like protein {Oryza sativa} | -1.31531362 | 0.02761637 | |
| **MZ00026538** | ZIM-motif family protein {Zea mays} | 1.72623912 | 0.01317232 | |
| **MZ00036019** | putative NAC-domain protein {Oryza sativa} | 1.19363088 | 0.00269634 | TF51 |
| **MZ00037092** | homeobox transcription factor KNOTTED1 (kn1) {Zea mays} | 2.37885291 | 0.01395867 | |
| **MZ00041768** | putative zinc finger protein {Zea mays} | 5.04517754 | 0.0018165 | |

**Tab.7. 14: Transcription factors in systemic induced leaves**

| MZ number | Annotation | fold expression (log10) | p-value | Abbrevation |
|---|---|---|---|---|
| **MZ00001373** | putative F-box protein Fbl2 {Oryza sativa} | -1.93695949 | 0.03356703 | |
| **MZ00016166** | putative transcription factor EREBP1 {Oryza sativa} | -1.0654935 | 0.02284059 | |
| **MZ00018541** | Putative EREBP-like protein {Oryza sativa} | -1.6199081 | 0.03713096 | TF38 |
| **MZ00020231** | zinc finger protein family-like {Oryza sativa} | -1.12971082 | 0.03208903 | |
| **MZ00030973** | putative NAC-domain protein {Oryza sativa} | -1.18177136 | 0.00056905 | |
| **MZ00032849** | putative phi-1 {Oryza sativa} | 1.30492278 | 0.00093883 | |
| **MZ00035947** | putative NAC-domain protein {Oryza sativa} | -1.44313555 | 1.05E-02 | TF22 |
| **MZ00036608** | putative transcription factor EREBP1 {Oryza sativa} | -1.9900955 | 0.01739547 | |
| **MZ00056649** | putative SWIb domain-containing protein {Oryza sativa} | -1.51655072 | 0.00947039 | |

## 7.8 Regulatory cis-elements of the 1.5 kb promoter fragment of *tps23* in *Zea mays* var. Delprim

**Tab.7. 15**

| tps23 1500 bp | Organism | Position | Strand | Sequence | Database |
|---|---|---|---|---|---|
| **-300ELEMENT** | | 377 | - | TGHAAARK | PLACE |
| **AACACOREOSGLUB1** | | 443 | + | AACAAAC | PLACE |
| **AAGAA-motif** | *Avena sativa* | 729 | - | GAAAGAA | PlantCARE |
| **AAGAA-motif** | *Avena sativa* | 1205 | - | GAAAGAA | PlantCARE |
| **AAGAA-motif** | *Avena sativa* | 978 | - | GAAAGAA | PlantCARE |
| **A-box** | *Petroselinum crispum* | 327 | - | CCGTCC | PlantCARE |
| **ABRE** | *Hordeum vulgare* | 41 | + | CGTACGTGCA | PlantCARE |
| **ABRE** | *Oryza sativa* | 44 | + | GACACGTACGT | PlantCARE |
| **ABRE** | *Hordeum vulgare* | 163 | + | CGTACGTGCA | PlantCARE |
| **ABRE** | *Arabidopsis thaliana* | 43 | + | TACGTG | PlantCARE |
| **ABRE** | *Arabidopsis thaliana* | 165 | + | TACGTG | PlantCARE |
| **ABRE** | *Arabidopsis thaliana* | 47 | - | TACGTG | PlantCARE |
| **ABRE** | *Arabidopsis thaliana* | 157 | - | CACGTG | PlantCARE |
| **ABRE** | *Hordeum vulgare* | 45 | - | CGTACGTGCA | PlantCARE |
| **ABRELATERD1** | | 163 | + | ACGTG | PLACE |
| **ABRELATERD1** | | 53 | + | ACGTG | PLACE |
| **ABRELATERD1** | | 170 | - | ACGTG | PLACE |
| **ABRELATERD1** | | 162 | - | ACGTG | PLACE |
| **ABRELATERD1** | | 48 | - | ACGTG | PLACE |
| **ABREOSRAB21** | | 166 | + | ACGTSSSC | PLACE |
| **ABREOSRAB21** | | 56 | + | ACGTSSSC | PLACE |
| **ABREOSRAB21** | | 170 | - | ACGTSSSC | PLACE |
| **ABRERATCAL** | | 164 | + | MACGYGB | PLACE |
| **ABRERATCAL** | | 163 | - | MACGYGB | PLACE |
| **ACA-motif** | *Arabidopsis* | 661 | + | AATCACAACCA | PlantCARE |

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|---|---|---|---|---|---|
| | *thaliana* | | | TA | |
| **ACGTABOX** | | 175 | + | TACGTA | PLACE |
| **ACGTABOX** | | 175 | - | TACGTA | PLACE |
| **ACGTATERD1** | | 1488 | + | ACGT | PLACE |
| **ACGTATERD1** | | 933 | + | ACGT | PLACE |
| **ACGTATERD1** | | 174 | + | ACGT | PLACE |
| **ACGTATERD1** | | 170 | + | ACGT | PLACE |
| **ACGTATERD1** | | 162 | + | ACGT | PLACE |
| **ACGTATERD1** | | 52 | + | ACGT | PLACE |
| **ACGTATERD1** | | 48 | + | ACGT | PLACE |
| **ACGTATERD1** | | 1488 | - | ACGT | PLACE |
| **ACGTATERD1** | | 933 | - | ACGT | PLACE |
| **ACGTATERD1** | | 174 | - | ACGT | PLACE |
| **ACGTATERD1** | | 170 | - | ACGT | PLACE |
| **ACGTATERD1** | | 162 | - | ACGT | PLACE |
| **ACGTATERD1** | | 52 | - | ACGT | PLACE |
| **ACGTATERD1** | | 48 | - | ACGT | PLACE |
| **ACGTOSGLUB1** | | 53 | + | GTACGTG | PLACE |
| **ACGTOSGLUB1** | | 172 | - | GTACGTG | PLACE |
| **ACGTOSGLUB1** | | 50 | - | GTACGTG | PLACE |
| **ACGTTBOX** | | 1489 | + | AACGTT | PLACE |
| **ACGTTBOX** | | 1489 | - | AACGTT | PLACE |
| **AE-box** | *Arabidopsis thaliana* | 1470 | + | AGAAACAA | PlantCARE |
| **ANAERO1CONSENSUS** | | 1543 | + | AAACAAA | PLACE |
| **ANAERO1CONSENSUS** | | 717 | + | AAACAAA | PLACE |
| **ANAERO1CONSENSUS** | | 442 | + | AAACAAA | PLACE |
| **ANAERO1CONSENSUS** | | 1476 | - | AAACAAA | PLACE |
| **ANAERO2CONSENSUS** | | 741 | + | AGCAGC | PLACE |
| **ARE** | *Zea mays* | 319 | - | TGGTTT | PlantCARE |
| **ARE** | *Zea mays* | 1427 | - | TGGTTT | PlantCARE |

| | | | | | |
|---|---|---|---|---|---|
| **ARR1AT** | | 1704 | + | NGATT | PLACE |
| **ARR1AT** | | 1562 | + | NGATT | PLACE |
| **ARR1AT** | | 1456 | + | NGATT | PLACE |
| **ARR1AT** | | 1223 | + | NGATT | PLACE |
| **ARR1AT** | | 1139 | + | NGATT | PLACE |
| **ARR1AT** | | 1037 | + | NGATT | PLACE |
| **ARR1AT** | | 990 | + | NGATT | PLACE |
| **ARR1AT** | | 896 | + | NGATT | PLACE |
| **ARR1AT** | | 791 | + | NGATT | PLACE |
| **ARR1AT** | | 769 | + | NGATT | PLACE |
| **ARR1AT** | | 674 | + | NGATT | PLACE |
| **ARR1AT** | | 577 | + | NGATT | PLACE |
| **ARR1AT** | | 1661 | - | NGATT | PLACE |
| **ARR1AT** | | 1337 | - | NGATT | PLACE |
| **ARR1AT** | | 706 | - | NGATT | PLACE |
| **ARR1AT** | | 777 | - | NGATT | PLACE |
| **ARR1AT** | | 1425 | - | NGATT | PLACE |
| **ARR1AT** | | 864 | - | NGATT | PLACE |
| **ASF1MOTIFCAMV** | | 658 | + | TGACG | PLACE |
| **BIHD1OS** | | 1557 | + | TGTCA | PLACE |
| **BIHD1OS** | | 1440 | - | TGTCA | PLACE |
| **BIHD1OS** | | 1234 | - | TGTCA | PLACE |
| **Box 4** | *Petroselinum crispum* | 788 | - | ATTAAT | PlantCARE |
| **Box I** | *Pisum sativum* | 344 | + | TTTCAAA | PlantCARE |
| **CAAT-box** | *Brassica rapa* | 179 | + | CAAAT | PlantCARE |
| **CAAT-box** | *Hordeum vulgare* | 190 | + | CAAT | PlantCARE |
| **CAAT-box** | *Glycine max* | 280 | + | CAATT | PlantCARE |
| **CAAT-box** | *Hordeum vulgare* | 281 | + | CAAT | PlantCARE |
| **CAAT-box** | *Brassica rapa* | 574 | + | CAAAT | PlantCARE |
| **CAAT-box** | *Glycine max* | 940 | + | CAATT | PlantCARE |
| **CAAT-box** | *Hordeum vulgare* | 941 | + | CAAT | PlantCARE |
| **CAAT-box** | *Hordeum vulgare* | 1259 | + | CAAT | PlantCARE |
| **CAAT-box** | *Brassica rapa* | 1381 | + | CAAAT | PlantCARE |
| **CAAT-box** | *Brassica rapa* | 1468 | + | CAAAT | PlantCARE |
| **CAAT-box** | *Hordeum vulgare* | 79 | - | CAAT | PlantCARE |

