Full Length Research Paper

Cloning and expression analysis of a blue copper-binding protein gene from *Dasypyrum Villosum*

Huagang He¹*, Shanying Zhu¹, Wenbing Wang¹, Tongde Bie² and Peidu Chen³

¹Jiangsu University. Zhenjiang 212013, P. R. China.
²Yangzhou Academy of Agricultural Sciences. Yangzhou 225007, P. R. China.
³Nanjing Agricultural University. Nanjing 210095, P. R. China.

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A differentially expressed fragment EST145 was isolated by suppression subtractive hybridization (SSH) method. Using EST145 as the probe, a blue copper-binding protein gene designated as *DvBCB* was screened from *Dasypyrum villosum* cDNA library. The *DvBCB* gene was 845 bp in length with an open reading frame (ORF) which encoded a 178-amino acid polypeptide and contained the deduced functional sites: H⁶⁶, C¹⁰⁷, H¹¹² and M¹²¹. Northern blot analysis showed that, the expression of *DvBCB* gene was enhanced in leaves after inoculation with *Erysiphe graminis*; reached a peak level at 24 h and decreased to constitutive level at 72 h after inoculation in resistant Gh21 line. The expression level in susceptible mutant M14S line was slightly lower than that in the resistant Gh21 line at all stages after inoculation, and the peak could not appear in M14S line. The function of *DvBCB* gene might include lignification of cell wall or scavenging of reactive oxygen species (ROS) during powdery mildew attack.

Key words: *Dasypyrum villosum*, powdery mildew, suppression subtractive hybridization, blue copper-binding protein gene.

INTRODUCTION

Powdery mildew caused by *Erysiphe graminis* Dc. f. sp. *tritici* Marchal is a serious disease of *Triticum aestivum* (common wheat). *Dasypyrum villosum*, a close relative to common wheat, carries powdery mildew resistance gene *Pm21* which confers effective resistance to all current powdery mildew races (Qi et al., 1995). Cloning resistance or pathogenesis-related genes from *D. villosum* is important to develop the resistance to powdery mildew in common wheat.

Blue copper-binding protein (BCB) can bind a single copper atom (Ryden and Hunt, 1993). The copper binding sites consist of two histidine (H), one cysteine (C) and one methionine (M) or glutamine (Q) (Garrett et al., 1984). BCB proteins can rapidly regulate Ca²⁺, Mg²⁺, Zn²⁺ or other ions in plants (Lin and Wu, 1994), whose functions include reactive reaction (Gysel et al., 1993) and/or lignification of cell wall (Drew and Gatehouse, 1994). The expression of BCB gene was enhanced by UV-light (John et al., 2001), ozone (Miller et al., 1999), aluminum (Richards et al., 1998), wounding (Kim et al., 1994) or other abiotic stresses. It was also reported that the expression of BCB gene was up-regulated by pathogens (Luo et al., 2002; Jansen et al., 2005).

A blue copper-binding protein gene (*DvBCB*) from *D. villosum* was cloned and its expression pattern was revealed for the first time in this study. The results shed light on the resistance mechanism of *D. villosum* to *E. graminis*.

MATERIALS AND METHODS

Growth and inoculation condition

Wild type *D. villosum* resistant Gh21 line and its susceptible mutant M14S line induced by EMS were grown separately without pathogens at 20°C for 14 days. The seedlings at two-leaf stage were inoculated with *E. graminis*. The temperature and humidity were kept in order to induce spores to germinate. The leaves were harvested and their surface was cleaned using sterile water. Total RNA was extracted by TRIZOL reagent (Invitrogen, USA). Poly (A)⁺ RNA was purified by PolyATtract® mRNA Isolation Systems

*Corresponding author. E-mail: hghe@ujs.edu.cn.

Abbreviations: SSH, Suppression subtractive hybridization; BCB, blue copper-binding protein; ORF, open reading frame; ROS, reactive oxygen species.
Suppression subtractive hybridization

Samples of total RNA of resistant Gh21 line inoculated by E. graminis at 15, 18 and 21 h were mixed with equal amounts and used to extract mRNA as tester, and mRNA of susceptible M14S line as driver. SSH procedures were performed according to the manual of PCR-Select™ cDNA Subtraction kit (Clontech, USA). Purified PCR products were cloned into pGEM-T easy vector (Promega, USA). PCR products of positive clones were denatured using NaOH solution and transferred onto the Hybond-N+ nylon membrane (Amersham, UK). Forward and reverse SSH products were labeled by $\alpha$-32P-dCTP and used to screen the differentially expressed clones according to the manual of PCR-Select Differential Screening kit (Clontech, USA).

Screening of cDNA library

The cDNA library from the leaves of D. villosum infected by E. graminis was constructed according to the manual of Superscript cDNA synthesis kit (Invitrogen, USA). A differentially expressed EST145 and a homolog of blue copper-binding protein gene, was used as probe labeled by $\alpha$-32P-dCTP to screen this cDNA library. The method was southern blot (Sambrook et al., 1989).

Sequence analysis

DNA sequencing of the positive clone was finished by Bioasia Biotechnological Company Ltd (Shanghai, China). Analysis of homology and open reading frame (ORF) were respectively based on BLAST program and ORF Finder program in GenBank. Multiple alignment analysis was performed by clustalW program and the result was visualized by BOXSHADE 3.21 software. Phylogenetic tree was constructed using neighbor-joining method by MEGA3.1 software.

