Induction of New Defensin Genes in Tomato Plants via Pathogens-Biocontrol Agent Interaction

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Abstract

Defensins and defensin-like peptides are functionally diverse and commonly presented as an immune reaction between plant and pathogen. Trichoderma viride and Bacillus subtilis as biological control agents, were inoculated into the soil, to suppress the activity of the pathogenic fungi Fusarium oxysporum and Rhizoctonia solani on tomato. The up- and down-regulated genes were examined in both treated and non-treated plants, using differential display technique. In treated plants, many up-regulated genes (21) with different molecular sizes, ranging from 50 to 7000 bp, were observed. Only four up-regulated genes were isolated from plants treated with B. subtilis+R. solani. The sequence analysis revealed that the identified genes were defensin genes; Amino Acid/Auxin Permease Family, Endopolygalacturonase PG1, Fructose-1,6-bisphosphatase and glycosyl transferase. Moreover, chitinase gene, defensin genes (DF1 and DF2) were quantitatively determined using RT-PCR. The comparative expression level of the three induced genes was exponentially increased as a function of time, after the application of the biological control agents. However, while the expression levels of DF1 and DF2 were high in plants infected with either F. oxysporum or R. solani in the beginning of the experiment, the highest expression level of these genes was attained in the tomato plant treated with either T. viride or B. subtilis, after 24 hour post inoculation.

Keywords: Bacillus subtilis; Defensin; Differential display; Fusarium oxysporum; Rhizoctonia solani; Trichoderma viride

Introduction

Tomato (Solanum lycopersicum L.) is one of the most economically important crops worldwide; however, it is susceptible to over 200 pathogens that cause severe destruction for this plant and consequent great reduction in the yield. Fusarium oxysporum is the main casual of the tomato root rot disease in tomato plants. Moreover, Rhizoctonia solani are highly destructive pathogens of both greenhouse and field grown tomatoes causing damping-off diseases [1]. Many strategies to control these diseases and others on tomato, have been developed. However, the major component used in integrated pest management (IPM) studies was the chemical fungicides. The implication of chemical fungicides in soil and water pollution has mandated the search for alternative approaches to disease control management [2].

A promising strategy for the replacement of chemicals fungicides that has been the implementation of biological control technology, used individually or with other IPM components. Among the promising biological control agents, Trichoderma spp. has attracted the attention for controlling various soil-borne fungi. In addition to the well-recognized mycoparasitic nature of Trichoderma spp., their role in induction of resistance against pathogens in plants and growth promotion had also been reported [3]. The induction of resistance in plants using Trichoderma spp. has been poorly studied, compared with the responses that are induced by rhizobacteria, perhaps because the Trichoderma research community has focused on factors that are associated with direct effects on other fungi, especially mycoparasitism and antibiosis.

Genetic and gene discovery studies have defined molecular pathways and cellular processes that are transcriptionally regulated during biotic interactions, and have expanded our understanding of how plants respond to pathogens and biological control agents.

Shoresh and Harman [4] reported that proteomic analysis of maize plants inoculated with T. harzianum T22 showed a total of 205 differentially expressed spots, over both roots and shoots were identified. Many proteins of defense/stress-related functions were up-regulated. Comparison of the interaction between plants and Trichoderma and plant-Trichoderma-pathogen indicated the activation of specific response to the biocontrol agent. Genes encoding extension like proteins were up-regulated in tomato plants [5], but down-regulated in cacao seedlings by several Trichoderma isolates [6]. Altogether, a whole array of stress- and defense-related proteins are up-regulated or primed in plant shoots, post Trichoderma inoculation of the roots, thus rendering plants to be more resistant to subsequent pathogen attack.

Another example of the biological control agents is the Gram-positive bacterium Bacillus subtilis, a bacteria widely distributed in nature, and which has been found to possess bio-control potential for a variety of phytopathogenic fungi [7]. The mechanisms by which B. subtilis reduces plant diseases include antagonism of fungal pathogens, by competing for niche and nutriments, by producing fungi-toxic compounds, and stimulating the defensive capacities of the host plant [8]. Yan et al. [7] studied the biocontrol efficiency of B. subtilis SL-13 and its antifungal chitinase. The control efficacies of B. subtilis SL-13 against tomato Rhizoctonia rot were 20.65% and 35.23% in the greenhouse and field, respectively.