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|---|---|---|---|---|---|
| **CAAT-box** | *Glycine max* | 177 | - | CAATT | PlantCARE |
| **CAAT-box** | *Hordeum vulgare* | 313 | - | CAAT | PlantCARE |
| **CAAT-box** | *Brassica rapa* | 402 | - | CAAAT | PlantCARE |
| **CAAT-box** | *Hordeum vulgare* | 621 | - | CAAT | PlantCARE |
| **CAAT-box** | *Brassica rapa* | 699 | - | CAAAT | PlantCARE |
| **CAAT-box** | *Hordeum vulgare* | 771 | - | CAAT | PlantCARE |
| **CAAT-box** | *Glycine max* | 1010 | - | CAATT | PlantCARE |
| **CAATBOX1** | | 1014 | + | CAAT | PLACE |
| **CAATBOX1** | | 775 | + | CAAT | PLACE |
| **CAATBOX1** | | 625 | + | CAAT | PLACE |
| **CAATBOX1** | | 317 | + | CAAT | PLACE |
| **CAATBOX1** | | 181 | + | CAAT | PLACE |
| **CAATBOX1** | | 83 | + | CAAT | PLACE |
| **CAATBOX1** | | 1509 | - | CAAT | PLACE |
| **CAATBOX1** | | 1263 | - | CAAT | PLACE |
| **CAATBOX1** | | 945 | - | CAAT | PLACE |
| **CAATBOX1** | | 285 | - | CAAT | PLACE |
| **CAATBOX1** | | 194 | - | CAAT | PLACE |
| **CACGTGMOTIF** | | 163 | + | CACGTG | PLACE |
| **CACGTGMOTIF** | | 163 | - | CACGTG | PLACE |
| **CACTFTPPCA1** | | 1375 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 1294 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 1269 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 1239 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 1052 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 910 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 485 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 310 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 232 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 177 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 150 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 92 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 16 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 1157 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 1119 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 145 | - | YACT | PLACE |

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|---|---|---|---|---|---|
| **CACTFTPPCA1** | | 71 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 1772 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 1690 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 1537 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 1513 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 1469 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 1153 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 1067 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 860 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 822 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 337 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 12 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 7 | - | YACT | PLACE |
| **CANBNNAPA** | | 1451 | - | CNAACAC | PLACE |
| **CARGCW8GAT** | | 788 | + | CWWWWWWWWG | PLACE |
| **CARGCW8GAT** | | 194 | + | CWWWWWWWWG | PLACE |
| **CARGCW8GAT** | | 128 | + | CWWWWWWWWG | PLACE |
| **CARGCW8GAT** | | 788 | - | CWWWWWWWWG | PLACE |
| **CARGCW8GAT** | | 194 | - | CWWWWWWWWG | PLACE |
| **CARGCW8GAT** | | 128 | - | CWWWWWWWWG | PLACE |
| **CBFHV** | | 708 | + | RYCGAC | PLACE |
| **CBFHV** | | 261 | + | RYCGAC | PLACE |
| **CCGTCC-box** | *Arabidopsis thaliana* | 327 | - | CCGTCC | PlantCARE |
| **CGACGOSAMY3** | | 223 | - | CGACG | PLACE |
| **CGTCA-motif** | *Hordeum vulgare* | 653 | + | CGTCA | PlantCARE |
| **CIACADIANLELHC** | | 1660 | + | CAANNNNATC | PLACE |
| **CIACADIANLELHC** | | 1081 | - | CAANNNNATC | PLACE |
| **circadian** | *Lycopersicon esculentum* | 1071 | + | CAANNNNATC | PlantCARE |

| | | | | | |
|---|---|---|---|---|---|
| **CMSRE1IBSPOA** | | 334 | - | TGGACGG | PLACE |
| **CURECORECR** | | 1691 | + | GTAC | PLACE |
| **CURECORECR** | | 1068 | + | GTAC | PLACE |
| **CURECORECR** | | 978 | + | GTAC | PLACE |
| **CURECORECR** | | 631 | + | GTAC | PLACE |
| **CURECORECR** | | 176 | + | GTAC | PLACE |
| **CURECORECR** | | 172 | + | GTAC | PLACE |
| **CURECORECR** | | 149 | + | GTAC | PLACE |
| **CURECORECR** | | 50 | + | GTAC | PLACE |
| **CURECORECR** | | 1691 | - | GTAC | PLACE |
| **CURECORECR** | | 1068 | - | GTAC | PLACE |
| **CURECORECR** | | 978 | - | GTAC | PLACE |
| **CURECORECR** | | 631 | - | GTAC | PLACE |
| **CURECORECR** | | 176 | - | GTAC | PLACE |
| **CURECORECR** | | 172 | - | GTAC | PLACE |
| **CURECORECR** | | 149 | - | GTAC | PLACE |
| **CURECORECR** | | 50 | - | GTAC | PLACE |
| **DOFCOREZM** | | 1745 | + | AAAG | PLACE |
| **DOFCOREZM** | | 1656 | + | AAAG | PLACE |
| **DOFCOREZM** | | 1523 | + | AAAG | PLACE |
| **DOFCOREZM** | | 1280 | + | AAAG | PLACE |
| **DOFCOREZM** | | 1214 | + | AAAG | PLACE |
| **DOFCOREZM** | | 1210 | + | AAAG | PLACE |
| **DOFCOREZM** | | 1117 | + | AAAG | PLACE |
| **DOFCOREZM** | | 1087 | + | AAAG | PLACE |
| **DOFCOREZM** | | 1022 | + | AAAG | PLACE |
| **DOFCOREZM** | | 987 | + | AAAG | PLACE |
| **DOFCOREZM** | | 983 | + | AAAG | PLACE |
| **DOFCOREZM** | | 867 | + | AAAG | PLACE |
| **DOFCOREZM** | | 820 | + | AAAG | PLACE |
| **DOFCOREZM** | | 734 | + | AAAG | PLACE |
| **DOFCOREZM** | | 718 | + | AAAG | PLACE |
| **DOFCOREZM** | | 698 | + | AAAG | PLACE |
| **DOFCOREZM** | | 639 | + | AAAG | PLACE |
| **DOFCOREZM** | | 557 | + | AAAG | PLACE |
| **DOFCOREZM** | | 473 | + | AAAG | PLACE |

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|---|---|---|---|---|---|
| **DOFCOREZM** | | 5 | + | AAAG | PLACE |
| **DOFCOREZM** | | 1764 | - | AAAG | PLACE |
| **DOFCOREZM** | | 1589 | - | AAAG | PLACE |
| **DOFCOREZM** | | 1551 | - | AAAG | PLACE |
| **DOFCOREZM** | | 950 | - | AAAG | PLACE |
| **DOFCOREZM** | | 761 | - | AAAG | PLACE |
| **DOFCOREZM** | | 745 | - | AAAG | PLACE |
| **DOFCOREZM** | | 373 | - | AAAG | PLACE |
| **DPBFCOREDCDC3** | | 279 | + | ACACNNG | PLACE |
| **DPBFCOREDCDC3** | | 1448 | - | ACACNNG | PLACE |
| **DRECRTCOREAT** | | 261 | + | RCCGAC | PLACE |
| **E2FCONSENSUS** | | 330 | + | WTTSSCSS | PLACE |
| **EBOXBNNAPA** | | 1614 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 1602 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 1545 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 1429 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 1377 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 1231 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 647 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 600 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 408 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 279 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 270 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 163 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 104 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 1614 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 1602 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 1545 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 1429 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 1377 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 1231 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 647 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 600 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 408 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 279 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 270 | - | CANNTG | PLACE |

