RNA Interference Mediated Serine Protease Gene (Spbtry1) Knockdown Affects Growth and Mortality in the Soybean Pod Borer (Lepidoptera: Olethreutidae)

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RNA interference mediated serine protease gene (Spbtry1) knockdown affects growth and mortality in the soybean pod borer (Lepidoptera: Olethreutidae)

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Abstract

The soybean pod borer, *Leguminivora glycinivorella* Matsumura (Lepidoptera: Tortricidae), is an economically significant soybean pest in northeastern Asia. Serine proteases are crucial enzymes responsible for protein digestion in herbivorous lepidopterans. In this study, a gene (Spbtry1) encoding a soybean pod borer serine protease was cloned from the organism’s midgut. The Spbtry1 open reading frame encoded a 269 amino acid protein with a predicted molecular mass of approximately 29 kDa. Alignment of Spbtry1 with trypsins and chymotrypsins from other insects revealed a high degree of conservation in the putative catalytic domain region. Analysis by reverse transcriptase polymerase chain reaction indicated that Spbtry1 was specifically expressed in the midgut, its transcript existed constitutively in the larval stage, and its expression was highest in the 3rd instar larval stage. RNA interference indicated that Spbtry1 expression levels decreased on diets containing Spbtry1 double-stranded RNA (dsRNA). Larvae had significantly lower body weight (18.7 ± 0.25 mg in the Spbtry1 dsRNA-fed group versus 30.1 ± 0.78 mg and 29.9 ± 0.88 mg in the phosphate buffered saline (PBS) and green fluorescent protein (GFP) dsRNA-fed groups, respectively (Student’s t-test, P < 0.01) and higher mortality (43.8%) than the control groups (20.8% in PBS-treated and 19.5% in GFP dsRNA-treated) after 15 d, suggesting that Spbtry1 is important for soybean pod borer larval growth and development.

Key Words: *Leguminivora glycinivorella;* gene expression; RNAi; larval development

Resumen

El barrenador de la vaina de la soja, *Leguminivora glycinivorella* Matsumura (Lepidoptera: Tortricidae), es una plaga económicamente significativa de la soja en el noreste de Asia. Las serinas proteasas son enzimas cruciales responsables de la digestión de proteínas en los lepidópteros herbívoros. En este estudio, se clonó un gen (Spbtry1) que codifica una serina proteasa del intestino medio del organismo del barrenador de vaina de la soja. El marco de lectura abierto Spbtry1 codificó una proteína de 269 aminoácidos con una masa molecular predicha de aproximadamente 29 kDa. La alineación de Spbtry1 con tripasinas y quimotripasinas de otros insectos reveló un alto grado de conservación en la región del dominio catalítico. El análisis por la reacción en cadena de la polimerasa de la transcriptasa inversa indicó que Spbtry1 se expresó específicamente en el intestino medio, su transcripción existió constativamente en la fase larvaria, y su expresión fue más alta en la fase larvaria del 3er instar. La interferencia de ARN indicó que los niveles de expresión de Spbtry1 disminuyeron en dietas que contenían ARN bicatenario Spbtry1 (dsRNA). Las larvas tuvieron significativamente menor peso corporal (18.7 ± 0.25 mg en el grupo alimentado con dsRNA de Spbtry1 frente a 30.1 ± 0.78 mg y 29.9 ± 0.88 mg en los grupos alimentados con dsRNA de PBS y GFP, respectivamente (prueba t de Student, P <0,01) y una mayor mortalidad (43,8%) que los grupos control (20,8% en PBS tratados y 19,5% en GFP dsRNA tratados) después de 15 d, lo que sugiere que Spbtry1es importante para la vaina de la soja barrenador de larvas de crecimiento y desarrollo.