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Material and Methods

Plant material and microorganisms

Tomato plant (Solanum lycopersicum L.) cultivar AUC 93 was obtained from Agricultural Research Center, Giza, Egypt, and used as a test plant in this work. Both pathogens and biological control agents were isolated during this work. Three isolates of Fusarium oxysporum and three of Rhizoctonia solani were isolated from diseased tomato plants showing wilt or root rot symptoms, cultivated in Alexandria governorate, Egypt. The pathogens were cultured on potato dextrose agar (PDA). Trichoderma viride and Bacillus subtilis were isolated from the rhizosphere of healthy tomato plants (from Alexandria governorate, Egypt) on PDA and nutrient agar, respectively.

Pathogenicity test

The pathogenicity ability of the six isolates of F. oxysporum and R. solani was evaluated on tomato seedlings (cv. AUC 93) in pots experiment. Tomato seedlings were sterilized (5 min in 0.5% NaOCl), rinsed in sterile distilled water, and seeded in plastic pots, 15 cm in diameter filled with sterile peat moss and clay (1:1 w/w). Inocula were produced by growing the fungi for 15 days at 25°C on a milled bran/sand mixture (1:1 w/w), autoclaved twice at 120°C for 60 min. Brani/sand inoculum was mixed into potting soil at 5 g per each pot, and seeded with the test plants (10 seeds per pot). For each isolate, 5 replicate pots were scored. The most potent isolates of F. oxysporum and R. solani were selected for the next experiments, according to this test.

A combined visual disease severity index was used. Each plant was graded on a scale of 0 to 5, based on the assessment of the disease symptoms degree (wilting, discoloration, and stem, and root rot). To estimate the disease severity (DS), plants were classified into five categories, where 0=healthy plant or undetectable symptoms; 1=up to 10%; 2=11-25%; 3= 26-50%, 4=51-75 %, and 5=76-100% of wilting, discoloration and root rot incidence. DS (%) was assessed twice after 3 and 5 weeks after inoculation, according to the following formula.

\[
\text{Disease severity} = \frac{\sum (a)(b) \times 100}{AK}
\]

Where, a=No. of diseased plants having the same degree of infection, b=Degree of infection, A=Total no. of examined plants, and K=Highest degree of infection.

The mean isolate effect was considered as the sum of DS (%) in the two periods, according the following formula:

Mean isolate effect (MIE)=(DS (%) after 3 weeks+DS (%) after 5 weeks)/2.

Molecular identification of the microorganisms

All microorganisms (two tested bioagents and two selected pathogenic fungi) were subjected into DNA extraction, using the Qiagen DNA extraction kit (Qiagen, Germany). These organisms were identified by amplification of ITS gene (in case of fungi) and 16S rRNA gene (in case of bacteria), using universal primers according to Hafiez and Elbestawy [9] method. The PCR amplicones were sequenced in Macrogene Company (Seoul, Korea). The DNA sequences were analyzed using the DNA BLAST.

In vitro antagonistic effect of B. subtilis and T. viride against F. oxysporum and R. solani

The antagonistic potentiality of T. viride and B. subtilis was tested against both F. oxysporum (F3) and R. solani (R2) in vitro, using dual culture method. PDA plates were inoculated with antagonistic isolated bacteria, as streak line with loop-full of two days old culture, for 48 h prior to the tested fungi. Mycelial disc (5 mm in diameter) of an actively growing culture of the tested fungi was placed at a constant distance (1.0 cm), opposite to other edge of the Petri plate, and incubated at 25°C for 3-7 days, and the inhibition zones were measured. To test the antagonistic effect of T. viride, 5 mm discs of advanced edge of one week old PDA culture and the target pathogen (F. oxysporum or R. solani) were inoculated at the opposite dish edge of the plate, and incubated at 25°C for 7 days. The fungal growth was examined for any change in growth shape or other antagonistic effects. All experiments were carried out with three replicates for each treatment.