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| **EBOXBNNAPA** | | 163 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 104 | - | CANNTG | PLACE |
| **EECCRCAH1** | | 1608 | + | GANTTNC | PLACE |
| **EECCRCAH1** | | 1293 | + | GANTTNC | PLACE |
| **EECCRCAH1** | | 1226 | + | GANTTNC | PLACE |
| **EECCRCAH1** | | 920 | + | GANTTNC | PLACE |
| **EECCRCAH1** | | 580 | + | GANTTNC | PLACE |
| **EECCRCAH1** | | 428 | - | GANTTNC | PLACE |
| **ERE** | *Dianthus caryophyllus* | 344 | + | ATTTCAAA | PLACE; PlantCARE |
| **GAG-motif** | *Arabidopsis thaliana* | 1291 | + | AGAGAGT | PlantCARE |
| **GATABOX** | | 1421 | + | GATA | PLACE |
| **GATABOX** | | 1050 | + | GATA | PLACE |
| **GATABOX** | | 564 | + | GATA | PLACE |
| **GATABOX** | | 462 | + | GATA | PLACE |
| **GATABOX** | | 1369 | - | GATA | PLACE |
| **GATABOX** | | 1325 | - | GATA | PLACE |
| **GATABOX** | | 1161 | - | GATA | PLACE |
| **GATABOX** | | 361 | - | GATA | PLACE |
| **GATABOX** | | 296 | - | GATA | PLACE |
| **G-Box** | *Antirrhinum majus* | 47 | + | CACGTA | PlantCARE |
| **G-box** | *Daucus carota* | 43 | + | TACGTG | PlantCARE |
| **G-box** | *Daucus carota* | 165 | + | TACGTG | PlantCARE |
| **G-Box** | *Antirrhinum majus* | 43 | - | CACGTA | PlantCARE |
| **G-Box** | *Pisum sativum* | 271 | - | CACACATGGAA | PlantCARE |
| **G-Box** | *Pisum sativum* | 157 | - | CACGTG | PlantCARE |
| **G-Box** | *Antirrhinum majus* | 165 | - | CACGTA | PlantCARE |
| **G-box** | *Daucus carota* | 47 | - | TACGTG | PlantCARE |
| **G-box** | *Zea mays* | 564 | - | CACGAC | PlantCARE |
| **G-box** | *Oryza sativa* | 46 | - | GTACGTG | PlantCARE |
| **G-box** | *Solanum tuberosum* | 273 | - | CACATGG | PlantCARE |
| **GT1CONSENSUS** | | 1751 | + | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 1727 | + | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 1423 | + | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 1008 | + | GRWAAW | PLACE |

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| **GT1CONSENSUS** | | 358 | + | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 872 | + | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 1767 | - | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 1325 | - | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 1226 | - | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 1018 | - | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 382 | - | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 204 | - | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 203 | - | GRWAAW | PLACE |
| **GT1CORE** | | 1759 | + | GGTTAA | PLACE |
| **GT1CORE** | | 1761 | - | GGTTAA | PLACE |
| **GT1CORE** | | 1143 | - | GGTTAA | PLACE |
| **GT1GMSCAM4** | | 872 | + | GAAAAA | PLACE |
| **GT1GMSCAM4** | | 203 | - | GAAAAA | PLACE |
| **GT1-motif** | *Avena sativa* | 1136 | + | GGTTAAT | PlantCARE |
| **GT1-motif** | *Arabidopsis thaliana* | 1137 | + | GGTTAA | PlantCARE |
| **GTGANTG10** | | 1232 | + | GTGA | PLACE |
| **GTGANTG10** | | 806 | + | GTGA | PLACE |
| **GTGANTG10** | | 620 | + | GTGA | PLACE |
| **GTGANTG10** | | 530 | + | GTGA | PLACE |
| **GTGANTG10** | | 523 | + | GTGA | PLACE |
| **GTGANTG10** | | 155 | + | GTGA | PLACE |
| **GTGANTG10** | | 1426 | - | GTGA | PLACE |
| **GTGANTG10** | | 1127 | - | GTGA | PLACE |
| **GTGANTG10** | | 962 | - | GTGA | PLACE |
| **GTGANTG10** | | 644 | - | GTGA | PLACE |
| **I-box** | *Flaveria trinervia* | 458 | - | GATATGG | PlantCARE |
| **IBOXCORE** | | 1422 | + | GATAA | PLACE |
| **IBOXCORE** | | 1325 | - | GATAA | PLACE |
| **INRNTPSADB** | | 1016 | + | YTCANTYY | PLACE |
| **INRNTPSADB** | | 183 | + | YTCANTYY | PLACE |
| **INRNTPSADB** | | 777 | + | YTCANTYY | PLACE |
| **INTRONLOWER** | | 604 | + | TGCAGG | PLACE |
| **IRO2OS** | | 164 | + | CACGTGG | PLACE |
| **JERE** | *Arabidopsis* | 507 | - | AGACCGCC | PlantCARE |

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|---|---|---|---|---|---|
| | *thaliana* | | | | |
| **LECPLEACS2** | | 1368 | + | TAAAATAT | PLACE |
| **LTRECOREATCOR15** | | 261 | + | CCGAC | PLACE |
| **MNF1** | *Zea mays* | 160 | + | GTGCCC(A/T)(A/T) | PlantCARE |
| **MNF1** | *Zea mays* | 50 | - | GTGCCC(A/T)(A/T) | PlantCARE |
| **MYB1AT** | | 1433 | - | WAACCA | PLACE |
| **MYB1AT** | | 325 | - | WAACCA | PLACE |
| **MYB1AT** | | 955 | - | WAACCA | PLACE |
| **MYB1AT** | | 669 | - | WAACCA | PLACE |
| **MYB2CONSENSUSAT** | | 802 | + | YAACKG | PLACE |
| **MYB2CONSENSUSAT** | | 1032 | - | YAACKG | PLACE |
| **MYBATRD22** | | 956 | - | CTAACCA | PLACE |
| **MYBCORE** | | 585 | + | CNGTTR | PLACE |
| **MYBCORE** | | 43 | + | CNGTTR | PLACE |
| **MYBCORE** | | 1032 | + | CNGTTR | PLACE |
| **MYBCORE** | | 1144 | - | CNGTTR | PLACE |
| **MYBCORE** | | 802 | - | CNGTTR | PLACE |
| **MYBCOREATCYCB1** | | 802 | + | AACGG | PLACE |
| **MYBCOREATCYCB1** | | 491 | + | AACGG | PLACE |
| **MYBCOREATCYCB1** | | 1352 | - | AACGG | PLACE |
| **MYBCOREATCYCB1** | | 1031 | - | AACGG | PLACE |
| **MYBPZM** | | 1194 | + | CCWACC | PLACE |
| **MYBST1** | | 1050 | + | GGATA | PLACE |
| **MYCATERD1** | | 1231 | + | CATGTG | PLACE |
| **MYCATERD1** | | 270 | + | CATGTG | PLACE |
| **MYCATERD1** | | 647 | - | CATGTG | PLACE |
| **MYCATERD1** | | 279 | - | CATGTG | PLACE |
| **MYCATRD22** | | 647 | + | CACATG | PLACE |
| **MYCATRD22** | | 279 | + | CACATG | PLACE |
| **MYCATRD22** | | 1231 | - | CACATG | PLACE |
| **MYCATRD22** | | 270 | - | CACATG | PLACE |
| **MYCCONSENSUSAT** | | 1614 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 1602 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 1545 | + | CANNTG | PLACE |

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| **MYCCONSENSUSAT** | | 1429 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 1377 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 1231 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 647 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 600 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 408 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 279 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 270 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 163 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 104 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 1614 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 1602 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 1545 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 1429 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 1377 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 1231 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 647 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 600 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 408 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 279 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 270 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 163 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 104 | - | CANNTG | PLACE |
| **NODCON1GM** | | 989 | + | AAAGAT | PLACE |
| **NODCON1GM** | | 641 | + | AAAGAT | PLACE |
| **NODCON1GM** | | 475 | + | AAAGAT | PLACE |
| **NODCON2GM** | | 1588 | + | CTCTT | PLACE |
| **NODCON2GM** | | 1303 | - | CTCTT | PLACE |
| **NODCON2GM** | | 1216 | - | CTCTT | PLACE |
| **NTBBF1ARROLB** | | 821 | - | ACTTTA | PLACE |
| **O2-site** | *Zea mays* | 679 | + | GATGATGTGG | PlantCARE |
| **O2-site** | *Zea mays* | 455 | - | GATGATATGG | PlantCARE |
| **OSE1ROOTNODULE** | | 989 | + | AAAGAT | PLACE |
| **OSE1ROOTNODULE** | | 641 | + | AAAGAT | PLACE |
| **OSE1ROOTNODULE** | | 475 | + | AAAGAT | PLACE |
| **OSE2ROOTNODULE** | | 1588 | + | CTCTT | PLACE |