Palabras Clave: *Leguminivora glycinivorella;* expresión de genes; ARN; desarrollo de larva

The soybean pod borer, *Leguminivora glycinivorella* Matsumura (Lepidoptera: Tortricidae), is one of the most serious soybean pests in northeastern Asia, including northeastern China, Korea, and Russia (Zhao et al. 2008). It is a univoltine insect, and the mature larvae make cocoons in the soil from Oct throughout the winter, pupate in mid-Jul, and then adults emerge from late Jul to early Aug. The females oviposit on young bean pods. The hatched larvae enter the pod and actively feed on the immature beans, resulting in up to 40% yield loss. The control of this insect is difficult, because when insecticide is applied to the plant, it does not make contact with the larvae inside the soybean pods (Wang et al. 2014).

Insecticides have been applied to control soybean pod borer adults for the last 3 decades and insecticide resistance in certain soybean pod borer populations is now a threat (Hu et al. 2013). Transgenic plants that over-express either insecticidal proteins or double-stranded RNA (dsRNA) specific to important insect genes might be a suitable alterna-

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tive. This has been demonstrated by transferring proteinase inhibitor oryzacystatin II (OCI) from rice to tobacco, which enhances tobacco resistance to the Colorado potato beetle, *Leptinotarsa decemlineata* (Say) (Coleoptera: Chrysomelidae) (Cingel et al. 2015). Additionally, transgenic plants that express dsRNA specific to the cytochrome P450 gene (CYP6AE14) have improved resistance to the cotton bollworm, *Helicoverpa armigera* Hübner (Lepidoptera: Noctuidae) (Mao et al. 2007).

The serine proteases are critical targets for insect control because of their importance in food digestion (Srinivasan et al. 2006). Serine proteases contribute approximately 95% of the total digestive activity in the herbivorous lepidopteran larvae (Chougule et al. 2005). Moreover, serine proteases are involved in various essential processes, such as intra- and extra-cellular protein metabolism, immune responses (Loof et al. 2011), molting (Wei et al. 2007), blood coagulation, fertilization, and developmental regulation (Rao et al. 1998). The plant protease inhibitor (PI) interaction with serine proteases in insects from a stable and inactive acyl enzyme distorts the serine protease active site (catalytic triad). The loss of protease activity retards digestion and leads to negative effects on both larval survival (Srinivasan et al. 2005) and adult moth fertility and fecundity (DeLeo & Gallerani 2002). However, PIs are highly specific to a particular class of digestive enzymes. Insects could overcome the deleterious effect of PI ingestion by overexpressing the existing proteases or synthesizing new proteases that are insensitive to the introduced PIs (Huma & Khalid 2007; Pawlowska et al. 2007). The polymerase chain reaction (PCR) cycles were as follows: denaturation at 94 °C for 30 s, annealing at 56 °C for 30 s, and elongation at 72 °C for 10 min using Taq polymerase (Takara) for 35 cycles.

The 3′- and 5′-ends of the transcript were cloned using 3′- and 5′-rapid amplification of cDNA ends (RACE), according to the manufacturer’s protocol (3′/5′ RACE Kit, Takara, Japan) with 2 gene-specific primers (Table 1). The PCR products were cloned into the pMD18-T vector (Takara), and sequenced by the Sanger method. The resulting overlapping sequences were assembled to obtain the full-length *Spbtry1* cDNA sequence. To confirm the assembled cDNA sequence from the overlapping PCR products, the entire *Spbtry1* coding region was amplified by PCR reactions with the *Spbtry1* F and *Spbtry1* R primers (Table 1). The PCR conditions were as follows: denaturation at 94 °C for 30 s, annealing at 58 °C for 30 s, and elongation at 72 °C for 10 min using Taq polymerase (Takara) for 40 cycles. The products were cloned into the pMD18-T vector (Takara) and sequenced from both directions as described above.

**Materials and Methods**

**INSECT REARING**

Soybean pod borer eggs were originally collected from a naturally infested field at the experimental station at Northeast Agricultural University, Harbin, China. The soybean pod borer eggs were hatched at 26 °C. The larvae were reared on an artificial diet at 80 to 90% RH, 18:6 h L:D, and 26 °C until they reached adulthood. The adult moths were fed a 5% honey solution and allowed to oviposit on young bean pods.