Effect of B. subtilis and T. viride against F. oxysporum and R. solani under greenhouse conditions

Antagonistic effect of B. subtilis and T. viride on the growth of F. oxysporum and R. solani were tested on tomato cultivar AUC 93. Preparation of the inocula of T. viride was made by inoculation of 50 ml of sterile PD broth medium in 250 ml Erlenmeyer flasks, with 5-mm plugs taken form a PDA Petri plate cultures (3-7 days-old). Flasks were incubated without shaking in the dark at 25°C for a week. Mycelial mat, on the surface of the medium, were then homogenized for 2 min in sterile water and mixed with the soil, at the ratio of 20 ml per pot. For inoculation of B. subtilis, the bacterium was inoculated into nutrient broth medium and cultured overnight at 30°C, with constant shaking. Then, 20 ml of the cell suspension was added to each pot. The biological control agents were added 3 days before transplanting. The inocula of virulent F. oxysporum and R. solani were prepared as mentioned above (in pathogenicity test), and were added to the soil in the same rate (5 g per pot), one day before tomato transplanting. Healthy control was considered as the treatment to which neither bioagents, nor the pathogens were added. The treatments applied in this study can be summarized as follows: Control (C), R. solani (R), F. oxysporum (F), R. solani+B. subtilis (RB), R. solani+T. viride (RT), F. oxysporum+B. subtilis (FB), and F. oxysporum+T. viride (FT). For each treatment, 3 pots were prepared and 10 plants were planted in each pot, with using control for each treatment. The trial was conducted twice and the experiment was arranged in a completely randomized block design. After transplanting, samples from treatments (C, RB, RT, FB and FT) were taken at different times (2, 4, 6, 8, and 24 h), to detect the induced defense genes using differential display technique and real-time PCR [10]. Three plants of each treatment were carefully harvested (Three weeks after inoculation with the pathogen), washed under running water to remove soil particles, and evaluated for the following growth parameters: shoot fresh and dry weights, and root fresh and dry weights. All the weights were expressed in grams; dry weights were recorded after drying the samples at 80°C for 48 h in a hot air oven, until constant weight. Disease severity of each treatment was estimated twice after 3 and 5 weeks after inoculation, according to the above equation in the pathogenicity test.

Extraction of total RNA from plant tissues

RNA isolation from plant roots (healthy and infected) was done using RNeasy Mini Kit, according to manufacturer’s instructions (QIAGEN, Germany). About 0.1 g of roots was subjected to RNA extraction,
and the resultant RNA was dissolved in diethylpyrocarbonate-treated water. To remove any DNA residue, the extracted RNA was incubated with DNase for one hour at 37°C. The purified RNA was quantitated spectrophotometrically, and analyzed on 1.2% agarose gel.

cDNA synthesis for the extracted RNA

Reverse transcription reactions were performed in reaction volume, 25 μl. The reaction mixture contains 2.5 μl of 5X buffer with MgCl₂, 2.5 μl of 2.5 mM dNTPs, 1 μl 10 pmol of each primer, 1.5 μl cDNA and 0.2 μl (5 units/μl) Taq DNA polymerase. PCR amplification was performed in a thermal cycler (Eppendorf, Germany), programmed for one cycle at 95°C for 5 min, then 34 cycles as follows: 30 sec at 95°C for denaturation, one minute at 45-48°C for annealing (Table 1), and one minute at 72°C for elongation. Reaction was then incubated at 72°C for 10 min for final extension. Two μl of loading dye was added prior to loading of 10 μl per gel slot. Electrophoresis was performed at 80 Volt with 0.5X TBE as running buffer in 1.5 % agarose/0.5X TBE gels, and then, the gel was stained in 0.5 μg/ml (w/v) ethidium bromide solutions and destained in deionized water. Finally, the gel was visualized and photographed using a gel documentation system. Unique bands that are only present in inoculated host plants, but not in control plants, were cut from the agarose gel and kept at -20°C for further study.