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| **OSE2ROOTNODULE** | | 1303 | - | CTCTT | PLACE |
| **OSE2ROOTNODULE** | | 1216 | - | CTCTT | PLACE |
| **PALBOXAPC** | | 333 | + | CCGTCC | PLACE |
| **P-box** | *Oryza sativa* | 740 | - | CCTTTTG | PlantCARE |
| **POLASIG1** | | 1485 | + | AATAAA | PLACE |
| **POLASIG1** | | 829 | + | AATAAA | PLACE |
| **POLASIG1** | | 471 | + | AATAAA | PLACE |
| **POLASIG1** | | 1631 | - | AATAAA | PLACE |
| **POLASIG2** | | 1059 | + | AATTAAA | PLACE |
| **POLASIG3** | | 833 | + | AATAAT | PLACE |
| **POLASIG3** | | 293 | + | AATAAT | PLACE |
| **POLASIG3** | | 1313 | - | AATAAT | PLACE |
| **POLLEN1LELAT52** | | 1416 | + | AGAAA | PLACE |
| **POLLEN1LELAT52** | | 1213 | + | AGAAA | PLACE |
| **POLLEN1LELAT52** | | 1086 | + | AGAAA | PLACE |
| **POLLEN1LELAT52** | | 986 | + | AGAAA | PLACE |
| **POLLEN1LELAT52** | | 870 | + | AGAAA | PLACE |
| **POLLEN1LELAT52** | | 733 | + | AGAAA | PLACE |
| **POLLEN1LELAT52** | | 1478 | - | AGAAA | PLACE |
| **POLLEN1LELAT52** | | 1436 | - | AGAAA | PLACE |
| **POLLEN1LELAT52** | | 592 | - | AGAAA | PLACE |
| **PREATPRODH** | | 1605 | - | ACTCAT | PLACE |
| **PYRIMIDINEBOXHVEPB1** | | 204 | + | TTTTTTCC | PLACE |
| **PYRIMIDINEBOXOSRAMY1A** | | 1765 | + | CCTTTT | PLACE |
| **PYRIMIDINEBOXOSRAMY1A** | | 746 | + | CCTTTT | PLACE |
| **PYRIMIDINEBOXOSRAMY1A** | | 1281 | - | CCTTTT | PLACE |
| **RAV1AAT** | | 315 | + | CAACA | PLACE |
| **RAV1AAT** | | 1342 | - | CAACA | PLACE |
| **RAV1AAT** | | 878 | - | CAACA | PLACE |
| **RAV1AAT** | | 765 | - | CAACA | PLACE |
| **RAV1AAT** | | 585 | - | CAACA | PLACE |
| **RAV1AAT** | | 321 | - | CAACA | PLACE |

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| **RAV1AAT** | | 43 | - | CAACA | PLACE |
| **RAV1BAT** | | 1429 | + | CACCTG | PLACE |
| **RAV1BAT** | | 104 | + | CACCTG | PLACE |
| **RBCSCONSENSUS** | | 769 | - | AATCCAA | PLACE |
| **REALPHALGLHCB21** | | 954 | - | AACCAA | PLACE |
| **REALPHALGLHCB21** | | 324 | - | AACCAA | PLACE |
| **RHERPATEXPA7** | | 170 | + | KCACGW | PLACE |
| **RHERPATEXPA7** | | 162 | + | KCACGW | PLACE |
| **RHERPATEXPA7** | | 48 | + | KCACGW | PLACE |
| **RHERPATEXPA7** | | 54 | - | KCACGW | PLACE |
| **RHERPATEXPA7** | | 530 | - | KCACGW | PLACE |
| **RHERPATEXPA7** | | 155 | - | KCACGW | PLACE |
| **ROOTMOTIFTAPOX1** | | 1627 | + | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 1274 | + | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 998 | + | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 797 | + | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 193 | + | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 1368 | - | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 997 | - | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 796 | - | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 787 | - | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 627 | - | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 360 | - | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 295 | - | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 249 | - | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 126 | - | ATATT | PLACE |
| **RYREPEATBNNAPA** | | 387 | + | CATGCA | PLACE |
| **RYREPEATBNNAPA** | | 90 | + | CATGCA | PLACE |
| **RYREPEATBNNAPA** | | 88 | - | CATGCA | PLACE |
| **RYREPEATGMGY2** | | 388 | + | CATGCAT | PLACE |
| **RYREPEATGMGY2** | | 88 | - | CATGCAT | PLACE |
| **RYREPEATLEGUMIN BOX** | | 388 | + | CATGCAY | PLACE |
| **RYREPEATLEGUMIN BOX** | | 91 | + | CATGCAY | PLACE |
| **RYREPEATLEGUMIN** | | 88 | - | CATGCAY | PLACE |

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| **BOX** | | | | | |
| **SEBFCONSSTPR10A** | | 1235 | - | YTGTCWC | PLACE |
| **SEF1MOTIF** | | 1631 | + | ATATTTAWW | PLACE |
| **SEF1MOTIF** | | 249 | - | ATATTTAWW | PLACE |
| **SEF4MOTIFGM7S** | | 1635 | + | RTTTTTR | PLACE |
| **SEF4MOTIFGM7S** | | 817 | + | RTTTTTR | PLACE |
| **SEF4MOTIFGM7S** | | 904 | - | RTTTTTR | PLACE |
| **SITEIIATCYTC** | | 1412 | + | TGGGCY | PLACE |
| **SITEIIATCYTC** | | 1578 | - | TGGGCY | PLACE |
| **SORLIP1AT** | | 1494 | + | GCCAC | PLACE |
| **SORLIP1AT** | | 517 | + | GCCAC | PLACE |
| **Sp1** | *Zea mays* | 513 | - | CC(G/A)CCC | PlantCARE |
| **SURECOREATSULTR11** | | 1462 | - | GAGAC | PLACE |
| **SURECOREATSULTR11** | | 610 | - | GAGAC | PLACE |
| **TAAAGSTKST1** | | 820 | + | TAAAG | PLACE |
| **TAAAGSTKST1** | | 639 | + | TAAAG | PLACE |
| **TAAAGSTKST1** | | 1590 | - | TAAAG | PLACE |
| **TAAAGSTKST1** | | 1552 | - | TAAAG | PLACE |
| **TATA-box** | *Arabidopsis thaliana* | 186 | + | TATAA | PlantCARE |
| **TATA-box** | *Zea mays* | 238 | + | TTTAAAAA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 240 | + | TATTTAAA | PlantCARE |
| **TATA-box** | *Lycopersicon esculentum* | 450 | + | TTTTA | PlantCARE |
| **TATA-box** | *Lycopersicon esculentum* | 467 | + | TTTTA | PlantCARE |
| **TATA-box** | *Lycopersicon esculentum* | 610 | + | TTTTA | PlantCARE |
| **TATA-box** | *Helianthus annuus* | 645 | + | TATACA | PlantCARE |
| **TATA-box** | *Glycine max* | 793 | + | TAATA | PlantCARE |
| **TATA-box** | *Zea mays* | 811 | + | TTTAAAAA | PlantCARE |
| **TATA-box** | *Lycopersicon esculentum* | 820 | + | TTTTA | PlantCARE |

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| **TATA-box** | *Glycine max* | 994 | + | TAATA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 1035 | + | TATAA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 1059 | + | TATAA | PlantCARE |
| **TATA-box** | *Glycine max* | 1270 | + | TAATA | PlantCARE |
| **TATA-box** | *Lycopersicon esculentum* | 1273 | + | TTTTA | PlantCARE |
| **TATA-box** | *Glycine max* | 1309 | + | TAATA | PlantCARE |
| **TATA-box** | *Lycopersicon esculentum* | 1360 | + | TTTTA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 5 | - | TATA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 10 | - | TATA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 75 | - | TATA | PlantCARE |
| **TATA-box** | *Glycine max* | 120 | - | TAATA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 123 | - | TATA | PlantCARE |
| **TATA-box** | *Brassica napus* | 185 | - | ATTATA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 187 | - | TATA | PlantCARE |
| **TATA-box** | *Lycopersicon esculentum* | 239 | - | TTTTA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 246 | - | TATA | PlantCARE |
| **TATA-box** | *Glycine max* | 286 | - | TAATA | PlantCARE |
| **TATA-box** | *Glycine max* | 289 | - | TAATA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 647 | - | TATA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 659 | - | TATA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 779 | - | TATA | PlantCARE |
| **TATA-box** | *Glycine max* | 781 | - | TAATA | PlantCARE |