**SPBTRY1 CLONING**

To obtain full-length *Spbtry1* cDNA, soybean pod borer 3rd instar larvae gut tissues were dissected. The 3rd instar larvae were anesthetized for 40 s with ethyl ether. A drop of diethyl pyrocarbonate–treated phosphate buffered saline (PBS) was placed onto a glass slide fixed under a stereomicroscope (Nikon® SMZ1270, Nikon, Tokyo, Japan). The larvae were transferred onto the prepared slide by stabbing the thorax with a needle-tip probe. While the larvae were held down with the probe, forceps were used to grasp the 2nd to the 4th abdominal segment to gently pull off the larva’s abdomen in a single motion. The gut should remain attached to the immobilized thorax. The abdomen was discarded, and forceps were used to detach the gut from the thorax (Supplementary Fig. S1; supplementary material is online at http://purl.fcla.edu/fcla/entomologist/browse). Total RNA was isolated from dissected gut tissues using Trizol™ reagent (Invitrogen, Carlsbad, California). Genomic DNA was removed from the isolated RNA by adding 2 μL (1 mg/μL) DNaseI (Invitrogen). The 1st-strand cDNA was synthesized using reverse transcriptase AMV (Takara, Dalian, China). The polymerase chain reaction (PCR) cycles were as follows: denaturation at 94 °C for 30 s, annealing at 56 °C for 30 s, and elongation at 72°C for 10 min using Taq polymerase (Takara) for 35 cycles.

**cDNA AND PROTEIN ALIGNMENT ANALYSIS**

The full-length *Spbtry1* cDNA obtained was analyzed using a basic local alignment search tool (BLAST) through the National Center for Biotechnology Information (NCBI) website (http://www.ncbi.nlm.nih.gov/). The *Spbtry1* amino acid sequence was deduced from the corresponding cDNA sequence using the translation tool at the ExPASy Proteomics website (http://expasy.org/tools/dna.html). Other protein sequence analysis tools used in this study, including molecular weight and isoelectric point, were verified from the ExPASy Proteomics website (http://expasy.org/). Multiple sequence alignments of deduced amino acid sequences were performed using the Multiple Alignment website (http://www.ebi.ac.uk/clustalw/index.html). The phylogenetic tree was constructed using MEGA 6 (Tamura et al. 2013) based on the amino acid sequences of known serine proteases. A bootstrap analysis with 1,000 permutations was carried out.

**SPBTRY1 GENE TRANSCRIPTION EXPRESSION PROFILES IN DIFFERENT TISSUES AND DEVELOPMENT STAGES**

Total RNA was isolated from different tissues (ganglion, cuticle, salivary, midgut, ovary, testis, and fat body) and whole soybean pod borers at different developmental stages (eggs, larvae, pupa, and adult females and males) using the Trizol™ reagent (Invitrogen) as described above. The cDNA prepared from total RNA was used as a template for quantitative real-time PCR (qPCR). The qPCR analysis was performed using a SYBR Green kit (Bio-Rad, Hercules, California) and a Bio-Rad iCycler IQs real-time PCR detection system. The primers used for qPCR analysis were designed using Primer-BLAST from NCBI. The efficiencies of the primer pairs were higher than 90% for all of the qPCR primer pairs used in this study (Table 1). The qPCR conditions were as follows: 95 °C for 5 min, 40 cycles at 95 °C for 30 s, 62 °C for 15 s, and 72 °C for 30 s.
Table 1. Primers used in cloning, reverse transcriptase polymerase chain reaction (RT-PCR), double-stranded RNA (dsRNA) synthesis, and quantitative real-time polymerase chain reaction (qPCR).