**Cloning and sequencing of up-regulated genes**

The PCR-amplified fragments were excised from the agarose gel and purified using Qiagen Gel Extraction kit (Qiagen, Germany). Purified DNA fragments were then cloned into pCR 4-TOPO vector and purified using Qiagen Gel Extraction kit (Qiagen, Germany). Plasmid DNA was sequenced in both directions, using BigDye Sequencing Kit and ABI 377 DNA sequencer (Macrogen Inc, Korea). DNA sequences reported in this study were deposited in the NCBI nucleotide sequence database, GenBank.

**Alignments and phylogenetic analysis**

Pair wise and multiple DNA sequence alignment were carried out using ClustalW (1.82) [11]. Neighbor-joining tree was generated using MEGA 3 [12], from CLUSTALW alignments.

**Comparative expression level of chitinase, defensin1 and defensin2 genes by quantitative real-time PCR (Q-PCR)**

Tomato leaves samples were taken at different intervals (2, 4, 6, 8, and 24 h), after inoculation with the pathogens and the bioagents, and the total extraction of RNA of plant tissue was performed as mentioned before. PCR reaction consists of 12.5 μl of 2X Quantitech SYBR® Green Mix (Fermentaz, USA), 150 ng of cDNA as template, 1 μl of 25 pM/μl forward primer, 1 μl of 25 pM/μl reverse primer (Table 1), 9.5 μl of RNA free water, for a total of 25 μl. Samples were spun before loading in the rotor’s wells. The real time PCR program was performed as follows: initial denaturation at 95°C for 10 min; 40 cycles of 95°C for 15 sec; annealing at 60°C for 30 sec, and extension at 72°C for 30 sec. Data acquisition performed during the extension step. This reaction was performed using Rotor-Gene 6000 system (Qiagen, USA).

**Data analysis**

Comparative quantitation analysis of samples was done using Rotor-Gene-6000 Series Software, based on the following equation.

\[ \text{Ratio target gene expression} = \frac{\text{target gene expression (sample)}}{\text{reference gene expression (sample)}} \]

Data presented in table 3 indicates that the isolate of *R. solani* (R2) was highly antagonized by *B. subtilis*, while its growth was inhibited by 76.19%. In the same time, the isolate of *F. oxysporum* (F3) was highly suppressed by *B. subtilis*.

**Results**

By the end of the isolation trials for the causal agent of wilt, root rot and damping-off diseases from diseased tomato plants, 3 isolates of *F. oxysporum* and 3 of *R. solani* were obtained. Data presented in table 2 shows that *F. oxysporum* isolate (F3) and *R. solani* isolate (R2) were the most virulent among the tested strains. The isolate main effect of *R. solani* isolate (R2) was 71.82. These two isolates were selected for further studies in this work. All microorganisms (two tested bioagents and two selected pathogenic fungi) were identified using ITS (in case of fungi) and 16S rRNA (in case of bacteria), and the obtained nucleotide sequences were deposited in the GenBank under accession numbers, which are listed in table 3.

One way analysis of variance (ANOVA) showed that *B. subtilis* had a significant antagonistic effect (P ≤ 0.001) on the linear growth of both *R. solani* (R2) and *F. oxysporum* (F3). Results obtained in table 4 indicate that the isolate of *R. solani* (R2) was highly antagonized by *B. subtilis*, and its growth was inhibited by 76.19%. In the same time, the growth of *F. oxysporum* (F3) was highly suppressed by *B. subtilis*.

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**Table 1:** Primers used in this study and their annealing temperature.