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| **TATA-box** | *Glycine max* | 790 | - | TAATA | PlantCARE |
| **TATA-box** | *Lycopersicon esculentum* | 812 | - | TTTTA | PlantCARE |
| **TATA-box** | *Lycopersicon esculentum* | 844 | - | TTTTA | PlantCARE |
| **TATA-box** | *Oryza sativa* | 895 | - | TACAAAA | PlantCARE |
| **TATA-box** | *Lycopersicon esculentum* | 988 | - | TTTTA | PlantCARE |
| **TATA-box** | *Glycine max* | 991 | - | TAATA | PlantCARE |
| **TATA-box** | *Brassica napus* | 1034 | - | ATTATA | PlantCARE |
| **TATA-box** | *Ac* | 1036 | - | TATAAAT | PlantCARE |
| **TATA-box** | *Brassica napus* | 1058 | - | ATTATA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 1060 | - | TATA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 1268 | - | TATA | PlantCARE |
| **TATA-box** | *Glycine max* | 1478 | - | TAATA | PlantCARE |
| **TATABOX2** | | 1043 | + | TATAAAT | PLACE |
| **TATABOX3** | | 1777 | + | TATTAAT | PLACE |
| **TATABOX3** | | 795 | - | TATTAAT | PLACE |
| **TATABOX5** | | 1632 | + | TTATTT | PLACE |
| **TATABOX5** | | 1753 | - | TTATTT | PLACE |
| **TATABOX5** | | 832 | - | TTATTT | PLACE |
| **TATABOX5** | | 828 | - | TTATTT | PLACE |
| **TATABOXOSPAL** | | 248 | - | TATTTAA | PLACE |
| **TBOXATGAPB** | | 558 | - | ACTTTG | PLACE |
| **TC-rich repeats** | *Nicotiana tabacum* | 1429 | - | GTTTTCTTAC | PlantCARE |
| **TGACG-motif** | *Hordeum vulgare* | 653 | - | TGACG | PlantCARE |
| **TGTCACACMCUCUMISIN** | | 1234 | - | TGTCACA | PLACE |
| **Unnamed__1** | *Zea mays* | 136 | - | CGTGG | PlantCARE |
| **Unnamed__1** | *Zea mays* | 159 | - | CGTGG | PlantCARE |
| **Unnamed__4** | *Petroselinum hortense* | 602 | + | CTCC | PlantCARE |
| **Unnamed__4** | *Petroselinum hortense* | 1302 | + | CTCC | PlantCARE |

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| **Unnamed__4** | *Petroselinum hortense* | 1128 | + | CTCC | PlantCARE |
| **Unnamed__4** | *Petroselinum hortense* | 139 | + | CTCC | PlantCARE |
| **Unnamed__4** | *Petroselinum hortense* | 27 | - | CTCC | PlantCARE |
| **Unnamed__4** | *Petroselinum hortense* | 962 | - | CTCC | PlantCARE |
| **Unnamed__4** | *Petroselinum hortense* | 534 | - | CTCC | PlantCARE |
| **Unnamed__4** | *Petroselinum hortense* | 834 | - | CTCC | PlantCARE |
| **Unnamed__4** | *Petroselinum hortense* | 1459 | - | CTCC | PlantCARE |
| **Unnamed__4** | *Petroselinum hortense* | 1102 | - | CTCC | PlantCARE |
| **Unnamed__4** | *Petroselinum hortense* | 549 | - | CTCC | PlantCARE |
| **Unnamed__4** | *Petroselinum hortense* | 1200 | - | CTCC | PlantCARE |
| **WBOXATNPR1** | | 657 | + | TTGAC | PLACE |
| **WBOXATNPR1** | | 1558 | - | TTGAC | PLACE |
| **WBOXHVISO1** | | 525 | + | TGACT | PLACE |
| **WBOXHVISO1** | | 1135 | - | TGACT | PLACE |
| **WBOXNTCHN48** | | 1136 | - | CTGACY | PLACE |
| **WBOXNTERF3** | | 525 | + | TGACY | PLACE |
| **WBOXNTERF3** | | 1135 | - | TGACY | PLACE |
| **WRKY71OS** | | 1439 | + | TGAC | PLACE |
| **WRKY71OS** | | 1233 | + | TGAC | PLACE |
| **WRKY71OS** | | 657 | + | TGAC | PLACE |
| **WRKY71OS** | | 524 | + | TGAC | PLACE |
| **WRKY71OS** | | 1557 | - | TGAC | PLACE |
| **WRKY71OS** | | 1135 | - | TGAC | PLACE |
| **WUN-motif** | *Brassica oleracea* | 684 | - | TCATTACGAA | PlantCARE |

## 7.9 Regulatory cis-elements in the 1.5 kb promoter fragment of *tps10* of *Zea mays* var. Delprim

**Tab.7. 16**

| tps10 1300 bp | Organism | Position | Strand | Sequence | Database |
|---|---|---|---|---|---|
| **-10PEHVPSBD** | | 635 | + | TATTCT | PLACE |
| **A-box** | *Petroselinum crispum* | 303 | - | CCGTCC | PlantCARE |
| **ABRE** | *Oryza sativa* | 152 | + | AGTACGTGGC | PlantCARE |
| **ABRE** | *Arabidopsis thaliana* | 455 | - | CACGTG | PlantCARE |
| **ABRELATERD1** | | 456 | + | ACGTG | PLACE |
| **ABRELATERD1** | | 457 | - | ACGTG | PLACE |
| **ABRELATERD1** | | 875 | - | ACGTG | PLACE |
| **ABRERATCAL** | | 455 | + | MACGYGB | PLACE |
| **ABRERATCAL** | | 844 | - | MACGYGB | PLACE |
| **ACGTATERD1** | | 114 | + | ACGT | PLACE |
| **ACGTATERD1** | | 281 | + | ACGT | PLACE |
| **ACGTATERD1** | | 296 | + | ACGT | PLACE |
| **ACGTATERD1** | | 457 | + | ACGT | PLACE |
| **ACGTATERD1** | | 875 | + | ACGT | PLACE |
| **ACGTATERD1** | | 114 | - | ACGT | PLACE |
| **ACGTATERD1** | | 281 | - | ACGT | PLACE |
| **ACGTATERD1** | | 296 | - | ACGT | PLACE |
| **ACGTATERD1** | | 457 | - | ACGT | PLACE |
| **ACGTATERD1** | | 875 | - | ACGT | PLACE |
| **ACGTTBOX** | | 295 | + | AACGTT | PLACE |
| **ACGTTBOX** | | 295 | - | AACGTT | PLACE |
| **ANAERO1CONSENSUS** | | 87 | + | AAACAAA | PLACE |
| **ANAERO2CONSENSUS** | | 5 | - | AGCAGC | PLACE |
| **ANAERO2CONSENSUS** | | 185 | - | AGCAGC | PLACE |
| **ARE** | *Zea mays* | 350 | - | TGGTTT | PlantCARE |

| | | | | | |
|---|---|---|---|---|---|
| **ARFAT** | | 410 | + | TGTCTC | PLACE |
| **ARFAT** | | 617 | + | TGTCTC | PLACE |
| **ARFAT** | | 988 | + | TGTCTC | PLACE |
| **ARR1AT** | | 434 | + | NGATT | PLACE |
| **ARR1AT** | | 763 | + | NGATT | PLACE |
| **ARR1AT** | | 915 | + | NGATT | PLACE |
| **ARR1AT** | | 948 | + | NGATT | PLACE |
| **ARR1AT** | | 493 | - | NGATT | PLACE |
| **ARR1AT** | | 952 | - | NGATT | PLACE |
| **ARR1AT** | | 1098 | - | NGATT | PLACE |
| **ARR1AT** | | 1143 | - | NGATT | PLACE |
| **ARR1AT** | | 128 | - | NGATT | PLACE |
| **ARR1AT** | | 592 | - | NGATT | PLACE |
| **ARR1AT** | | 701 | - | NGATT | PLACE |
| **ASF1MOTIFCAMV** | | 45 | + | TGACG | PLACE |
| **ASF1MOTIFCAMV** | | 23 | - | TGACG | PLACE |
| **BIHD1OS** | | 577 | + | TGTCA | PLACE |
| **BIHD1OS** | | 1000 | - | TGTCA | PLACE |
| **BIHD1OS** | | 1263 | - | TGTCA | PLACE |
| **Box 4** | *Petroselinum crispum* | 668 | - | ATTAAT | PlantCARE |
| **Box 4** | *Petroselinum crispum* | 944 | - | ATTAAT | PlantCARE |
| **Box 4** | *Petroselinum crispum* | 932 | - | ATTAAT | PlantCARE |
| **Box 4** | *Petroselinum crispum* | 1115 | - | ATTAAT | PlantCARE |
| **BOXIINTPATPB** | | 710 | + | ATAGAA | PLACE |
| **BP5OSWX** | | 873 | - | CAACGTG | PLACE |
| **CAAT-box** | *Hordeum vulgare* | 129 | + | CAAT | PLACE; PlantCARE |
| **CAAT-box** | *Hordeum vulgare* | 147 | + | CAAT | PLACE; PlantCARE |
| **CAAT-box** | *Glycine max* | 319 | + | CAATT | PlantCARE |
| **CAAT-box** | *Arabidopsis thaliana* | 320 | + | gGCAAT | PlantCARE |