| Gene Names          | Primer sequences for cloning and RT-PCR                                                                 | Product length (bp) |
|---------------------|--------------------------------------------------------------------------------------------------------|---------------------|
| SP-F                | 5'-GGGT (A/C/G/T)GT (A/C/G/T)AC (A/C/G/T)GC (A/C/G/T)GC (A/C/G/T)CA (T/C)TG                          |                     |
| SP-R                | 5'-A(A/G) (A/C/G/T)GGG (T/C)CC (A/C/G/T)CC (A/C/G/T)CC (A/G/T)F-C (A/C/G/T)CC                        |                     |
| Spbtry1 3'race GPS1 | 5'-CTACAAATGTCGCGGATAACC                                                                   |                     |
| Spbtry1 3'race GPS2 | 5'-TGCGTGCTGCTGCTAACA                                                                     |                     |
| Spbtry1 5'race GPS inner Primer | 5'-CGTTGTCGCGGCTGTTGC                                                |                     |
| Spbtry1 5'race GPS outer Primer | 5'-ACTAAAGACGGCGACTGCAACA                                         |                     |
| Spbtry1F            | 5'-AAGACAGTCA GCTTGAAGACC                                                               |                     |
| Spbtry1R            | 5'-CTTCCGCAAACATCTCCACC                                                              |                     |
| Spbtry1-E-F         | 5'-CGGGTTTAAA AAGGACAAATA TC                                                            |                     |
| Spbtry1-E-R         | 5'-TCGCGCGACATTGTTAGCGG                                                              |                     |
| Spbactin-E-F        | 5'-GGCGACATAGCAAGCTTCTC                                                               |                     |
| Spbactin-E-R        | 5'-ATCTCCGGT CTGGACTTGGC                                                             |                     |

| Gene Names          | primer sequences for dsRNA synthesis                                                                 | Product length (bp) |
|---------------------|--------------------------------------------------------------------------------------------------------|---------------------|
| Spbtry-70-T7-F      | 5'-GGATCTCAATACGACCTCAGCTTAGGGCGGTGTA TGATACT                                                   | 70                  |
| Spbtry-70-T7-R      | 5'-GGATCTCAATACGACCTCAGCTTAGGGCGGTGTA TGATACT                                                   |                     |
| Spbtry-343-T7-F     | 5'-GGATCTCAATACGACCTCAGCTTAGGGCGGTGTA TGATACT                                                   | 343                 |
| Spbtry-343-T7-R     | 5'-GGATCTCAATACGACCTCAGCTTAGGGCGGTGTA TGATACT                                                   |                     |
| Spbtry-41-T7-F      | 5'-GGATCTCAATACGACCTCAGCTTAGGGCGGTGTA TGATACT                                                   | 41                  |
| Spbtry-41-T7-R      | 5'-GGATCTCAATACGACCTCAGCTTAGGGCGGTGTA TGATACT                                                   |                     |
| GFP-T7-F            | 5'-GGATCTCAATACGACCTCAGCTTAGGGCGGTGTA TGATACT                                                   | 370                 |
| GFP-T7-R            | 5'-GGATCTCAATACGACCTCAGCTTAGGGCGGTGTA TGATACT                                                   |                     |

| Gene Names          | primer sequences for qPCR                                                                         | Product length (bp) | slope  | R2     | Primer efficiency (%) |
|---------------------|--------------------------------------------------------------------------------------------------|---------------------|--------|--------|-----------------------|
| Spbtry1-Q-F         | 5'-TCTGTGACACCACTCAGTAAGGCAGAAAG                                                              | 154                | -3.166 | 0.999  | 91.02                 |
| Spbtry1-Q-R         | 5'-CGGTTAGACGCGGTGAAAGA                                                                      |                     |        |        |                       |
| Spbactin-Q-F        | 5'-GGCGACATACGACAGCTTCTC                                                                     | 149                | -3.218 | 0.997  | 97.32                 |
| Spbactin-Q-R        | 5'-ATCTCCGGT CTGGACTTGGC                                                                     |                     |        |        |                       |

*Underlined sequence corresponds to T7 promoter; F, forward; R, reverse.*
45 s, followed by 95 °C for 1 min and 55 °C for 1 min. At the end of each qPCR experiment, a melt curve was generated to rule out the possibility of primer-dimer formation. Each experimental group contained 3 biological replications, and each biological replication had 2 technical replications. The relative expression analysis for qPCR was performed using the soybean pod borer actin gene as an internal reference. For PCR analysis, 25 cycles were used for the Spbry1 and actin genes, each cycle consisted of 94 °C for 30 s, 55 °C for 60 s, and 72 °C for 60 s. The forward and reverse Spbry1-E primers and LgActin-E primers (Table 1) were used for the Spbry1 and actin genes, respectively.