<table>
<thead>
<tr>
<th>Primer</th>
<th>Primer sequence 3’→5’</th>
<th>Annealing °C</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Real time PCR</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Chitinase1 Forward</td>
<td>TTG GTG GAG TGC ATC GGT</td>
<td>60</td>
</tr>
<tr>
<td>Chitinase1 Reverse</td>
<td>TAN GG CIN NNN NCC NIGG RIT</td>
<td></td>
</tr>
<tr>
<td>Defensin1 Forward</td>
<td>CAA TGT AAC TTAAG TGC GTAAT ATG</td>
<td>55</td>
</tr>
<tr>
<td>Defensin1 Reverse</td>
<td>CCT ATC AGA TGT CAA TGG AGA AAT C</td>
<td></td>
</tr>
<tr>
<td>Defensin2 Forward</td>
<td>TCA CCA AAT TAT TGG ATT TCA A</td>
<td>57</td>
</tr>
<tr>
<td>Defensin2 Reverse</td>
<td>TCA CCA AAT TAT TGG ATT TCA C</td>
<td></td>
</tr>
<tr>
<td><strong>Differential PCR</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>EZ2</td>
<td>GCCATCAACAGACCTGTATTACGCC</td>
<td>45</td>
</tr>
<tr>
<td>Chi 15</td>
<td>GCCGTTGCTGATGARGG</td>
<td>55</td>
</tr>
<tr>
<td>EzA1A13</td>
<td>CAG GCC CTT CCA GCA CCCAC</td>
<td>53</td>
</tr>
<tr>
<td>Chi 25</td>
<td>GGTGTTGGGATAKCC</td>
<td>52</td>
</tr>
<tr>
<td>PR1</td>
<td>CCAGAAGCTTTTTGTTACGTTTCCTGTC</td>
<td>40</td>
</tr>
<tr>
<td>PR2</td>
<td>CCGGATCTACTGGCTATTCTG - GATTATTATCG</td>
<td>40</td>
</tr>
</tbody>
</table>

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by 40.48%. On the other hand, both isolates of \( \text{F. oxysporum} \) (R2) and \( \text{Rhizoctonia solani} \) (R3) were greatly inhibited, as a result of application of \( \text{Bacillus subtilis} \) or \( \text{Rhizoctonia solani} \), when compared with the control. Effect of treatments on growth parameters is presented in table 6. Results obtained indicate that both biological control agents stimulated the growth of tomato plants, compared to either infected or healthy plants. Treatment with \( \text{B. subtilis} \) or \( \text{T. viride} \) significantly increased the growth parameters of tomato plants infected with either \( \text{R. solani} \) or \( \text{F. oxysporum} \), when compared with the control.

To study the induced defensin genes as a result of application of bioagents, plant samples were collected after 2, 4, 6, 8 and 24 h post-inoculation, and were subjected to differential display and real-time PCR analysis. PCR differential display was performed using six different primers (Table 1). The most prevalent observation was an induction of new defensin genes in tomato plants via pathogenic-biocontrol agent interaction. J Plant Pathol Microb 4: 167 doi:10.4172/2157-7471.1000167

Table 6: Effect of \( \text{Bacillus subtilis} \) and \( \text{Trichoderma viride} \) on the growth parameters.

<table>
<thead>
<tr>
<th>Treatment</th>
<th>Shoot dry weight (g)</th>
<th>Root dry weight (g)</th>
</tr>
</thead>
<tbody>
<tr>
<td>C</td>
<td>3.64 ± 1.0</td>
<td>0.55 ± 0.3</td>
</tr>
<tr>
<td>B</td>
<td>3.51 ± 0.9</td>
<td>0.09 ± 0.4</td>
</tr>
<tr>
<td>T</td>
<td>3.91 ± 1.1</td>
<td>0.85 ± 0.7</td>
</tr>
<tr>
<td>R</td>
<td>0.37 ± 0.8</td>
<td>0.03 ± 1.0</td>
</tr>
<tr>
<td>RB</td>
<td>0.17 ± 0.7</td>
<td>0.07 ± 0.6</td>
</tr>
<tr>
<td>RT</td>
<td>2.82 ± 1.0</td>
<td>0.40 ± 0.9</td>
</tr>
<tr>
<td>FB</td>
<td>3.22 ± 1.1</td>
<td>0.50 ± 0.8</td>
</tr>
<tr>
<td>FT</td>
<td>3.88 ± 0.3</td>
<td>0.62 ± 0.4</td>
</tr>
</tbody>
</table>