Northern blot analysis

The resistant Gh21 line and its susceptible mutant M14S line were inoculated at 0, 6, 12, 24, 48 and 72 h, respectively. Total RNA was extracted by TRIZOL reagent and detected by agarose gel electrophoresis and UV-spectrophotometer at the wavelength of 260 and 280 nm. 15 µg of the total RNA in each lane was separated by electrophoresis on 1.0% formaldehyde agarose gel and blotted on Hybond-N+ nylon membrane. The full-length DvBCB cDNA was labeled by $\alpha$-32P-dCTP using random primer method. Northern blot was performed at 42°C and the details were according to Sambrook et al. (1989).

RESULTS

Cloning and sequence analysis of DvBCB gene

In order to clone defense-related genes to powdery mildew in D. villosum, a suppression subtractive hybridization library was constructed from the leaves infected by E. graminis and 218 differentially expressed DNA fragments were screened between the resistant Gh21 line and its susceptible mutant M14S line. EST145, 255 bp in length, was a homolog of blue copper-binding protein gene. EST145 was employed as probe to screen a cDNA library from the leaves of D. villosum infected by E. graminis and a positive cDNA clone was obtained.

The full-length cDNA, designated as DvBCB (accession number: EU070903), was 845 bp in length with an ORF which encoded a 178-amino acid polypeptide (Figure 1). The molecular weight of this deduced DvBCB protein was about 17.6 kDa and the pl was about 5.05. DvBCB protein contained a 25-amino acid signal peptide in the N-terminal and a 24-amino acid transmembrane region in the C-terminal. According to Garrett et al. (1984), this DvBCB protein also contained the possible copper-binding sites which were H$_66$, C$_{107}$, H$_{112}$ and M$_{121}$.

Blast analysis showed that the deduced BCB protein of D. villosum and the ones of wheat, barley, rice and Arabidopsis thaliana had 75, 66, 58 and 45% identity, respectively (Figure 2). Phylogenetic analysis of DvBCB and other plant BCB proteins indicated that DvBCB protein might share the same origin with the ones of wheat, barley and rice which belongs to grass (Figure 3).

Northern blot analysis of DvBCB gene

Northern blot analysis showed that DvBCB gene was constitutively expressed and greatly induced by E. graminis in resistant Gh21 line and its susceptible mutant M14S line (Figure 4). In Gh21 line, the expression of DvBCB gene reached a peak level at 24 h after inoculation and decreased to constitutive level at 72 h. In M14S line, the level was a little lower than that in Gh21 line at all stages after inoculation and the peak could not appear.

DISCUSSION

Cell wall is the first physical block when pathogens invade plant hosts. Lignification can fortify cell wall and increase the resistance to pathogens in plants (Moerschbacher et al., 1990). It was reported that the blue copper-binding protein of pea is correlated with lignin deposition in pod endocarp (Drew and Gatehouse, 1994). Under aluminium stress, AtBCB protein of A. thaliana was localized to cell membrane region by transient expression in onion epidermal cells. In transgenic A. thaliana, in which AtBCB gene was over-expressed, lignin production was constitutive in the whole roots and could be increased by aluminium stress in the root-tip region (Ezaki et al., 2005). In this research, the deduced BCB protein of D. villosum contained a transmembrane domain. So we proposed that DvBCB protein might be localized to cell membrane and be correlated with lignin deposition in the invaded epidermal cells of D. villosum. Reactive oxygen species (ROS) play crucial dual roles during defense against pathogens in plants.
Figure 1. The nucleotide sequence of BCB gene and its deduced amino acid sequence. Each amino acid is below its correspondent codon. The asterisk represents the stop codon. The predicted signal peptide is underlined and the transmembrane region is boxed. The four amino acid residues shade form the possible copper-binding site.

(Vandenabeele et al., 2000). On one hand, ROS can trigger hypersensitive response at the local site invaded by pathogens and induce systemic acquired resistance in the whole plant. On the other hand, the accumulation of ROS can harm the host cells. So, plants have developed a series of enzymes as ROS-scavengers for defense against ROS stress. According to the conserved domain, Gysel et al. (1993) identified a blue copper-binding protein (AtBCB) of A. thaliana as a cupredoxin-like protein which could catalyze oxygenic Cu$^{2+}$ to reactive Cu$^+$, and proposed that AtBCB gene might be involved in electron transfer reactions in the cell membrane region. Ezaki et al. (2005) found that the concentration of lipid peroxides was rather low at the site of lignin accumulation which was considered to be related to BCB protein. It is also considered that oxidative burst appears at early stage after inoculation (Lamb and Dixon, 1997). In our research, the expression of DvBCB gene was rapidly induced and reached the peak level at 24 h after inoculation. This result indicated that the expression...
pattern of DvBCB gene in resistant Gh21 line was in accordance with the accumulation pattern of ROS. So, we report that DvBCB protein might be involved in the scavenging of ROS to protect host cells during defense against powdery mildew in D. villosum.

Overall, DvBCB gene from D. villosum might have multiple functions during infection by E. graminis. This study could contribute more to the understanding of the
Figure 3. Phylogenetic analysis of the deduced BCB in *D. villosum* with other plant BCBs. The accession numbers of BCBs are shown in the brackets. The DvBCB protein is marked by an asterisk.

Figure 4. Northern blot analysis of DvBCB gene. A, Northern blot results using total RNA of Gh21 and M14S; B, electrophoresis results of 18S rRNA and 28S rRNA of Gh21 and M14S. The resistant Gh21 line and its susceptible mutant M14S line were inoculated at 0, 6, 12, 24, 48 and 72 h, respectively.

resistance mechanism of *D. Villosum* to *E. graminis*.

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REFERENCES


Garrett TPJ, Clingeleffer DJ, Guss JM, Rogers SJ, Freeman HC (1984). The crystal structure of poplar apoplastocyanin at 1.8Å resolution. The geometry of the copper-binding site is created by the polypeptide. J. Biol. Chem. 259: 1822-1825.