**dsRNA SYNTHESIS**

The complete serine protease coding sequence for soybean pod borer was sub-cloned into a pGEM-T vector and used as a template for the target sequence amplification. The Spbry1 dsRNA was designed based on the sequence similarity among Spbry1 and 13 homologous trypsin-like proteases from other lepidopteran insects (Supplementary Fig. S2). The dsRNA fragment target regions and sequences are illustrated in Supplementary Fig. S3. The target dsRNA nucleotide and protein sequences were analyzed using blastn and blastp on the NCBI website. The target sequence's E-value, similarity, and identity to other insects are shown in Supplementary Tables S1–S6. Three serine protease gene target sequences were amplified by reverse transcriptase PCR (RT-PCR) using specific primers conjugated with 23 bases of the T7 RNA polymerase promoter (Table 1). For the negative control, the green fluorescent protein (GFP) gene was amplified from the PCAMBIA1302 expression vector using gene-specific primers (Table 1). The RT-PCR products amplified for Spbry1 and GFP were used as templates for dsRNA synthesis using Promega T7 RioMAX Express Large Scale RNA Production Systems (Promega, Wisconsin) according to the manufacturer’s protocol. The dsRNA was purified by a phenol–chloroform extraction followed by ammonium acetate precipitation. The dsRNA was resuspended in ultrapure water and quantified spectrophotometrically at 260 nm. The product was stored at −80 °C.

**SOYBEAN POD BORER FEEDING BIOASSAY**

The 2nd instar larvae were provided with dsRNA in an artificial diet. The dsRNA was carefully mixed with the artificial diet. The final concentration of dsRNA in the diet was 10 μg per ml. Control larvae were treated with either the same concentration of GFP dsRNA or the same volume of PBS. Each treatment was carried out on 50 larvae and conducted in triplicate; thus, 150 larvae were analyzed in each treatment. The larvae were reared at 26 °C, 80 to 90% humidity, and 16:8 h L:D for 15 days. The dsRNA artificial diet was replaced with a new one every 3 days. Soybean pod borer body weight and mortality were recorded 15 days. The dsRNA artificial diet was subsequently obtained by larval body weight and mortality.

**DETERMINATION OF SERINE PROTEASE GENE SILENCING**

Six individual larvae were randomly collected at each time point from 1 to 15 days after feeding on Spbry1 dsRNA. Total RNA was extracted from 3 pools of 6 larvae using Trizol®. The extracted RNA samples were subjected to qPCR amplification as described above. To evaluate the off-target effect, soybean pod borer serine protease mRNA levels were determined and compared between the dsRNA soybean serine protease treated insects and the controls. The qPCR experiment was performed in triplicate. Statistical significance between the controls and the serine protease dsRNA-treated group was determined by 1-way ANOVA test. The putative serine protease mRNA levels from 3rd instar gut tissues using degenerate primers (from the regions of conserved amino acids flanking the active site of the His75 and Ser220 residues) amplified a 400 bp fragment. Sequence analysis of 6 clones from this fragment resulted in a unique sequence homologous to serine proteases in other lepidopteran species. The full-length serine protease cDNA was subsequently obtained using 5’ and 3’ RACE. The gene was 891 nt long, containing a 27 bp putative 5’ untranslated region, an 84 bp 3’ untranslated region, and a 780 bp open reading frame (NCBI accession number JQ340915). The cDNA sequence contained a stop codon (TGA) at position 805–807 bp and a polyadenylation signal (AATAAA) located 12 bp upstream of the poly (A) tail (Fig. 1). The mRNA sequence open reading frame encoded a putative protein of 259 amino acid residues with a predicted molecular mass of 29 kD and an isoelectric point of 5.64. Comparison of the deduced protein sequence with other sequences from the databases using Blastp showed 30 to 78% identity to trypsin-like proteases from other insect species (data not shown). Therefore, the protein was named Spbry1.