- C=control, B=\( \text{Bacillus subtilis} \), T=\( \text{Trichoderma viride} \), R=\( \text{Rhizoctonia solani} \), F=\( \text{F. oxysporum} \), \( \text{B}+\text{F}=\text{Bacillus subtilis}+\text{F. oxysporum} \), \( \text{RT}+\text{RB}=\text{Rhizoctonia solani}+\text{Trichoderma viride} \), \( \text{FB}+\text{FT}=\text{F. oxysporum}+\text{Trichoderma viride} \).
In this study, two sets of primers were synthesized for two defensin genes based on the Arabidopsis genome, to examine their expression in the tomato plant treated with pathogen, in the presence of the bioagents. Meanwhile, the defensin 1 gene expression was fluctuated among the tested samples. The highest expression observed after 24 h in treatments contain F. oxysporum + B. subtilis (0.69), F. oxysporum + T. viride (0.68) (Figure 3). However, the highest gene expression in case of treatment of R. solani + B. subtilis was achieved after 6 h (0.63), and r RNA gene (Reference data). Data in figure 2 show that the increase in time incubation after treatment with bio-agents, the increase in Chitinase (PR protein) gene expression in plants. The highest expression of chitinase gene was observed after 24 h post treatments. The gene expression in treatment of R. solani + T. viride after 24 h was 2.76. But in case of R. solani + B. subtilis, chitinase expression was 1.932. The level of gene expression was 1.823 in plants treated with F. oxysporum + T. viride; however, in plants treated with F. oxysporum + B. subtilis, the chitinase expression level was 1.681. It is worth to mention that chitinase expression in infested control did not exceed than 0.31, which is relatively close to the expression level obtained in the healthy plants (0.26).

In case of primer ch25, after 2 h two up-regulated genes were observed with fragments length 1300 and 1500 bp in sample 4 (plant infected with R. solani and T. viride), however, only one gene with fragment length of 700 bp was observed in sample 1 (plant infected with F. oxysporum and B. subtilis). Monomorphic genes were observed, highly expressed in samples 1 and 4, compared with the others. After 4 h post treatment, high expression level was dramatic in samples 2 (plant infected with F. oxysporum and T. viride) and sample 3 (plant infected with R. solani and B. subtilis), and after 6 h, in sample 3. Moreover, 8 h post inoculation induced expression level in samples 1 and 4, however this induction was approached after 24 h in samples 3 and 4. Genes with fragment length 1700 bp emerged in samples 2 and 4, but one gene with MW 300 bp was observed in sample 4 only. Primer chi15 was succeed to differentiate the examined samples. In case of primer EZ, only one up-regulated gene with fragment length 7000 bp was obtained in sample 3. The same gene with the same fragment length was experiential after 4 h in samples 2 and 3. On the other hand, three down regulation genes were noticed in all examined samples, compared with control, these genes were with fragment length 7 kbp, 6.5 kbp and 50 bp, respectively.

The band pattern initiated by primer EzA1A13 demonstrates that, after 2 h, all the scanned genes are polymorphic in the treated samples, compared with control. However, only high expression level was observed in two genes with fragment length 500 bp and 300 bp in sample 4. But, after 4 h, the same observation was demonstrated in samples 2 and 3. Three up-regulation genes were induced in sample 2 (1000 and 7000 bp) and 400 bp in sample 3. After 6 h, all genes are polymorphic and the expression level was the same. After 8 h, high expression level was recorded with samples 1, 2 and 4, combined with up-regulated gene with fragment length 200 bp. After 24 h, high expression was perceived in all evolved genes in samples 2, 3 and 4. In case of primer PR1, after 2 h post treatment, only one up-regulated gene was obtained in sample 1 with fragment length 500 bp, and another up-regulated gene was raised in samples 3 and 4 with MW 300 bp. After 4 h, two down regulated genes were observed in sample 3, with fragment length 750 and 300 bp. Down regulation of the most scanned genes, especially in samples 3 and 4 after 8 h post treatment, was common. After 24 h, one up-regulated gene was observed in samples 1 and 3, with fragment length 600 bp. Down regulation was observed in genes with fragment length 9 kbp, 7 kbp and 6 kbp in samples 1, 2, 3 and 4. In case of PR2, different band pattern was obtained in all samples after 2 h. After 4 h, eight up regulated genes were exhibited (10 kbp to 150 bp) in samples 1, 2 and 3. After 6 h, there was only one up-regulated gene with fragment length 5 kbp was observed in samples 1, 2 and 3, and two different genes were demonstrated in sample 4, with fragment length 250 and 250 bp. A unique band pattern contains up-regulated gene (5 kbp) was obtained in all samples, except sample 4; after 8 h, however, gene with fragment length 3 kbp was observed in sample 2 after 24 hours.