| | | | | | |
|---|---|---|---|---|---|
| **CAAT-box** | *Hordeum vulgare* | 446 | + | CAAT | PLACE; PlantCARE |
| **CAAT-box** | *Hordeum vulgare* | 451 | + | CAAT | PLACE; PlantCARE |
| **CAAT-box** | *Glycine max* | 483 | + | CAATT | PlantCARE |
| **CAAT-box** | *Hordeum vulgare* | 484 | + | CAAT | PLACE; PlantCARE |
| **CAAT-box** | *Hordeum vulgare* | 494 | + | CAAT | PLACE; PlantCARE |
| **CAAT-box** | *Brassica rapa* | 724 | + | CAAAT | PlantCARE |
| **CAAT-box** | *Arabidopsis thaliana* | 893 | + | CCAAT | PlantCARE |
| **CAAT-box** | *Brassica rapa* | 1060 | + | CAAAT | PlantCARE |
| **CAAT-box** | *Brassica rapa* | 1236 | + | CAAAT | PlantCARE |
| **CAAT-box** | *Hordeum vulgare* | 178 | - | CAAT | PLACE; PlantCARE |
| **CAAT-box** | *Hordeum vulgare* | 368 | - | CAAT | PLACE; PlantCARE |
| **CAAT-box** | *Brassica rapa* | 426 | - | CAAAT | PlantCARE |
| **CAAT-box** | *Hordeum vulgare* | 554 | - | CAAT | PLACE; PlantCARE |
| **CAAT-box** | *Brassica rapa* | 811 | - | CAAAT | PlantCARE |
| **CAAT-box** | *Hordeum vulgare* | 1089 | - | CAAT | PLACE; PlantCARE |
| **CAAT-box** | *Brassica rapa* | 1183 | - | CAAAT | PlantCARE |
| **CAATBOX1** | | 321 | + | CAAT | PLACE |
| **CAATBOX1** | | 894 | + | CAAT | PLACE |
| **CACGTGMOTIF** | | 456 | + | CACGTG | PLACE |
| **CACGTGMOTIF** | | 456 | - | CACGTG | PLACE |
| **CACTFTPPCA1** | | 111 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 138 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 210 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 394 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 1013 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 1162 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 1202 | + | YACT | PLACE |

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|---|---|---|---|---|---|
| **CACTFTPPCA1** | | 1224 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 1261 | + | YACT | PLACE |
| **CACTFTPPCA1** | | 359 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 732 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 1177 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 1277 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 159 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 263 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 589 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 652 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 720 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 759 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 767 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 961 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 994 | - | YACT | PLACE |
| **CACTFTPPCA1** | | 1121 | - | YACT | PLACE |
| **CANBNNAPA** | | 1173 | - | CNAACAC | PLACE |
| **CAREOSREP1** | | 421 | + | CAACTC | PLACE |
| **CARGCW8GAT** | | 888 | + | CWWWWWWWWG | PLACE |
| **CARGCW8GAT** | | 888 | - | CWWWWWWWWG | PLACE |
| **CCAATBOX1** | | 894 | + | CCAAT | PLACE |
| **CCGTCC-box** | *Arabidopsis thaliana* | 303 | - | CCGTCC | PlantCARE |
| **CEREGLUBOX2PSLEGA** | | 1054 | + | TGAAAACT | PLACE |
| **CGACGOSAMY3** | | 42 | + | CGACG | PLACE |
| **CGCGBOXAT** | | 845 | + | VCGCGB | PLACE |
| **CGCGBOXAT** | | 845 | - | VCGCGB | PLACE |
| **CGTCA-motif** | *Hordeum vulgare* | 22 | + | CGTCA | PlantCARE |
| **CGTCA-motif** | *Hordeum vulgare* | 44 | - | CGTCA | PlantCARE |
| **circadian** | *Lycopersicon esculentum* | 687 | + | CAANNNNATC | PlantCARE; PLACE |
| **circadian** | *Lycopersicon esculentum* | 872 | - | CAANNNNATC | PlantCARE; PLACE |

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|---|---|---|---|---|---|
| **CMSRE1IBSPOA** | | 304 | + | TGGACGG | PLACE |
| **CTRMCAMV35S** | | 612 | + | TCTCTCTCT | PLACE |
| **CURECORECR** | | 112 | + | GTAC | PLACE |
| **CURECORECR** | | 158 | + | GTAC | PLACE |
| **CURECORECR** | | 249 | + | GTAC | PLACE |
| **CURECORECR** | | 262 | + | GTAC | PLACE |
| **CURECORECR** | | 476 | + | GTAC | PLACE |
| **CURECORECR** | | 112 | - | GTAC | PLACE |
| **CURECORECR** | | 158 | - | GTAC | PLACE |
| **CURECORECR** | | 249 | - | GTAC | PLACE |
| **CURECORECR** | | 262 | - | GTAC | PLACE |
| **CURECORECR** | | 476 | - | GTAC | PLACE |
| **DOFCOREZM** | | 85 | + | AAAG | PLACE |
| **DOFCOREZM** | | 104 | + | AAAG | PLACE |
| **DOFCOREZM** | | 515 | + | AAAG | PLACE |
| **DOFCOREZM** | | 734 | + | AAAG | PLACE |
| **DOFCOREZM** | | 1017 | + | AAAG | PLACE |
| **DOFCOREZM** | | 1152 | + | AAAG | PLACE |
| **DOFCOREZM** | | 1194 | + | AAAG | PLACE |
| **DOFCOREZM** | | 1253 | + | AAAG | PLACE |
| **DOFCOREZM** | | 1294 | + | AAAG | PLACE |
| **DOFCOREZM** | | 1244 | - | AAAG | PLACE |
| **DOFCOREZM** | | 1285 | - | AAAG | PLACE |
| **DPBFCOREDCDC3** | | 1160 | + | ACACNNG | PLACE |
| **DPBFCOREDCDC3** | | 1259 | + | ACACNNG | PLACE |
| **DPBFCOREDCDC3** | | 251 | - | ACACNNG | PLACE |
| **DPBFCOREDCDC3** | | 1176 | - | ACACNNG | PLACE |
| **DPBFCOREDCDC3** | | 1276 | - | ACACNNG | PLACE |
| **E2FCONSENSUS** | | 321 | - | WTTSSCSS | PLACE |
| **EBOXBNNAPA** | | 16 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 456 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 471 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 623 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 812 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 836 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 908 | + | CANNTG | PLACE |

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|---|---|---|---|---|---|
| **EBOXBNNAPA** | | 1060 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 1236 | + | CANNTG | PLACE |
| **EBOXBNNAPA** | | 16 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 456 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 471 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 623 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 812 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 836 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 908 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 1060 | - | CANNTG | PLACE |
| **EBOXBNNAPA** | | 1236 | - | CANNTG | PLACE |
| **EECCRCAH1** | | 319 | - | GANTTNC | PLACE |
| **EECCRCAH1** | | 421 | - | GANTTNC | PLACE |
| **Gap-box** | *Arabidopsis thaliana* | 1055 | + | CAAATGAA(A/G)A | PlantCARE |
| **GATABOX** | | 400 | + | GATA | PLACE |
| **GATABOX** | | 639 | + | GATA | PLACE |
| **GATABOX** | | 659 | + | GATA | PLACE |
| **GATABOX** | | 883 | + | GATA | PLACE |
| **GATABOX** | | 978 | + | GATA | PLACE |
| **GATABOX** | | 233 | - | GATA | PLACE |
| **GATABOX** | | 573 | - | GATA | PLACE |
| **GATABOX** | | 959 | - | GATA | PLACE |
| **GATABOX** | | 1021 | - | GATA | PLACE |
| **G-Box** | *Pisum sativum* | 873 | + | CACGTT | PlantCARE |
| **G-box** | *Zea mays* | 873 | + | CACGTT | PlantCARE |
| **G-Box** | *Pisum sativum* | 455 | - | CACGTG | PlantCARE |
| **G-box** | *Arabidopsis thaliana* | 455 | - | CACGTG | PlantCARE |
| **GCCCORE** | | 324 | - | GCCGCC | PLACE |
| **GT1CONSENSUS** | | 79 | + | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 976 | + | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 1129 | + | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 1137 | + | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 398 | + | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 707 | + | GRWAAW | PLACE |