**SERINE PROTEASE CDNA CLONING AND SEQUENCE ANALYSIS**

The full-length soybean pod borer serine protease cDNA sequence was obtained by RT-PCR and 5’/3’ RACE. RT-PCR amplification of total RNA from the soybean pod borer 3rd instar gut tissues using degenerate primers (from the regions of conserved amino acids flanking the active site of the His75 and Ser220 residues) amplified a 400 bp fragment. Sequence analysis of 6 clones from this fragment resulted in a unique sequence homologous to serine proteases in other lepidopteran species. The full-length serine protease cDNA was subsequently obtained using 5’ and 3’ RACE. The gene was 891 nt long, containing a 27 bp putative 5’ untranslated region, an 84 bp 3’ untranslated region, and a 780 bp open reading frame (NCBI accession number JQ340915). The cDNA sequence contained a stop codon (TGA) at position 805–807 bp and a polyadenylation signal (AATAAA) located 12 bp upstream of the poly (A) tail (Fig. 1). The cDNA sequence open reading frame encoded a putative protein of 259 amino acid residues with a predicted molecular mass of 29 kD and an isoelectric point of 5.64. Comparison of the deduced protein sequence with other sequences from the databases using Blastp showed 30 to 78% identity to trypsin-like proteases from other insect species (data not shown). Therefore, the protein was named Spbry1.

**Results**

**Fig. 1.** Nucleotide and deduced amino acid sequences of Spbry1 cDNA cloned from *Leguminivora glycinivorella*. The numbers on the left and right refer to the amino acid sequence. The putative signal peptide of 17 amino acids is in bold and the cleavage site is indicated by an arrow. The cleavage site for the putative propeptide removal is indicated by an arrowhead. The stop codon TAA is indicated by an asterisk. The putative polyadenylation signal (AATAAA) is underlined. The putative serine protease conserved motif (GDSGGPL) is boxed. The 3 amino acid residues (His72, Asp118, and Ser216) of the catalytic triad (active site) are indicated with white letters on a gray background. GenBank accession no. JQ340915.
MULTIPLE SEQUENCE ALIGNMENT AND PHYLOGENETIC ANALYSIS

Multi-sequence alignment of Spbtry1 and 13 homologous trypsin-like proteases from other lepidopteran insects are shown in Supplementary Fig. S3. The cleavage site (RIVGG) for removal of the propeptide from the mature protein was identical in all of the proteins, except for the European corn borer, Ostrinia nubilalis Hübner (Lepidoptera: Crambidae) (AAX62030), in which the Val residue at the 3rd place was substituted by Trp. The catalytic motif (GDSGGPL) was also highly conserved among the sequences. There were 81 amino acid residues that were identical in all of the aligned sequences, particularly in the AAHC regions and the catalytic motif (GDSGGPL), implying that these amino acids might be essential for either secretory or functional activity in these serine proteases. The 3 catalytic triads (His72, Asp118, and Ser216) for serine protease activity were highly conserved in these trypsin-like proteases. The residues, aspartate (210), glycine (218), and glycine (228), from the substrate-binding pocket were conserved in the trypsin-like proteases.