Our results reveal that the relative amounts of mRNA detected from target genes (Chitinase, Defensin1 and Defensin2), present in samples collected 2, 4, 6, 8 and 24 h post inoculation for each treatment, were compared with plant infected with F. oxysporum and R. solani (genetic pool) and uninfected plant (healthy control). Results normalized to 18S
Solanum, Arabidopsis, Penicillum and Trichophyton, with different identity. The gene was grouped with Phytophthora genes, and it was considered as outer group for Solanum and Arabidopsis (Figure 5). Data in figure 6 revealed that the nine aligned genes were grouped into two main groups which had one ancestor. The first group contains the obtained gene, and other one isolated from Glomerella and the second group, included the rest of genes.

The isolated fructose 1,6 biphosphatase gene showed similarity with other genes isolated from tomato, yeast, and exons 3,4,6,7 in human (Figure 7). A phylogenetic tree was constructed for the isolated glycolyl transferase group1 gene, with other 11 different genes isolated from different organisms, and the obtained gene grouped as a separate group (Figure 8).

**Discussion**

*In vitro* test showed that *B. subtilis* and *T. viride* greatly suppressed the growth of the two pathogens. The reduction in linear growth was 79.72% in case of *R. solani* and 79.41%, in case of *F. oxysporum*, when *T. viride* was applied. *Trichoderma* spp. is well known for their antagonism against several soil-phytopathogens. The main mechanisms of action involved in the antagonism of *Trichoderma* are mycoparasitism, secretion of bioactive molecules (i.e. antibiotics and cell wall degrading enzymes), competition for space and nutrients and stimulation of the plant’s defensive capacity [13]. Also, *Bacillus* spp. was used as biological control agents against many soil borne pathogens. It was mentioned to...
Development of real-time PCR (RT-PCR) has provided a powerful tool for pathogen monitoring. It allows detecting the pathogen earlier than symptoms of the disease appear on the plants. With the use of RT-PCR, it is possible to perform a semiquantification of fungal pathogens, such as *F. oxysporum*, *Fusarium solani*, *Pythium ultimum* and *R. solani* in a single assay [18]. Our results revealed that the relative amounts of mRNA detected from target genes (Chitinase, Defensin1 and Defensin2), present in samples collected 2, 4, 6, 8 and 24 h post inoculation for each treatment, were compared with plant infested with *F. oxysporum* and *R. solani* (genetic pool) and uninfested plant (healthy control).

The chitinase gene was gradually increased in all examined samples and reached its peak with samples 21. But, the expression of the F1 gene was fluctuated, but the highest expression level was precieved in samples 18 and 19. Gene F2 showed the same observation obtained by the F1 gene. Chitinases are key enzymes involved in plant-microbe interactions, and are grouped in the pathogen-related protein type three families (PR-3). Five classes of plant chitinases have been proposed based on their peptidic sequences, conserved domains and specific activities [19]. Because chitin is a primary structural component of the wall of all true fungi, chitinases are considered to play a major role during pathogenic plant-fungal interactions [20]. The combined expression of chitinases with other plant-defense proteins, such as glucanases and ribosome-inactivating proteins further enhances the plant’s resistance to fungal attack. The time for chitinase induction is also dependent on the specific pathogen-host interaction, and varies from minutes to 15-20 h [20].