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|---|---|---|---|---|---|
| **GT1CONSENSUS** | | 1168 | + | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 66 | - | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 346 | - | GRWAAW | PLACE |
| **GT1CONSENSUS** | | 1241 | - | GRWAAW | PLACE |
| **GT1CORE** | | 826 | - | GGTTAA | PLACE |
| **GT1GMSCAM4** | | 707 | + | GAAAAA | PLACE |
| **GT1GMSCAM4** | | 1168 | + | GAAAAA | PLACE |
| **GT1-motif** | *Avena sativa* | 825 | - | GGTTAAT | PlantCARE |
| **GTGANTG10** | | 336 | + | GTGA | PLACE |
| **GTGANTG10** | | 470 | + | GTGA | PLACE |
| **GTGANTG10** | | 545 | + | GTGA | PLACE |
| **GTGANTG10** | | 731 | + | GTGA | PLACE |
| **GTGANTG10** | | 211 | - | GTGA | PLACE |
| **GTGANTG10** | | 459 | - | GTGA | PLACE |
| **GTGANTG10** | | 507 | - | GTGA | PLACE |
| **GTGANTG10** | | 877 | - | GTGA | PLACE |
| **IBOX** | | 1021 | - | GATAAG | PLACE |
| **IBOXCORE** | | 399 | + | GATAA | PLACE |
| **IBOXCORE** | | 977 | + | GATAA | PLACE |
| **IBOXCORE** | | 1021 | - | GATAA | PLACE |
| **IBOXCORENT** | | 1021 | - | GATAAGR | PLACE |
| **INRNTPSADB** | | 780 | - | YTCANTYY | PLACE |
| **INRNTPSADB** | | 730 | - | YTCANTYY | PLACE |
| **INTRONLOWER** | | 12 | + | TGCAGG | PLACE |
| **INTRONLOWER** | | 36 | - | TGCAGG | PLACE |
| **LECPLEACS2** | | 1081 | - | TAAAATAT | PLACE |
| **MBS** | *Arabidopsis thaliana* | 622 | + | CAACTG | PlantCARE |
| **MNF1** | *Zea mays* | 627 | - | GTGCCC(A/T)(A/T) | PlantCARE |
| **MYB1AT** | | 351 | + | WAACCA | PLACE |
| **MYB2CONSENSUSAT** | | 623 | + | YAACKG | PLACE |
| **MYBCORE** | | 623 | - | CNGTTR | PLACE |
| **MYBCORE** | | 825 | - | CNGTTR | PLACE |
| **MYBST1** | | 400 | + | GGATA | PLACE |
| **MYBST1** | | 572 | - | GGATA | PLACE |

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|---|---|---|---|---|---|
| **MYCATERD1** | | 16 | + | CATGTG | PLACE |
| **MYCATERD1** | | 471 | + | CATGTG | PLACE |
| **MYCATRD22** | | 16 | - | CACATG | PLACE |
| **MYCATRD22** | | 471 | - | CACATG | PLACE |
| **MYCCONSENSUSAT** | | 16 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 456 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 471 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 623 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 812 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 836 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 908 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 1060 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 1236 | + | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 16 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 456 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 471 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 623 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 812 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 836 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 908 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 1060 | - | CANNTG | PLACE |
| **MYCCONSENSUSAT** | | 1236 | - | CANNTG | PLACE |
| **NODCON1GM** | | 102 | + | AAAGAT | PLACE |
| **NODCON2GM** | | 1286 | + | CTCTT | PLACE |
| **NODCON2GM** | | 1192 | - | CTCTT | PLACE |
| **NODCON2GM** | | 1251 | - | CTCTT | PLACE |
| **NTBBF1ARROLB** | | 733 | - | ACTTTA | PLACE |
| **OSE1ROOTNODULE** | | 102 | + | AAAGAT | PLACE |
| **OSE2ROOTNODULE** | | 1286 | + | CTCTT | PLACE |
| **OSE2ROOTNODULE** | | 1192 | - | CTCTT | PLACE |
| **OSE2ROOTNODULE** | | 1251 | - | CTCTT | PLACE |
| **PALBOXAPC** | | 304 | - | CCGTCC | PLACE |
| **P-box** | *Oryza sativa* | 83 | - | CCTTTTG | PlantCARE |
| **POLASIG1** | | 1186 | - | AATAAA | PLACE |
| **POLASIG1** | | 1229 | - | AATAAA | PLACE |

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|---|---|---|---|---|---|
| **POLASIG2** | | 429 | - | AATTAAA | PLACE |
| **POLASIG2** | | 1269 | - | AATTAAA | PLACE |
| **POLLEN1LELAT52** | | 709 | + | AGAAA | PLACE |
| **PREATPRODH** | | 779 | - | ACTCAT | PLACE |
| **PYRIMIDINEBOXOSRAMY1A** | | 84 | - | CCTTTT | PLACE |
| **RAV1AAT** | | 20 | + | CAACA | PLACE |
| **RAV1AAT** | | 142 | + | CAACA | PLACE |
| **RAV1AAT** | | 684 | + | CAACA | PLACE |
| **REALPHALGLHCB21** | | 532 | + | AACCAA | PLACE |
| **RGATAOS** | | 228 | - | CAGAAGATA | PLACE |
| **RHERPATEXPA7** | | 457 | + | KCACGW | PLACE |
| **RHERPATEXPA7** | | 875 | + | KCACGW | PLACE |
| **RHERPATEXPA7** | | 455 | - | KCACGW | PLACE |
| **ROOTMOTIFTAPOX1** | | 637 | + | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 930 | + | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 1084 | + | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 1113 | + | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 77 | - | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 854 | - | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 892 | - | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 931 | - | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 1085 | - | ATATT | PLACE |
| **ROOTMOTIFTAPOX1** | | 1114 | - | ATATT | PLACE |
| **RYREPEATBNNAPA** | | 215 | + | CATGCA | PLACE |
| **RYREPEATBNNAPA** | | 222 | + | CATGCA | PLACE |
| **RYREPEATBNNAPA** | | 378 | + | CATGCA | PLACE |
| **RYREPEATBNNAPA** | | 224 | - | CATGCA | PLACE |
| **RYREPEATGMGY2** | | 214 | + | CATGCAT | PLACE |
| **RYREPEATGMGY2** | | 221 | + | CATGCAT | PLACE |
| **RYREPEATGMGY2** | | 377 | + | CATGCAT | PLACE |
| **RYREPEATLEGUMINBOX** | | 214 | + | CATGCAY | PLACE |
| **RYREPEATLEGUMINBOX** | | 221 | + | CATGCAY | PLACE |
| **RYREPEATLEGUMIN** | | 377 | + | CATGCAY | PLACE |

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|---|---|---|---|---|---|
| **BOX** | | | | | |
| **S1FBOXSORPS1L21** | | 70 | - | ATGGTA | PLACE |
| **SEBFCONSSTPR10A** | | 410 | + | YTGTCWC | PLACE |
| **SEF4MOTIFGM7S** | | 783 | - | RTTTTTR | PLACE |
| **SEF4MOTIFGM7S** | | 603 | - | RTTTTTR | PLACE |
| **IIATCYTC** | | 300 | - | TGGGCY | PLACE |
| **IIATCYTC** | | 382 | - | TGGGCY | PLACE |
| **Skn-1_motif** | *Oryza sativa* | 575 | + | GTCAT | PlantCARE |
| **SORLIP1AT** | | 327 | - | GCCAC | PLACE |
| **SORLIP1AT** | | 801 | - | GCCAC | PLACE |
| **SORLIP2AT** | | 301 | - | GGGCC | PLACE |
| **SORLREP3AT** | | 738 | + | TGTATATAT | PLACE |
| **SP8BFIBSP8BIB** | | 767 | - | TACTATT | PLACE |
| **SREATMSD** | | 399 | - | TTATCC | PLACE |
| **SURE1STPAT21** | | 708 | + | AATAGAAAA | PLACE |
| **SURECOREATSULTR11** | | 192 | - | GAGAC | PLACE |
| **SURECOREATSULTR11** | | 237 | - | GAGAC | PLACE |
| **SURECOREATSULTR11** | | 410 | - | GAGAC | PLACE |
| **SURECOREATSULTR11** | | 617 | - | GAGAC | PLACE |
| **SURECOREATSULTR11** | | 988 | - | GAGAC | PLACE |
| **T/GBOXATPIN2** | | 874 | - | AACGTG | PLACE |
| **TAAAGSTKST1** | | 515 | + | TAAAG | PLACE |
| **TAAAGSTKST1** | | 734 | + | TAAAG | PLACE |
| **TAAAGSTKST1** | | 1243 | - | TAAAG | PLACE |
| **TATA-box** | *Glycine max* | 77 | + | TAATA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 161 | + | TATAA | PlantCARE |
| **TATA-box** | *Glycine max* | 276 | + | TAATA | PlantCARE |
| **TATA-box** | *Daucus carota* | 671 | + | ccTATAAATT | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 732 | + | taTATAAAgg | PlantCARE |