A phylogenetic tree was constructed for Spbtry1 and 13 homologous serine proteases from other insects (Fig. 2). Two major groups were formed for the insect serine proteases, and the deduced Spbtry1 amino acid sequence had 33 to 62% identity at the amino acid level to the lepidopteran species homologues. Chymotrypsins and trypsins are the major serine protease enzymes present in the gut of most insect species. Spbtry1 belongs to the 2nd group and this group includes Chilo suppressalis Walker (Lepidoptera: Crambidae) trypsin-like proteinase (AFK64829), Manduca sexta L. (Lepidoptera: Sphingidae) trypsin (AAF29341), Spodoptera frugiperda Smith & Abbot (Lepidoptera: Noctuidae) trypsin (ACR25157), H. armigera trypsin-like protease (CA97948), Heliotris virescens F. (Lepidoptera: Noctuidae) trypsin T2a (ABR688242), O. nubilalis trypsin-like protease T23 precursor (AAP98919), and Plodia interpunctella Hübner (Lepidoptera: Pyralidae) trypsin-like piT2b precursor (AF173495). This group had more conserved sequences for the signal peptides, propeptides, catalytic motif region, and substrate-binding pocket than the members of the 1st group (Fig. 2).

TISSUE AND DEVELOPMENT STAGE DEPENDENT SPBTRY1 EXPRESSION

The Spbtry1 gene transcript levels in different soybean pod border larvae tissues were determined by RT-PCR and qPCR. The RT-PCR analysis showed that Spbtry1 was specifically expressed at the transcript level in the midgut, but was not detectable in the ganglion, cuticle, salivary, ovary, testis, and fat body. The qPCR analysis of Spbtry1 tissue-specific expression resulted in the same expression pattern (Fig. 3A). RT-PCR and qPCR were carried out to analyze Spbtry1 expression patterns during different L. glycinivorella developmental stages. The results indicated that the Spbtry1 transcript was expressed throughout different feeding stages, with the highest expression level in the 3rd instar larvae, no expression was detected in eggs, pupae, and adults (Fig. 3B).
Three days after the 2nd instar larvae were fed *Spbtry1* dsRNA, the *Spbtry1* gene transcript decreased compared to the control larvae fed either GFP dsRNA or PBS. This decrease in the *Spbtry1* transcript level continued until the 15th day (Fig. 4). The larvae fed either GFP dsRNA or PBS exhibited a greater increase in body size than those fed *Spbtry1* dsRNA after 15 days (Fig. 5B). The body weight of larvae from the 3 groups was recorded before feeding. The average weight of unfed larvae from the fed-*Spbtry1* dsRNA group (12.8 ± 0.82 mg) was not significantly different from that of either the PBS fed group (12.8 ± 0.98 mg) or the GFP dsRNA-fed group (13.4 ± 0.67 mg). The body weight of the PBS and GFP dsRNA-fed groups increased significantly with increased feeding time, but body weight did not increase significantly in the *Spbtry1* dsRNA-fed group. There was a significant difference in body weight between the *Spbtry1* dsRNA-fed and the control groups after 15 days (18.7 ± 0.25 mg in the *Spbtry1* dsRNA-fed group vs. 30.1 ± 0.78 and 29.9 ± 0.88 mg in the PBS and GFP dsRNA-fed groups, respectively, Student’s *t*-test, *P* < 0.01) (Fig. 5A).
The cumulative larval mortality increased significantly after 3 days in the Spbtry1 dsRNA-fed group. The final mortality rate in the larvae fed Spbtry1 dsRNA was 43.8%, this mortality rate was significantly higher than the 20.8% and 19.5% in the PBS and GFP dsRNA-fed larvae (Fig. 6).

**Discussion**

The RT-PCR and qPCR analysis results revealed that the Spbtry1 transcript is predominately expressed in the midgut and the larval feeding stages, whereas, the transcript was not detected during the
non-feeding egg, pupae, and adult stages. Similar results have been reported in *Spodoptera litura* F. (Lepidoptera: Noctuidae) (Zhan et al. 2011), *M. sexta* (Felföldi et al. 2011), *S. frugiperda* (Rodríguez-Cabrera et al. 2010), and *Tribolium castaneum* Herbst (Coleoptera: Tenebrionidae) (Oppert et al. 2005). Furthermore, the *Spbtry1* gene deduced amino acid sequence had a putative signal peptide and an activation site, indicating that it is a secretory protein synthesized in the midgut and activated after secretion into the midgut lumen, where it likely digests dietary proteins (Zhang et al. 2010a). The tissue- and stage-dependent expression pattern of the *Spbtry1* gene implied that it might be involved in protein digestion in the *L. glycinivorella* midgut during the feeding stages.