Plant activation of host defense against pathogenic microbes requires significant host transcriptional reprogramming [21]. Moreover, within the subset of genes that are regulated by both pathogens, many genes show inverse regulation. Stotz et al. [22] studied the expression of the defensin gene DEF2 in tomato, and they found that defensin mRNA expression processing is differentially regulated in developing flowers. Antisense suppression or constitutive over expression of DEF2 reduces pollen viability and seed production. Furthermore, over expression of DEF2 pleiotropically alters the growth of various organs, and enhances foliar resistance to the fungal pathogen *Botrytis cinerea*. Most plant defensins are active against fungi [23].

PG1 is the major endopolygalacturonase of the vascular wilt pathogen, *Fusarium oxysporum* [24]. The tomato vascular wilt pathogen, *Fusarium oxysporum f. sp. lycopersici*, produces an array of pectinolytic enzymes that may contribute to penetration and colonization of the host plant [24]. Here, in our study, we isolated this gene as up-regulated gene from tomato plant leaves infected with *Fusarium oxysporum*. Different nine Endopolygalacturonase PG1 genes were aligned with the obtained gene. On the other hand, *F. oxysporum* causes vascular wilt disease on a wide variety of crops, and produces a wide variety of extracellular cell wall degrading enzymes (CWDEs), including xylanases, cellulases, proteases, pectate lyases, and exo- and endoPGs. To counteract the action of PGs, plants express polygalacturonase-inhibiting proteins (PGIPs), that have been shown to inhibit a variety of PGs with different inhibition kinetics, both competitive and noncompetitive [25].

Transcript analysis has been effectively employed to probe defense responses induced by elicitors, including yeast activated tomato genes encoding SAR-dependent PRs (chitinase and glucanase), cytochrome P450s and cell wall loosening enzymes (e.g. expansin, xyloligucan endoglycosl transferase, polygalacturonase) [26]. In *Arabidopsis*, transcriptional analysis has identified elicitor induced acclamatory

![Figure 8: Phylogenetic tree showing evolutionary relationship between glycotransferase gene of tomato plants and the others presented in GenBank. The Neighbor-Joining method was used to construct the tree. The numbers on the branches represent bootstrap support for 1,000 replicates. Names refer to the accession number of the nucleotide sequences that encode the corresponding glycotransferase genes.](image-url)
responses to stress, such as recovery of the cell redox balance (glutathione transferase, UDP glycosyltransferase and glutaredoxins), intracellular stress signaling and improved pathogen recognition [27]. While activation of defense responses by plant elicitors can protect against pathogens, an inhibition of the biosynthesis of photosynthetic pigments and photosynthetic activity reducing plant productivity can also occur [28].

Zhu-Salzman et al. [29] identified an LRR-containing glycoprotein sequence that is differentially expressed in leaves of Sorghum bicolor (L.) infested by S. graminum. LRR-containing glycoproteins are extracellular, membrane-anchored compounds that in some cases recognize specific tomato leaf mold pathogen, Cladosporium fulvum (Cf)-encoded virulence gene products. Results of Rooney et al. [30] indicated that Cf-2 and its Avr2 protein trigger a hypersensitive (resistance) response, that also requires an extracellular tomato cysteine protease Rcr3. The binding of Avr2 with and resulting Rcr3 inhibitions proposed as the event that enables the Cf-2 protein to activate a resistance response. A sequence similar to the Xa1 gene encoding the protein that confers resistance to bacterial blight, by recognizing a sequence that is differentially expressed in leaves of S. bicolor.

The functions of plant RLKs can be divided into two broad categories. The first category includes RLKs, involved in the control of plant growth and development, under normal growth conditions [33]. The second category includes RLKs involved in plant-microbe interactions and stress responses. The evolutionary relationships between these proteins, and what appear to be overlapping functions, suggest that the kinases ancestral to these two gene families may have been involved in these two “functions”, before the divergence between plants and animals [33].

References