| | | | | | |
|---|---|---|---|---|---|
| **TATA-box** | *Lycopersicon esculentum* | 733 | + | taTATAAAg | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 734 | + | TATAAA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 735 | + | TATATAA | PlantCARE |
| **TATA-box** | *Glycine max* | 769 | + | TAATA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 783 | + | ccTATAAAaa | PlantCARE |
| **TATA-box** | *Helianthus annuus* | 850 | + | TATACA | PlantCARE |
| **TATA-box** | *Glycine max* | 854 | + | TAATA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 889 | + | TATAA | PlantCARE |
| **TATA-box** | *Glycine max* | 931 | + | TAATA | PlantCARE |
| **TATA-box** | *Lycopersicon esculentum* | 971 | + | TTTTA | PlantCARE |
| **TATA-box** | *Lycopersicon esculentum* | 1033 | + | TTTTA | PlantCARE |
| **TATA-box** | *Lycopersicon esculentum* | 1047 | + | TTTTA | PlantCARE |
| **TATA-box** | *Lycopersicon esculentum* | 1080 | + | TTTTA | PlantCARE |
| **TATA-box** | *Glycine max* | 1114 | + | TAATA | PlantCARE |
| **TATA-box** | *Lycopersicon esculentum* | 1225 | + | TTTTA | PlantCARE |
| **TATA-box** | *Lycopersicon esculentum* | 1230 | + | TTTTA | PlantCARE |
| **TATA-box** | *Lycopersicon esculentum* | 1271 | + | TTTTA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 73 | - | TATA | PlantCARE |
| **TATA-box** | *Brassica napus* | 74 | - | ATATAT | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 75 | - | TATA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 162 | - | TATA | PlantCARE |

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|---|---|---|---|---|---|
| **TATA-box** | *Arabidopsis thaliana* | 736 | - | TATATATA | PlantCARE |
| **TATA-box** | *Brassica napus* | 737 | - | ATATAT | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 738 | - | TATA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 740 | - | TATA | PlantCARE |
| **TATA-box** | *Oryza sativa* | 772 | - | TACAAAA | PlantCARE |
| **TATA-box** | *Lycopersicon esculentum* | 784 | - | TTTTA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 852 | - | TATA | PlantCARE |
| **TATA-box** | *Brassica napus* | 888 | - | ATTATA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 890 | - | TATA | PlantCARE |
| **TATA-box** | *Arabidopsis thaliana* | 1041 | - | TATA | PlantCARE |
| **TATA-box** | *Glycine max* | 1111 | - | TAATA | PlantCARE |
| **TATA-box** | *Glycine max* | 1117 | - | TAATA | PlantCARE |
| **TATABOX3** | | 1116 | + | TATTAAT | PLACE |
| **TATABOX3** | | 932 | - | TATTAAT | PLACE |
| **TATABOX3** | | 1115 | - | TATTAAT | PLACE |
| **TATABOX4** | | 736 | + | TATATAA | PLACE |
| **TATABOX5** | | 1185 | + | TTATTT | PLACE |
| **TATABOX5** | | 1228 | + | TTATTT | PLACE |
| **TATAPVTRNALEU** | | 735 | - | TTTATATA | PLACE |
| **TC-rich repeats** | *Nicotiana tabacum* | 648 | - | ATTTTCTTCA | PlantCARE |
| **TGACG-motif** | *Hordeum vulgare* | 44 | + | TGACG | PlantCARE |
| **TGACG-motif** | *Hordeum vulgare* | 22 | - | TGACG | PlantCARE |
| **TRANSINITDICOTS** | | 444 | + | AMNAUGGC | PLACE |
| **TRANSINITMONOCOTS** | | 444 | + | RMNAUGGC | PLACE |
| **Unnamed__4** | *Petroselinum hortense* | 26 | + | CTCC | PlantCARE |
| **Unnamed__4** | *Petroselinum hortense* | 1075 | + | CTCC | PlantCARE |

| | | | | | |
|---|---|---|---|---|---|
| **Unnamed__4** | *Petroselinum hortense* | 419 | + | CTCC | PlantCARE |
| **Unnamed__4** | *Petroselinum hortense* | 1246 | + | CTCC | PlantCARE |
| **Unnamed__4** | *Petroselinum hortense* | 315 | + | CTCC | PlantCARE |
| **Unnamed__4** | *Petroselinum hortense* | 540 | + | CTCC | PlantCARE |
| **WBBOXPCWRKY1** | | 201 | + | TTTGACY | PLACE |
| **WBOXATNPR1** | | 202 | + | TTGAC | PLACE |
| **WBOXATNPR1** | | 1001 | + | TTGAC | PLACE |
| **WBOXATNPR1** | | 1264 | + | TTGAC | PLACE |
| **WBOXATNPR1** | | 22 | - | TTGAC | PLACE |
| **WBOXHVISO1** | | 201 | + | TGACT | PLACE |
| **WBOXHVISO1** | | 543 | + | TGACT | PLACE |
| **WBOXNTERF3** | | 201 | + | TGACY | PLACE |
| **WBOXNTERF3** | | 543 | + | TGACY | PLACE |
| **WRKY71OS** | | 46 | + | TGAC | PLACE |
| **WRKY71OS** | | 202 | + | TGAC | PLACE |
| **WRKY71OS** | | 544 | + | TGAC | PLACE |
| **WRKY71OS** | | 1001 | + | TGAC | PLACE |
| **WRKY71OS** | | 1264 | + | TGAC | PLACE |
| **WRKY71OS** | | 23 | - | TGAC | PLACE |
| **WRKY71OS** | | 577 | - | TGAC | PLACE |
| **WUN-motif** | *Brassica oleracea* | 1088 | - | TCATTACGAA | PlantCARE |

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## Publications

**Erb, M., C. Lenk, et al.** (2009). "The underestimated role of roots in defense against leaf attackers." Trends in Plant Science **14**(12): 653-659.

**Köllner, T. G., M. Held, et al.** (2008). "A maize (E)-beta-caryophyllene synthase implicated in indirect defense responses against herbivores is not expressed in most American maize varieties." Plant Cell **20**(2): 482-494.

**Köllner, T. G., C. Lenk, et al.** (2010). "Herbivore-Induced SABATH Methyltransferases of Maize That Methylate Anthranilic Acid Using S-Adenosyl-L-Methionine." Plant Physiology **153**(4): 1795-1807.

**Lenk, C., Köllner, T.G., et al. (2011).** "Two enzymes responsible for the formation of herbivore-induced volatiles of maize (*Zea mays* L.), the methyltransferase AAMT1 and the terpene synthase TPS23, are regulated by a similar signal transduction pathway." Entomologia in press

## Posters/Talks

**Köllner, T.G., Lenk, C. et al. (2006).** "A Maize (*E*)-ß-Caryophyllene Synthase Takes Part in Two Plant Defense Responses Which Are Directed Against Herbivores Above or Below Ground. " MPI Fachbeirat

**Lenk, C., Köllner, T.G., et al. (2009)**. Identification of transcription factors involved in herbivore-induced terpene biosynthesis in leaves and roots of maize. Terpnet Meeting

**Lenk, C. (2009).** "The regulation of herbivore-induced terpene biosynthesis in maize." SFB Meeting (Talk)

**Lenk, C., Köllner, T.G., et al. (2010)**. "Mechanical damage and insect elicitors induce maize volatiles by separate pathways" Gordon Conference: Plant molecular biology

**Lenk, C. (2010).** "The role of different stimuli for the induction of terpene biosynthesis." SFB Meeting (Talk)

**Lenk, C., Assefa, C., et al. (2011).** "Identification of promoter regulatory elements of *tps10* and *tps23* from *Zea mays* in *Arabidopsis thaliana.*" Maize Genetic Conference

**Lenk, C. (2011).** "Functional analysis of herbivore-induced promoters." SFB Meeting (Talk)

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| | |
|---|---|
| **Sprachkenntnisse** | Englisch: fließend in Wort und Schrift<br>Japanisch, Russisch: Grundkenntnisse |

## Halle, den 20.02.2012

Selbstständigkeitserklärung

Hiermit versichere ich, dass diese Arbeit in gleicher oder ähnlicher Form bisher keiner anderen Prüfbehörde zur Erlangung des Doktorgrades vorgelegt wurde. Ferner erkläre ich, gemäß der Promotionsordnung der Naturwissenschaftlichen Fakultät I – Biowissenschaften der Martin-Luther-Universität, dass ich die vorliegende Arbeit selbstständig verfasst und keine anderen als die angegebenen Quellen und Hilfsmittel benutzt habe. Alle Stellen, die wörtlich oder sinngemäß aus Veröffentlichungen entnommen sind, habe ich als solche kenntlich gemacht.

**Halle, den 20.02.2012** **Claudia Lenk**