RNA interference (RNAi), 1st characterized in the nematode *Caenorhabditis elegans* (Nematoda: Rhabditidae), has been the most powerful method for the rapid analysis of gene function in organisms (Whyard et al. 2009); the use of dsRNA-mediated RNAi to control insect pests of agriculturally important crops has been investigated (Zhang et al. 2015). When western corn rootworm, *Diabrotica virgifera virgifera* LeConte Coleoptera: Chrysomelidae) larvae were fed transgenic plants expressing dsRNA specific to a vacuolar ATPase subunit, the transgenic corn plants were less damaged by western corn rootworm larvae than the control (Baum et al. 2007). The gap gene hunchback (*hb*) is of crucial importance in insect axial patterning, and *hb* knockdown is lethal to the next generation. When *Myzus persicae* Sulzer (Hemiptera: Aphididae) nymphs were fed *Mphb* dsRNA-expressing tobacco, the transgenic diet reduced *Mphb* mRNA levels in the aphids and inhibited insect reproduction (Mao et al. 2014). These studies suggest that genes encoding proteins with essential functions in insects are the best RNAi targets for increasing mortality and deformity (Liu et al. 2015).

In this study, we performed RNAi for *Spbtry1* by orally feeding dsRNA to assess the use of dsRNA approaches to control the soybean pod borer. The insect serine protease gene family has 8 to 11 members (Saikia et al. 2011; Ge et al. 2013). Three dsRNA fragments were synthesized (Supplementary Fig. S3) and incorporated into the soybean pod borer diet to silence the *Spbtry1* gene. After 15 days, the relative expression of *Spbtry1* in soybean pod borer fed dsRNAs to dsSpbtry70, dsSpbtry343, and dsSpbtry41 were between 27% and 36%, and no significant differences were observed. Whereas the Spbtry41 dsRNA from the conserved region resulted in greater mortality and lower body weight than the Spbtry70 and Spbtry343 dsRNA from variable regions (Supplementary Fig. S4). These results suggest that Spbtry41 dsRNA targeted *Spbtry1* and other serine protease genes, while Spbtry70 and Spbtry343 dsRNA had lower impact because they only target the *Spbtry1* gene. Furthermore, the target Spbtry70 nucleotide and protein sequences shared no similarity or identity with those of other insects, except for *Cimex lectularius* L. (Hemiptera: Cimicidae) (Supplementary Tables S1 and S2). The Spbtry70 dsRNA was specific to *L. glycinivorella* and had no effect on other insects. Based on this experiment, Spbtry70 dsRNA caused moderate suppression of *Spbtry1* expression in the soybean pod borer. Treated larvae continued to demonstrate developmental stunting, which was not observed in the PBS and GFP controls, suggesting that larval digestion was conspicuously blocked by *Spbtry1* knockdown. The RNAi-mediated gene silencing also led to high mortality (43.8% of the larvae fed *Spbtry1* dsRNA) in *L. glycinivorella*, which is similar to RNAi in Locusta migratoria manilensis (Meyen) (Orthoptera: Acrididae) (Whyard et al. 2009; Zhang et al. 2010b). These results further indicated that *Spbtry1* is involved in protein digestion in the *L. glycinivorella* midgut, which subsequently affects larval growth and development rates. Thus, our results indicate that *Spbtry1* is important for *L. glycinivorella* growth and development, and *Spbtry1* gene silencing is lethal to the soybean pod borer. These results support the potential use of RNAi technology, by transferring *Spbtry1* gene dsRNA into soybeans, to control the soybean pod borer.

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